

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 5, 2005, 17:19:28 ; Search time 93.2556 Seconds
(without alignments)
1197.068 Million cell updates/sec
Title: US-10-063-510-6_COPY_17_234
Perfect score: 1125
Sequence: 1 TRLVQGSRLABELSIQVSC.....ETEPFVENKAAPKNEAGFG 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length	Description
1	1125	100.0	322	Q9UNF4
2	1111	98.8	322	Q8TC18
3	1106	98.3	322	Q9Y5Y7
4	719	63.9	322	Q6UC88
5	669	59.5	318	Q99NE4
6	669	59.5	318	Q8BHC0
7	520.5	46.3	201	Q7YS22
8	241	21.4	441	Q6QM56
9	226	20.1	437	Q6P8A2
10	213.5	19.0	503	CD44_RAT
11	213.5	19.0	780	Q08779
12	211.5	18.8	364	Q70509
13	211	18.8	265	Q98SR5
14	209.5	18.6	398	Q90ZL8
15	209.5	18.6	778	CD44_MOUSE
16	207	18.4	362	CD44_CRIGR
17	205	18.2	431	CD44_MESAU
18	203.5	18.1	362	Q60522_m cd44 anti
19	203	18.0	742	CD44_FAPHA
20	202	18.0	742	CD44_HUMAN
21	200.5	17.8	580	Q80X37
22	198.5	17.6	168	Q90ZL6
23	198.5	17.6	493	Q86Z27
24	197	17.5	396	Q9W6S4
25	197	17.5	719	Q9H5A5
26	196	17.4	294	Q92493
27	196	17.4	361	Q8N694
28	196	17.4	361	Q86T72
29	195	17.3	364	Q97569
30	194	17.2	351	CD44_CANFA
31	194	17.2	366	Q29423 bos taurus

32	191.5	17.0	676	Q9H5A7	Q9H5a7 homo sapien
33	191	17.0	271	Q9H5A3	Q9H5a3 homo sapien
34	191	17.0	338	Q9H5A4	Q9H5a4 homo sapien
35	191	17.0	470	Q9H5A6	Q9H5a6 homo sapien
36	183.5	16.3	359	CD44_HORSE	Q05078 equus caball
37	150	13.3	537	PGCA_PIG	Q29011 sus scrofa
38	145.5	12.9	494	Q9BGH3	Q9bgh3 sus scrofa
39	145.5	12.9	3562	PGV_CHICK	Q90953 gallus gall
40	145	12.9	277	TSG6_HUMAN	P98066 homo sapien
41	144	12.8	275	TSG6_MOUSE	O08859 mus musculus
42	143	12.7	2109	PGCA_CHICK	P07998 gallus gall
43	140	12.4	2571	SGN1_MOUSE	Q8r3y4 mus musculus
44	139.5	12.4	2333	PGCA_CANFA	Q28343 canis famil
45	139	12.4	2109	P79787	P79787 gallus gall
46	137	12.2	276	TSG6_RABIT	P98065 oryctolagus
47	133	11.8	514	Q62913	Q62913 rattus norv
48	132.5	11.8	721	Q6PID9	Q6pid9 homo sapien
49	131.5	11.7	2124	PGCA_RAT	P07897 rattus norv
50	131	11.6	2132	PGCA_MOUSE	Q61282 mus musculus
51	130.5	11.6	883	PGCB_MOUSE	Q61361 mus musculus
52	130.5	11.6	883	Q80WT7	Q80wt7 mus musculus
53	130.5	11.6	2415	PGCA_HUMAN	P16112 homo sapien
54	129	11.5	1431	SN2_RAT	Q8cFm6 rattus norv
55	128	11.4	2149	Q6XL68	Q6xl68 bos taurus
56	128	11.4	2364	PGCA_BOVIN	P13508 bos taurus
57	128	11.4	2365	Q6XL67	Q6xl67 bos taurus
58	127.5	11.3	883	PGCB_RAT	P55068 rattus norv
59	127.5	11.3	911	PGCB_HUMAN	Q96cw7 homo sapien
60	123	10.9	2570	SGN1_HUMAN	Q9ny15 homo sapien
61	122	10.8	394	PGCA_RABIT	Q28670 oryctolagus
62	121.5	10.8	360	HPL3_HUMAN	Q96886 homo sapien
63	121	10.8	516	Q8IWX2	Q8iwx2 homo sapien
64	121	10.8	1152	Q90WM2	Q90wm2 xenopus lae
65	120.5	10.7	912	PGCB_BOVIN	Q28062 bos taurus
66	120.5	10.7	1570	Q75Z13	Q75zi3 brachydanio
67	120.5	10.7	2559	SN2_MOUSE	Q8riu0 mus musculus
68	119	10.6	359	Q7ZX17	Q7zx17 xenopus lae
69	118.5	10.5	3396	PGCV_HUMAN	P13611 homo sapien
70	116	10.3	368	Q8BS97	Q8bs97 mus musculus
71	116	10.3	2738	PGCV_RAT	Q9erb4 rattus norv
72	116	10.3	3358	PGCV_MOUSE	Q62059 mus musculus
73	115	10.2	370	Q7M2W7	Q7m2w7 sus scrofa
74	115	10.2	394	Q6DCI6	Q6dc16 xenopus lae
75	115	10.2	3381	PGCV_BOVIN	P81282 bos taurus
76	113.5	10.1	341	HPL2_MOUSE	Q9esm3 mus musculus
77	112.5	10.0	340	HPL2_HUMAN	Q9gvv7 homo sapien
78	112.5	10.0	417	PGCB_FELCA	P41725 felis silve
79	112	10.0	210	Q8C9U7	Q8c9u7 mus musculus
80	112	10.0	2551	SN2_HUMAN	Q8cwq8 h stabilin
81	111	9.9	354	Q86W61	Q86w61 homo sapien
82	110	9.8	363	Q6NV41	Q6nv41 brachydanio
83	110	9.8	1290	Q9W6E1	Q9w6e1 gallus gall
84	109.5	9.7	1257	PGCN_RAT	P55067 rattus norv
85	109	9.7	1321	PGCN_HUMAN	O14594 homo sapien
86	108.5	9.6	341	HPL2_RAT	Q9esm2 rattus norv
87	108	9.6	354	HPL1_HUMAN	P10915 homo sapien
88	108	9.6	359	HPL3_MOUSE	Q80wm5 mus musculus
89	107	9.5	354	HPL1_RAT	P03994 rattus norv
90	107	9.5	355	HPL1_CHICK	P07354 gallus gall
91	107	9.5	356	HPL1_MOUSE	Q9qup5 mus musculus
92	107	9.5	862	Q9UF98	Q9uf98 homo sapien
93	107	9.5	1268	PGCN_MOUSE	P55066 mus musculus
94	107	9.5	1268	Q6P1E3	Q6pie3 mus musculus
95	106.5	9.5	816	Q70474	Q70474 rattus norv
96	105	9.3	354	HPL1_BOVIN	P55252 bos taurus
97	104.5	9.3	862	PGCV_MACNE	Q28858 macaca neme
98	104	9.2	139	Q95370	Q95370 homo sapien
99	104	9.2	354	HPL1_HORSE	Q28381 equus caball
100	104	9.2	354	HPL1_PIG	P10859 sus scrofa
101	103	9.2	80	Q86UZ1	Q86uz1 homo sapien
102	102	9.1	739	Q02360	Q02360 caenorhabdi
103	101.5	9.0	380	Q02343	Q02343 caenorhabdi
104	101.5	9.0	411	Q702X4	Q702x4 human herpe

105	101.5	9.0	1853	2	Q7KT96	Q7kt96 drosophila	178	88	7.8	1051	2	Q6CLJ9	Q6clj9 yarrowia li
106	101.5	9.0	1893	2	Q9NKC9	Q9nkc9 drosophila	179	88	7.8	1254	2	Q94185	Q94185 caenorhabdi
107	101.5	9.0	2008	2	Q18175	Q18175 caenorhabdi	180	87.5	7.8	555	2	Q9U6R7	Q9u6r7 dermatophag
108	101	9.0	2535	2	Q755B8	Q755b8 ashbya goes	181	87.5	7.8	653	2	Q8NK55	Q8nk55 candida alb
109	100.5	8.9	402	1	HPL4_HUMAN	Q8quw8 homo sapien	182	87.5	7.8	987	1	VGNM_APMV	P38485 andean taura
110	100.5	8.9	665	2	Q7Q4E5	Q7q4e5 anopheles g	183	87.5	7.8	1085	1	CASR_BOVIN	P35384 bos taurus
111	99.5	8.8	397	2	Q702X3	Q702x3 human herpe	184	87.5	7.8	9234	2	Q7KTES	Q7kt95 drosophila
112	98.5	8.8	573	2	Q8CJD9	Q8cjd9 rattus norv	185	87	7.7	235	2	Q63349	Q63349 rattus norv
113	98	8.7	2112	2	Q9VEL9	Q9vel9 drosophila	186	87	7.7	264	2	Q80X85	Q80x85 mus musculu
114	97.5	8.7	260	2	Q7PR65	Q7pr65 anopheles g	187	87	7.7	391	2	Q753G3	Q753g3 ashbya goes
115	97	8.6	390	1	VGL1_HRV11	P06487 human herpe	188	87	7.7	661	2	O13444	O13444 cladosporiu
116	97	8.6	390	2	Q702X7	Q702x7 human herpe	189	87	7.7	673	2	Q7QJB6	Q7qjb6 anopheles g
117	96	8.5	3178	1	YS89_CAEEL	Q09624 caenorhabdi	190	87	7.7	701	2	Q8ZMG4	Q8zmg4 pyrobaculum
118	95.5	8.5	481	2	Q9XUF4	Q9xuf4 caenorhabdi	191	87	7.7	721	2	Q97UG7	Q97ug7 sulfolobus
119	95	8.4	424	2	Q8FGW0	Q8fgw0 arabidopsis	192	87	7.7	722	2	O59644	O59644 sulfolobus
120	94.5	8.4	182	2	Q810D8	Q810d8 drosophila	193	87	7.7	1506	2	P79927	P79927 xenopus lae
121	94.5	8.4	183	2	Q9VT37	Q9vt37 drosophila	194	86.5	7.7	260	2	Q7PYX0	Q7pyx0 anopheles g
122	94.5	8.4	519	2	Q7YTR7	Q7ytr7 caenorhabdi	195	86.5	7.7	400	1	MUAI_XENLA	P10667 xenopus lae
123	94.5	8.4	1079	2	Q9N4S7	Q9n4s7 caenorhabdi	196	86.5	7.7	768	2	O60279	O60279 homo sapien
124	94.5	8.4	1795	2	Q76894	Q76894 drosophila	197	86.5	7.7	838	2	Q7UNP4	Q7unp4 rhodopirell
125	93.5	8.3	397	2	Q702X6	Q702x6 human herpe	198	86.5	7.7	941	2	Q9LTH0	Q9lth0 arabidopsis
126	93	8.3	405	2	Q66H22	Q66h22 brachydanio	199	86.5	7.7	965	2	Q22286	Q22286 caenorhabdi
127	93	8.3	478	2	Q7YX15	Q7yx15 caenorhabdi	200	86.5	7.7	980	2	Q84FU6	Q84fu6 chlamydia t
128	93	8.3	916	2	Q7YZI0	Q7yzi0 monosiga br	201	86.5	7.7	980	2	Q84FU8	Q84fu8 chlamydia t
129	92.5	8.2	247	2	Q8MKY7	Q8mky7 drosophila	202	86.5	7.7	981	2	Q84FU7	Q84fu7 chlamydia t
130	92.5	8.2	248	2	Q9NED0	Q9ned0 leishmania	203	86	7.6	477	2	Q86YCS	Q86yc5 homo sapien
131	92.5	8.2	400	1	HPL4_MOUSE	Q80wm4 mus musculu	204	85.5	7.6	178	2	Q8FQU3	Q8fqu3 corynebacte
132	92	8.2	347	2	Q8SYW5	Q8syw5 drosophila	205	85.5	7.6	510	2	Q6SCJ8	Q6scj8 aspergillus
133	92	8.2	500	2	Q864U4	Q864u4 bos taurus	206	85.5	7.6	616	2	Q8R0X0	Q8r0x0 mus musculu
134	92	8.2	846	2	O01699	O01699 caenorhabdi	207	85.5	7.6	656	2	Q8BUE7	Q8bue7 mus musculu
135	92	8.2	989	2	Q83U76	Q83u76 chlamydia t	208	85.5	7.6	734	2	Q7S939	Q7s939 neurospora
136	92	8.2	989	2	Q84FU9	Q84fu9 chlamydia t	209	85.5	7.6	786	2	Q21027	Q21027 caenorhabdi
137	92	8.2	1121	2	Q72884	Q72884 candida alb	210	85.5	7.6	841	2	Q6R8J4	Q6r8j4 brachydanio
138	91.5	8.1	288	2	Q6QPC9	Q6qpc9 simian aden	211	85.5	7.6	895	2	O80973	O80973 arabidopsis
139	91.5	8.1	860	2	Q7RZN3	Q7rzn3 neurospora	212	85.5	7.6	935	2	Q6R8J3	Q6r8j3 brachydanio
140	91.5	8.1	1126	2	Q9VGK5	Q9vgk5 drosophila	213	85.5	7.6	951	2	Q9FVX8	Q9fvx8 oryza sativ
141	91	8.1	174	2	Q7VTP1	Q7vtp1 caenorhabdi	214	85.5	7.6	977	2	Q6R8J2	Q6r8j2 brachydanio
142	91	8.1	488	2	Q05586	Q05586 caenorhabdi	215	85.5	7.6	1367	1	AMYH_YEAST	P08640 saccharomyc
143	91	8.1	624	2	Q19780	Q19780 caenorhabdi	216	85.5	7.6	1367	2	Q6LCS8	Q6lcs8 saccharomyc
144	90.5	8.0	411	2	Q6P6W1	Q6p6w1 rattus norv	217	85.5	7.6	2448	2	Q8WMQ5	Q8wmq5 homo sapien
145	90.5	8.0	497	2	Q8QVC4	Q8qvc4 eyach virus	218	85.5	7.6	6995	2	Q96RK2	Q96rk2 homo sapien
146	90.5	8.0	699	2	Q8QVE9	Q8qve9 eyach virus	219	85	7.6	172	2	Q8VC95	Q8vc95 mus musculu
147	90.5	8.0	952	2	Q86AH0	Q86ah0 dictyosteli	220	85	7.6	265	2	Q9GZES	Q9gze5 caenorhabdi
148	90.5	8.0	1175	2	Q9VRL7	Q9vrl7 drosophila	221	85	7.6	319	2	Q7QJA0	Q7qja0 anopheles g
149	90.5	8.0	1376	2	Q9V5I8	Q9v5i8 drosophila	222	85	7.6	345	2	Q691Y8	Q691y8 anolis sagr
150	90	8.0	388	1	VE2_HPV27	P36789 human papil	223	85	7.6	429	2	O76430	O76430 caenorhabdi
151	90	8.0	402	1	ODP2_MYCPN	P75392 mycoplasma	224	85	7.6	449	2	Q71UN8	Q71un8 caenorhabdi
152	90	8.0	948	2	Q86AV9	Q86av9 dictyosteli	225	85	7.6	569	2	Q9KGV9	Q9kgv9 listeria mo
153	90	8.0	1167	2	Q7RWQ7	Q7rwq7 neurospora	226	85	7.6	626	2	Q9NDD1	Q9ndd1 leishmania
154	89.5	8.0	411	1	LMP2_RAT	P17046 rattus norv	227	85	7.6	627	1	PKNB_LACUA	Q9cef5 lactococcus
155	89.5	8.0	440	2	Q9P566	Q9p566 neurospora	228	85	7.6	852	2	Q6CIA5	Q6cia5 yarrowia li
156	89.5	8.0	471	2	Q9VMG7	Q9vmg7 drosophila	229	85	7.6	961	2	Q92223	Q92223 emericeella
157	89.5	8.0	1349	2	Q8WQ4	Q8wmq4 homo sapien	230	85	7.6	991	2	Q83UW2	Q83uw2 chlamydia t
158	89	7.9	307	1	SGS3_DROME	P02840 drosophila	231	85	7.6	991	2	Q84FV0	Q84fv0 chlamydia t
159	89	7.9	416	1	LMP1_HUMAN	P11279 homo sapien	232	85	7.6	991	2	Q84FV1	Q84fv1 chlamydia t
160	89	7.9	417	2	Q8WU33	Q8wu33 homo sapien	233	85	7.6	1016	1	PMFH_CHLTR	Q84880 chlamydia t
161	89	7.9	429	2	P79046	P79046 humicola gr	234	85	7.6	1049	2	Q960E6	Q960e6 drosophila
162	89	7.9	482	2	Q6BSZ9	Q6bsz9 debaryomyce	235	85	7.6	1049	2	Q9V6L1	Q9v6l1 drosophila
163	89	7.9	503	2	Q19269	Q19269 caenorhabdi	236	85	7.6	1170	2	Q95011	Q95011 caenorhabdi
164	89	7.9	603	2	Q6CE49	Q6ce49 yarrowia li	237	85	7.6	1225	2	Q9VR49	Q9vr49 drosophila
165	89	7.9	1708	2	Q7XWZ9	Q7xwz9 oryza sativ	238	85	7.6	3150	2	Q7PMD5	Q7pmd5 anopheles g
166	88.5	7.9	316	2	Q9U9J0	Q9u9j0 toxocara ca	239	84.5	7.5	220	2	Q9EQG0	Q9eqg0 mus musculu
167	88.5	7.9	582	2	Q8IR74	Q8ir74 drosophila	240	84.5	7.5	350	2	Q7Q1R0	Q7q1r0 anopheles p
168	88.5	7.9	901	2	Q9H195	Q9h195 homo sapien	241	84.5	7.5	752	2	Q9YLC6	Q9ylc61 aeropyrum p
169	88.5	7.9	1101	1	GUNC_CELFI	P14090 cellulomona	242	84.5	7.5	814	2	Q6C247	Q6c247 yarrowia li
170	88.5	7.9	1148	2	Q6CBJ2	Q6cbj2 yarrowia li	243	84.5	7.5	834	2	Q877B7	Q877b7 aspergillus
171	88.5	7.9	2273	2	Q63HU2	Q63hu2 burkholderi	244	84.5	7.5	1161	1	DAN4_YEAST	P47179 saccharomyc
172	88	7.8	103	2	Q9TTB3	Q9ttb3 sus scrofa	245	84.5	7.5	2152	2	Q8WXI7	Q8wxi7 homo sapien
173	88	7.8	382	2	Q6C971	Q6c971 yarrowia li	246	84	7.5	259	2	Q9N3B9	Q9n3b9 caenorhabdi
174	88	7.8	456	2	Q9U2W2	Q9u2w2 caenorhabdi	247	84	7.5	262	2	P74577	P74577 synechocyst
175	88	7.8	602	2	Q8YV91	Q8yv91 anabaena sp	248	84	7.5	273	2	Q61002	Q61002 mus musculu
176	88	7.8	716	2	Q9NVE4	Q9nye4 homo sapien	249	84	7.5	335	2	Q9C7W2	Q9c7w2 arabidopsis
177	88	7.8	730	2	Q86AZ8	Q86az8 dictyosteli	250	84	7.5	421	2	Q6KCA6	Q6kca6 candida dub

251	84	7.5	475	2	Q8FQJ1	Q8fgj1 corynebacte	324	82	7.3	483	2	Q9W4M2	Q9w4m2 drosophila
252	84	7.5	543	2	Q14879	Q14879 homo sapien	325	82	7.3	538	2	Q76H84	Q76h84 streptococc
253	84	7.5	641	2	Q6AJU8	Q6aju8 desulfotale	326	82	7.3	630	2	Q96YH6	Q96yh6 sulfolobus
254	84	7.5	648	2	Q95QX0	Q95qx0 caenorhabdi	327	82	7.3	644	2	Q6CF33	Q6cf33 yarrowia li
255	84	7.5	662	1	MUC1_XENLA	Q05049 xenopus lae	328	82	7.3	693	2	Q27J394	Q27j394 caenorhabdi
256	84	7.5	927	1	Q21811	Q21811 caenorhabdi	329	82	7.3	966	2	Q27J394	Q27j394 caenorhabdi
257	84	7.5	1331	1	MANP_CALISA	F22533 caldocellum	330	82	7.3	973	2	Q7CZH1	Q7czh1 agrobacteri
258	84	7.5	1362	2	Q9V294	Q9v294 pyrococcus	331	82	7.3	977	2	Q8UFQ8	Q8ufq8 agrobacteri
259	84	7.5	1370	2	Q6C3B8	Q6c3b8 yarrowia li	332	82	7.3	1099	2	Q7TUJ6	Q7tuj6 prochloroco
260	84	7.5	1779	2	Q52374	Q52374 caldicellul	333	82	7.3	1266	2	Q6CAR3	Q6car3 yarrowia li
261	84	7.5	1832	2	Q96503	Q96503 cryptospori	334	81.5	7.2	147	2	Q61043	Q61043 trypanosoma
262	83.5	7.4	216	2	Q28501	Q28501 macaca mula	335	81.5	7.2	171	1	NUOE_BUCBP	Q89au3 buchnera ap
263	83.5	7.4	279	2	Q14888	Q14888 homo sapien	336	81.5	7.2	386	2	Q97G38	Q97g38 clostridium
264	83.5	7.4	615	2	Q9M6E8	Q9m6e8 phaseolus v	337	81.5	7.2	388	2	Q7Q1W8	Q7q1w8 anopheles g
265	83.5	7.4	743	2	Q7PQ19	Q7pq19 anopheles g	338	81.5	7.2	390	2	Q6PND6	Q6pnd6 emericelella
266	83.5	7.4	788	2	Q18510	Q18510 trichoplusi	339	81.5	7.2	411	2	Q702X9	Q702x9 human herpe
267	83.5	7.4	800	2	Q8TFG4	Q8tfq4 schizosacch	340	81.5	7.2	460	2	Q18984	Q18984 cercopithec
268	83.5	7.4	807	2	Q18511	Q18511 trichoplusi	341	81.5	7.2	584	1	CEUL_CABEL	Q17802 caenorhabdi
269	83.5	7.4	892	1	LDL2_XENLA	Q99088 xenopus lae	342	81.5	7.2	612	2	Q6CD44	Q6cd44 yarrowia li
270	83.5	7.4	1286	2	Q9TXR6	Q9txr6 caenorhabdi	343	81.5	7.2	741	2	Q6CH88	Q6ch88 yarrowia li
271	83.5	7.4	5179	1	MUC2_HUMAN	Q02817 homo sapien	344	81.5	7.2	808	2	Q81123	Q81123 caenorhabdi
272	83	7.4	269	2	Q9U9J2	Q9u9j2 toxocara ca	345	81.5	7.2	846	2	Q6ZKY0	Q6zky0 oryza sativ
273	83	7.4	309	2	Q63549	Q63549 rattus norv	346	81.5	7.2	860	1	MUTS_LISIN	Q92bv3 listeria in
274	83	7.4	316	2	Q8TDP14	Q8tdl4 homo sapien	347	81.5	7.2	860	1	VG12_BPB03	Q37893 bacterioph
275	83	7.4	329	2	Q7QB72	Q7qb72 anopheles g	348	81.5	7.2	913	2	Q7NP28	Q7np28 gloebacter
276	83	7.4	337	2	Q7Z5K8	Q7z5k8 homo sapien	349	81.5	7.2	957	2	Q9UKN0	Q9ukn0 homo sapien
277	83	7.4	378	2	Q8SX58	Q8sxs5 drosophila	350	81.5	7.2	1216	1	VPX5_CAEEL	Q92777 caenorhabdi
278	83	7.4	404	2	Q702X0	Q702x0 human herpe	351	81.5	7.2	1320	2	Q96KF5	Q96kf5 homo sapien
279	83	7.4	404	2	Q702Y3	Q702y3 human herpe	352	81.5	7.2	1354	2	Q9VKA7	Q9vka7 drosophila
280	83	7.4	409	1	R23B_HUMAN	P54727 homo sapien	353	81.5	7.2	1500	2	Q6AUW2	Q6auw2 oryza sativ
281	83	7.4	419	2	Q8TDL1	Q8tdl1 homo sapien	354	81.5	7.2	1844	2	Q22579	Q22579 caenorhabdi
282	83	7.4	422	2	Q8TDL3	Q8tdl3 homo sapien	355	81.5	7.2	2338	2	Q6Z9N6	Q6z9n6 burkholderi
283	83	7.4	477	2	Q14887	Q14887 homo sapien	356	81.5	7.2	3175	1	RPOA_EAV	P19811 equine arte
284	83	7.4	485	2	Q9V8B0	Q9v8b0 drosophila	357	81	7.2	184	2	Q7PPK1	Q7ppk1 anopheles g
285	83	7.4	492	2	Q6GCG6	Q6gcg6 yarrowia li	358	81	7.2	221	1	RL1_SULAC	P35024 sulfolobus
286	83	7.4	559	2	Q9VNS36	Q9vns36 drosophila	359	81	7.2	301	2	Q9X2G0	Q92490 cratogeomys
287	83	7.4	605	1	WSC4_YEAST	P38739 saccharomyc	360	81	7.2	315	2	Q9VX11	Q9vx11 drosophila
288	83	7.4	769	2	Q17921	Q17921 caenorhabdi	361	81	7.2	345	2	Q691X0	Q691x0 anolis sagr
289	83	7.4	993	2	Q83TJ6	Q83tj6 chlamydia t	362	81	7.2	355	2	Q9NP13	Q9np13 homo sapien
290	83	7.4	1002	2	Q6CBD5	Q6cbd5 yarrowia li	363	81	7.2	403	2	Q702W8	Q702w8 human herpe
291	83	7.4	1030	2	Q7QV30	Q7qv30 giardia lam	364	81	7.2	404	2	Q702W6	Q702w6 human herpe
292	83	7.4	1066	2	Q76NW3	Q76nw3 dictyosteli	365	81	7.2	404	2	Q702Y0	Q702y0 human herpe
293	82.5	7.3	197	2	Q26878	Q26878 trypanosoma	366	81	7.2	404	2	Q702Y6	Q702y6 human herpe
294	82.5	7.3	252	2	Q6GZ06	Q6gz06 avian pneum	367	81	7.2	453	2	Q9U301	Q9u301 caenorhabdi
295	82.5	7.3	383	1	VE2_HPV57	P22155 human papil	368	81	7.2	668	2	Q6FWR2	Q6fwr2 candida gla
296	82.5	7.3	389	2	Q64BB8	Q64bb8 uncultured	369	81	7.2	746	2	Q82GM0	Q82gm0 streptomyc
297	82.5	7.3	389	2	Q6GXX0	Q6gxx0 swine hepat	370	81	7.2	782	2	Q6CNV3	Q6cnv3 kluyveromyc
298	82.5	7.3	389	2	Q6GXX2	Q6gxx2 swine hepat	371	81	7.2	967	2	Q08294	Q08294 saccharomyc
299	82.5	7.3	389	2	Q6GXX3	Q6gxx3 swine hepat	372	81	7.2	1001	2	Q05164	Q05164 saccharomyc
300	82.5	7.3	540	1	CH60_STRAP	Q8KJ20 streptococc	373	81	7.2	1128	1	BEM3_YEAST	P32873 saccharomyc
301	82.5	7.3	599	2	Q6C2K2	Q6c2k2 yarrowia li	374	81	7.2	1163	2	Q8GAR1	Q8gar1 dictyosteli
302	82.5	7.3	627	2	Q7RWT2	Q7rwt2 neurospora	375	81	7.2	1537	1	FLO1_YEAST	P32768 saccharomyc
303	82.5	7.3	635	2	Q6G065	Q6g065 fibrobacter	376	81	7.2	1569	2	Q6W4X9	Q6w4x9 homo sapien
304	82.5	7.3	726	1	NF11_YEAST	Q12216 saccharomyc	377	81	7.2	1609	1	FIG2_YEAST	P25653 saccharomyc
305	82.5	7.3	825	2	Q03088	Q03088 saccharomyc	378	81	7.2	1713	2	Q8TGE1	Q8tge1 saccharomyc
306	82.5	7.3	843	2	Q9VYH8	Q9vyh8 drosophila	379	81	7.2	2282	1	ZAN_RABIT	P57999 oryctolagus
307	82.5	7.3	876	2	Q6XLI5	Q6xli5 brachydanio	380	81	7.2	2977	2	Q9VAP9	Q9vap9 drosophila
308	82.5	7.3	1206	1	FM14_MOUSE	Q05859 mus musculu	381	80.5	7.2	148	1	SV02_RAT	P14844 rattus norv
309	82.5	7.3	1261	2	Q7R2F4	Q7r2f4 giardia lam	382	80.5	7.2	165	2	Q66877	Q26877 trypanosoma
310	82.5	7.3	1371	2	Q9VU22	Q9vu22 drosophila	383	80.5	7.2	242	2	Q66R88	Q66r88 caenorhabdi
311	82.5	7.3	1468	1	FMN1_MOUSE	Q05860 mus musculu	384	80.5	7.2	334	2	Q66VAV6	Q6vav6 anopheles g
312	82.5	7.3	1472	2	Q6V9R4	Q6v9r4 strongyloce	385	80.5	7.2	391	1	VE2_HPV2A	P25482 human papil
313	82.5	7.3	1478	1	LHN2_BOVIN	Q97817 bos taurus	386	80.5	7.2	410	1	LMP2_CRIGR	P49130 cricetus
314	82.5	7.3	1851	2	Q9ESP3	Q9esp3 rattus norv	387	80.5	7.2	441	2	Q9U2W3	Q9u2w3 caenorhabdi
315	82	7.3	236	2	Q9LMO0	Q9lmo0 pinus taeda	388	80.5	7.2	540	1	CH60_STRAS	Q8cx22 streptococc
316	82	7.3	318	2	Q86HN3	Q86hn3 dictyosteli	389	80.5	7.2	540	1	CH60_STRAS	Q8cx22 streptococc
317	82	7.3	339	2	Q9VUX8	Q9vux8 drosophila	390	80.5	7.2	659	2	Q86AI8	Q86ai8 dictyosteli
318	82	7.3	345	2	Q690W2	Q690w2 anolis sagr	391	80.5	7.2	747	2	Q7S8F0	Q7s8f0 neurospora
319	82	7.3	346	2	Q7S973	Q7s973 neurospora	392	80.5	7.2	758	2	Q8TZI4	Q8tzi4 caenorhabdi
320	82	7.3	374	2	Q9Z209	Q9z209 cricetus	393	80.5	7.2	765	2	Q75I27	Q75i27 oryza sativ
321	82	7.3	389	2	Q76573	Q76573 caenorhabdi	394	80.5	7.2	860	2	Q71ZR7	Q71zr7 listeria mo
322	82	7.3	463	2	Q42665	Q42665 schizosacch	395	80.5	7.2	896	2	Q20253	Q20253 caenorhabdi
323	82	7.3	477	1	MYPH_HUMAN	Q13203 homo sapien	396	80.5	7.2	971	2	Q6W3C4	Q6w3c4 caenorhabdi

397	80.5	7.2	989	2	Q19930	Q19930 caenorhabdi	470	79	7.0	213	2	Q6ZU27	Q6ZU27 homo sapien
398	80.5	7.2	1184	2	Q6F3A8	Q6f3a8 oryza sativ	471	79	7.0	249	2	Q6BVX5	Q6bvxs5 debaryomyce
399	80.5	7.2	1300	2	Q6BZP6	Q6bzp6 yarrowia li	472	79	7.0	249	2	Q8BJQ4	Q8bjq4 arabidopsis
400	80.5	7.2	1372	2	Q8SX99	Q8sx99 drosophila	473	79	7.0	261	2	Q70CC2	Q70cc2 eimeria ten
401	80.5	7.2	1372	2	Q9VNV46	Q9vn46 drosophila	474	79	7.0	308	2	Q74KF4	Q74kf4 lactobacill
402	80.5	7.2	2225	2	Q45881	Q45881 caenorhabdi	475	79	7.0	333	2	Q6VAV8	Q6vav8 anopheles g
403	80.5	7.2	3295	2	Q66GT3	Q66gt3 rattus norv	476	79	7.0	345	2	Q691T8	Q691t8 anolis sagr
404	80	7.1	103	2	Q64380	Q64380 oryctolagus	477	79	7.0	352	2	Q49782	Q49782 arabidopsis
405	80	7.1	272	2	Q6ZSN5	Q6zsn5 homo sapien	478	79	7.0	353	2	Q8VPM3	Q8vpm3 micrococcus
406	80	7.1	291	2	Q6QFG5	Q6qpg5 simian aden	479	79	7.0	359	2	Q9XZT0	Q9xzt0 drosophila
407	80	7.1	334	2	Q6VAM0	Q6vaw0 anopheles g	480	79	7.0	390	2	Q702W4	Q702w4 human herpe
408	80	7.1	349	2	Q7XEC9	Q7xec9 oryza sativ	481	79	7.0	390	2	Q702W9	Q702w9 human herpe
409	80	7.1	390	2	Q7XET5	Q7xets5 phlebia rad	482	79	7.0	410	1	LMP2_HUMAN	P13473 homo sapien
410	80	7.1	390	2	Q70LM3	Q70lm3 phlebia rad	483	79	7.0	411	2	Q6Q3G8	Q6q3g8 homo sapien
411	80	7.1	410	2	Q9UD93	Q9ud93 homo sapien	484	79	7.0	446	2	Q9U137	Q9u137 leishmania
412	80	7.1	429	2	Q95Y50	Q95y50 caenorhabdi	485	79	7.0	447	2	Q8BIY6	Q8biy6 mus musculu
413	80	7.1	449	2	Q9VKS4	Q9vks4 drosophila	486	79	7.0	486	2	Q8FRY2	Q8fry2 corynebacte
414	80	7.1	569	2	Q71X10	Q71x10 listeria mo	487	79	7.0	489	2	Q95Q80	Q95q80 caenorhabdi
415	80	7.1	657	2	Q6AM00	Q6am00 desulfotale	488	79	7.0	503	2	Q95Q82	Q95q82 caenorhabdi
416	80	7.1	725	1	AGAL_YEAST	P32323 sacharomyc	489	79	7.0	503	2	Q9VCF0	Q9vcf0 mus musculu
417	80	7.1	729	2	Q8QWY2	Q8ow2 mus musculu	490	79	7.0	534	2	Q86AL2	Q86al2 dictyosteli
418	80	7.1	732	2	Q8QWY1	Q8ow1 mus musculu	491	79	7.0	555	2	Q9VH46	Q9vh46 drosophila
419	80	7.1	747	2	Q8CCZ1	Q8ccz1 mus musculu	492	79	7.0	575	2	Q6Z223	Q6z223 caenorhabdi
420	80	7.1	881	1	PRY3_YEAST	P47033 sacharomyc	493	79	7.0	594	2	Q6PAN1	Q6pan1 mus musculu
421	80	7.1	1082	1	YK02_SCHPO	Q9hdy9 schizosacch	494	79	7.0	601	2	Q6V6S1	Q6v6s1 drosophila
422	80	7.1	1168	2	Q9VZ8	Q9vze8 drosophila	495	79	7.0	601	2	Q8V6S2	Q8v6s2 drosophila
423	80	7.1	1324	2	Q8MMQ2	Q8mmq2 dictyosteli	496	79	7.0	629	2	Q8KDU5	Q8kdu5 synechococc
424	80	7.1	1325	2	Q9BKV7	Q9bkv7 leishmania	497	79	7.0	629	2	Q24017	Q24017 drosophila
425	80	7.1	4262	2	Q685J2	Q685j2 homo sapien	498	79	7.0	629	2	Q9V3H7	Q9v3h7 drosophila
426	80	7.1	4493	2	Q685J3	Q685j3 homo sapien	499	79	7.0	669	2	Q7EZY9	Q7ezy9 oryza sativ
427	79.5	7.1	129	2	Q6UNH4	Q6unh4 ictalurus p	500	79	7.0	729	2	Q8BW38	Q8bw38 mus musculu
428	79.5	7.1	161	2	Q6IGP4	Q6igp4 drosophila	501	79	7.0	785	2	Q7QO15	Q7qo15 giardia lam
429	79.5	7.1	272	2	Q8A3G1	Q8a3g1 bacteroides	502	79	7.0	893	2	Q9LHT1	Q9lht1 arabidopsis
430	79.5	7.1	273	2	Q6QK85	Q6jqk85 neodiprion	503	79	7.0	919	2	Q76EQ4	Q76eq4 streptococc
431	79.5	7.1	333	2	Q6VAV7	Q6vav7 anopheles g	504	79	7.0	980	2	Q9MA13	Q9ma13 arabidopsis
432	79.5	7.1	354	2	Q25402	Q25402 litomosoid	505	79	7.0	1031	2	Q925N8	Q925n8 mus musculu
433	79.5	7.1	363	2	Q91YK8	Q91yk8 mus musculu	506	79	7.0	1031	2	Q9D071	Q9d071 m mus muscu
434	79.5	7.1	373	2	Q76810	Q76810 anopheles g	507	79	7.0	1048	2	Q9LAU3	Q9lau3 legionella
435	79.5	7.1	403	2	Q8MVA9	Q8mva9 ixodes scap	508	79	7.0	1142	2	Q8CCL7	Q8ccl7 yarrowia li
436	79.5	7.1	433	2	Q88VC0	Q88vc0 lactobacill	509	79	7.0	1689	2	Q8QZF4	Q8qzf4 crimean-con
437	79.5	7.1	461	2	Q6C2X8	Q6c2x8 yarrowia li	510	79	7.0	1689	2	Q8QZF5	Q8qzf5 crimean-con
438	79.5	7.1	462	2	Q8TUE0	Q8tue0 methanosarc	511	79	7.0	1689	2	Q991H9	Q991h9 crimean-con
439	79.5	7.1	463	2	Q7RNE3	Q7rne3 plasmodium	512	79	7.0	1752	2	Q9AE52	Q9ae52 ruminococcu
440	79.5	7.1	495	2	Q9CV82	Q9cv82 mus musculu	513	79	7.0	2616	1	NOL_DROME	P98159 drosophila
441	79.5	7.1	497	2	Q8QVC5	Q8qvc5 eyach virus	514	79	7.0	3550	2	Q86GT4	Q86gt4 rattus norv
442	79.5	7.1	511	2	Q8UYA8	Q8uya8 human herpe	515	78.5	7.0	94	2	Q61030	Q61030 trypanosoma
443	79.5	7.1	511	2	Q8UZ60	Q8uz60 human herpe	516	78.5	7.0	142	2	Q26943	Q26943 trypanosoma
444	79.5	7.1	511	2	Q8UZ61	Q8uz61 human herpe	517	78.5	7.0	161	2	Q6CPZ3	Q6cpz3 kluveromyc
445	79.5	7.1	511	2	Q8UZ64	Q8uz64 human herpe	518	78.5	7.0	164	2	Q14851	Q14851 homo sapien
446	79.5	7.1	511	2	Q8UZ66	Q8uz66 human herpe	519	78.5	7.0	224	2	Q8KKT9	Q8kkt9 rhizobium e
447	79.5	7.1	511	2	Q8UZ67	Q8uz67 human herpe	520	78.5	7.0	231	2	Q8EZM6	Q8ezm6 leptospira
448	79.5	7.1	689	2	Q7QN60	Q7qn60 anopheles g	521	78.5	7.0	232	2	Q27423	Q27423 drosophila
449	79.5	7.1	796	2	Q8MRG9	Q8mr99 drosophila	522	78.5	7.0	252	2	Q80G93	Q80g93 avian pneum
450	79.5	7.1	796	2	Q9VTR4	Q9vtr4 drosophila	523	78.5	7.0	258	2	Q6TV72	Q6tv72 bovine papu
451	79.5	7.1	860	1	MUTS_L1SMO	Q8y789 listeria mo	524	78.5	7.0	262	2	Q9JMF0	Q9jmf0 mus musculu
452	79.5	7.1	873	2	Q9W458	Q9w458 drosophila	525	78.5	7.0	271	2	Q71DD6	Q71dd6 drosophila
453	79.5	7.1	873	2	Q9Y076	Q9y076 leishmania	526	78.5	7.0	283	2	Q6CIR8	Q6cir8 kluveromyc
454	79.5	7.1	887	2	Q6XD56	Q6xd56 gallus gall	527	78.5	7.0	285	2	Q86H76	Q86h76 dictyosteli
455	79.5	7.1	985	2	Q67643	Q67643 gallid herp	528	78.5	7.0	294	2	Q99322	Q99322 homo sapien
456	79.5	7.1	1203	2	Q6ZQ56	Q6zq56 mus musculu	529	78.5	7.0	322	2	Q62605	Q62605 rattus norv
457	79.5	7.1	1237	2	Q7WYN2	Q7wyn2 acetivibrio	530	78.5	7.0	334	2	Q6VAV5	Q6vav5 anopheles g
458	79.5	7.1	1441	2	Q8S628	Q8s628 oryza sativ	531	78.5	7.0	334	2	Q6VAV9	Q6vav9 anopheles g
459	79.5	7.1	1441	2	Q8GU94	Q8gu94 oryza sativ	532	78.5	7.0	338	2	Q95Y19	Q95y19 caenorhabdi
460	79.5	7.1	1459	1	LHN2_HUMAN	Q95490 homo sapien	533	78.5	7.0	402	2	Q9N503	Q9n503 caenorhabdi
461	79.5	7.1	1486	2	Q95RE5	Q95re5 drosophila	534	78.5	7.0	410	1	GC5B_MOUSE	Q92320 mus musculu
462	79.5	7.1	1486	2	Q967Y2	Q967y2 drosophila	535	78.5	7.0	430	2	Q9N4F8	Q9n4f8 caenorhabdi
463	79.5	7.1	1486	2	Q7KRP7	Q7krp7 drosophila	536	78.5	7.0	525	2	Q6CAQ5	Q6caq5 yarrowia li
464	79.5	7.1	1582	2	Q7KRP6	Q7krp6 drosophila	537	78.5	7.0	540	1	CH60_STRAG	Q6caq5 yarrowia li
465	79.5	7.1	1707	2	Q6PWR4	Q6pmr4 swine hepat	538	78.5	7.0	562	1	NUPL_HUMAN	Q9ame7 streptococc
466	79.5	7.1	1806	2	Q6B5R4	Q6b5r4 dictyosteli	539	78.5	7.0	581	2	Q7R0Z5	Q7roz5 giardia lam
467	79.5	7.1	5703	1	MUSB_HUMAN	Q9hc84 homo sapien	540	78.5	7.0	589	2	Q43419	Q43419 homo sapien
468	79	7.0	195	2	Q9W4V3	Q9w4v3 drosophila	541	78.5	7.0	627	2	Q8MP19	Q8mp19 dictyosteli
469	79	7.0	202	2	Q7XLD8	Q7xld8 oryza sativ	542	78.5	7.0	647	2	Q7RY11	Q7ry11 neurospora

543	78.5	7.0	657	2	Q86ID0	Q86id0 dictyosteli	616	77.5	6.9	1212	2	O42347	O42347 gallus gall
544	78.5	7.0	763	2	Q965Y7	Q965y7 caenorhabdi	617	77.5	6.9	1383	2	Q874K9	Q874k9 candida alb
545	78.5	7.0	830	2	Q6CAY0	Q6cay0 yarrowia li	618	77.5	6.9	1845	2	Q86JH8	Q86jh8 dictyosteli
546	78.5	7.0	858	2	Q9H8D9	Q9h8d9 homo sapien	619	77.5	6.9	1873	2	Q6S003	Q6s003 dictyosteli
547	78.5	7.0	1236	2	Q9C105	Q9c105 schizosacch	620	77.5	6.9	1878	2	Q6CP24	Q6cp24 kluyveromyc
548	78.5	7.0	1241	2	Q75JC0	Q75jc0 dictyosteli	621	77.5	6.9	2761	2	Q19522	Q19522 caenorhabdi
549	78.5	7.0	1487	1	LNH2_RAT	LNH2r23 rattus norv	622	77.5	6.9	4630	2	Q7UWM5	Q7uwm5 rhodopirell
550	78.5	7.0	1740	2	Q8ML25	Q8ml25 rattus norv	623	77.5	6.9	4630	2	Q77AU9	Q77au9 lymphocytic
551	78.5	7.0	1983	2	Q9N7Y6	Q9n7y6 drosophila	624	77.5	6.9	187	2	Q77AV0	Q77av0 lymphocytic
552	78.5	7.0	2378	2	Q7N7Y6	Q7n7y6 photorhabdu	625	77.5	6.9	187	2	Q9YJ85	Q9yj85 lymphocytic
553	78.5	7.0	5374	2	Q99ND0	Q99nd0 mus musculu	626	77.5	6.9	187	2	Q9YPM0	Q9ypm0 lymphocytic
554	78.5	7.0	119	2	Q61034	Q61034 trypanosoma	627	77.5	6.9	213	2	Q6M9S9	Q6m9s9 neurospora
555	78.5	7.0	248	2	Q6CFU5	Q6cfu5 yarrowia li	628	77.5	6.9	262	2	Q7PRM2	Q7prm2 anopheles g
556	78.5	7.0	293	2	P74526	P74526 synechocycat	629	77.5	6.9	340	2	Q8ZKQ1	Q8zkg1 salmonella
557	78.5	7.0	452	2	Q9CCE9	Q9cce9 mycobacteri	630	77.5	6.9	341	2	Q8IMS9	Q8ime9 drosophila
558	78.5	7.0	334	2	Q6VAV4	Q6vav4 anopheles g	631	77.5	6.9	345	2	Q6S0T8	Q6sot8 anolis sagr
559	78.5	7.0	338	2	Q7WZ11	Q7wz11 bacillus th	632	77.5	6.9	345	2	Q6S0U2	Q6s0u2 anolis sagr
560	78.5	7.0	345	2	Q6S0V2	Q6s0v2 anolis sagr	633	77.5	6.9	345	2	Q6S0U5	Q6s0u5 anolis sagr
561	78.5	7.0	345	2	Q6S0V6	Q6s0v6 anolis sagr	634	77.5	6.9	345	2	Q6S0U6	Q6s0u6 anolis sagr
562	78.5	7.0	345	2	Q6S0V7	Q6s0v7 anolis sagr	635	77.5	6.9	345	2	Q6S0U8	Q6s0u8 anolis sagr
563	78.5	7.0	345	2	Q6S0X3	Q6s0x3 anolis sagr	636	77.5	6.9	345	2	Q6S0V1	Q6s0v1 anolis sagr
564	78.5	7.0	345	2	Q6S2A4	Q6s2a4 anolis sagr	637	77.5	6.9	345	2	Q6S0W8	Q6s0w8 anolis sagr
565	78.5	7.0	345	2	Q6S2C2	Q6s2c2 anolis quad	638	77.5	6.9	345	2	Q6S0X6	Q6s0x6 anolis sagr
566	78.5	7.0	345	2	Q7TFJ3	Q7tfj3 rheus cyco	639	77.5	6.9	345	2	Q6S0X8	Q6s0x8 anolis sagr
567	78.5	7.0	379	2	Q42763	Q42763 gossypium h	640	77.5	6.9	345	2	Q6S1U6	Q6s1u6 anolis sagr
568	78.5	7.0	400	2	Q9SQF7	Q9sqf7 brassica ju	641	77.5	6.9	345	2	Q6S1Y0	Q6s1y0 anolis sagr
569	78.5	7.0	405	2	Q9SXXV0	Q9sxxv0 caenorhabdi	642	77.5	6.9	345	2	Q6S1Y1	Q6s1y1 anolis sagr
570	78.5	7.0	434	2	Q9SKN2	Q9skn2 arabidopsis	643	77.5	6.9	345	2	Q6S1Y6	Q6s1y6 anolis sagr
571	78.5	7.0	453	2	Q870S8	Q870s8 neurospora	644	77.5	6.9	345	2	Q6S1Z2	Q6s1z2 anolis sagr
572	78.5	7.0	495	2	Q74847	Q74847 human immun	645	77.5	6.9	350	2	Q9RT72	Q9rt72 deinococcus
573	78.5	7.0	513	2	Q43418	Q43418 homo sapien	646	77.5	6.9	453	1	Q7YUQ4	Q7yuyq4 trypanosoma
574	78.5	7.0	530	2	Q07701	Q07701 herpesvirus	647	77.5	6.9	549	2	Q7L8E3	Q7l8e3 homo sapien
575	78.5	7.0	573	2	Q8TOR9	Q8tor9 drosophila	648	77.5	6.9	577	2	Q6FSJ1	Q6fsj1 candida gla
576	78.5	7.0	637	1	C2AP_MOUSE	C2apm0 mus musculu	649	77.5	6.9	598	2	Q20747	Q20747 caenorhabdi
577	78.5	7.0	637	2	Q7TS55	Q7ts55 rattus norv	650	77.5	6.9	708	2	Q7R9K7	Q7r9k7 plasmodium
578	78.5	7.0	689	2	Q724Q0	Q724q0 listeria mo	651	77.5	6.9	713	2	Q9Y253	Q9y253 homo sapien
579	78.5	7.0	699	2	Q6CSM7	Q6csm7 kluyveromyc	652	77.5	6.9	717	2	Q8U1H5	Q8u1h5 pyrococcus
580	78.5	7.0	759	2	Q05143	Q05143 ruminococcu	653	77.5	6.9	750	2	Q8HFZ4	Q8hfz4 candida alb
581	78.5	7.0	823	2	Q6C159	Q6c159 yarrowia li	654	77.5	6.9	771	1	TM88_HUMAN	TM88h8 homo sapien
582	78.5	7.0	925	2	Q7XFP0	Q7xfp0 oryza sativ	655	77.5	6.9	772	2	Q82YF8	Q82yf8 streptomyce
583	78.5	7.0	1000	2	Q9SQH6	Q9sqh6 caenorhabdi	656	77.5	6.9	802	2	Q7YVP9	Q7yvp9 trypanosoma
584	78.5	7.0	1091	1	NCAL_CHICK	NCALc0 gallus gall	657	77.5	6.9	902	2	Q8Q7H5	Q8q7h5 human immun
585	78.5	7.0	1822	2	Q7ROW4	Q7row4 giardia lam	658	77.5	6.9	941	2	Q7Z5R7	Q7z5r7 homo sapien
586	78.5	7.0	1955	1	AGRN_CHICK	AGRNc0 gallus gall	659	77.5	6.9	979	2	Q8NDA4	Q8nda4 homo sapien
587	78.5	7.0	2162	2	Q70PP2	Q70pp2 drosophila	660	77.5	6.9	1092	1	NCAC_XENLA	NCACc0 yarrowia li
588	78.5	7.0	3218	2	Q9W3V6	Q9w3v6 drosophila	661	77.5	6.9	1168	2	Q7XC17	Q7xc17 oryza sativ
589	78.5	7.0	3529	2	Q9CP30	Q9cp30 theileria p	662	77.5	6.9	1203	2	Q6IE70	Q6ie70 rattus norv
590	77.5	6.9	215	2	Q6CBZ1	Q6cbz1 yarrowia li	663	77.5	6.9	1223	2	Q6ZS17	Q6zsl7 homo sapien
591	77.5	6.9	238	1	COR3_MOUSE	COR3m0 mus musculu	664	77.5	6.9	1462	2	Q86AR5	Q86ar5 dictyosteli
592	77.5	6.9	250	2	Q8FSI6	Q8fsi6 corynebacte	665	77.5	6.9	1513	1	MUC2_RAT	MUC2r3 rattus norv
593	77.5	6.9	260	2	Q6ND60	Q6nd60 rhodopeudo	666	77.5	6.9	1521	2	Q8CHS9	Q8chs9 mus musculu
594	77.5	6.9	270	2	Q821Y9	Q821y9 streptomyce	667	77.5	6.9	1706	2	Q7TGF2	Q7tgf2 hepatitis e
595	77.5	6.9	370	2	Q9XWNS	Q9xwn5 caenorhabdi	668	77.5	6.9	1711	1	N214_DROME	N214d0 drosophila
596	77.5	6.9	425	2	Q702W3	Q702w3 human herpe	669	77.5	6.9	2112	2	Q8OU93	Q8ou93 mus musculu
597	77.5	6.9	430	2	Q6K4M7	Q6k4m7 oryza sativ	670	77.5	6.9	2187	2	P70670	P70670 mus musculu
598	77.5	6.9	447	2	Q8S8G8	Q8s8g8 bacterioph	671	77.5	6.9	2300	2	Q7SFP6	Q7sfp6 neurospora
599	77.5	6.9	497	2	Q7XHL3	Q7xhl3 oryza sativ	672	77.5	6.9	2316	1	PTP2_RAT	PTP2r3 rattus norv
600	77.5	6.9	511	2	Q8UZ62	Q8uz62 human herpe	673	77.5	6.9	2566	2	Q8TSE7	Q8tse7 methanogarc
601	77.5	6.9	514	1	AVP2_XENLA	AVP2c0 xenopus lae	674	77.5	6.9	4782	2	Q8K1G6	Q8klg6 mus musculu
602	77.5	6.9	540	1	CH60_STRSA	CH60s0 streptococc	675	77.5	6.9	123	2	Q15773	Q15773 trypanosoma
603	77.5	6.9	547	2	Q8IV81	Q8iv81 homo sapien	676	77.5	6.9	185	2	Q7PEQ9	Q7peq9 anopheles g
604	77.5	6.9	592	2	Q23036	Q23036 caenorhabdi	677	77.5	6.9	185	2	Q7PZX2	Q7pzx2 anopheles g
605	77.5	6.9	624	2	Q8MQZ8	Q8mqz8 drosophila	678	76.5	6.8	232	2	Q69EW2	Q69ew2 streptococ
606	77.5	6.9	658	2	Q9VNZ5	Q9vnz5 drosophila	679	76.5	6.8	250	2	Q9HFS1	Q9hfs1 candida alb
607	77.5	6.9	706	2	Q9VCQ7	Q9vcq7 drosophila	680	76.5	6.8	299	2	Q825U2	Q825u2 streptomyce
608	77.5	6.9	753	2	Q6EJF7	Q6ejf7 homo sapien	681	76.5	6.8	300	2	Q6CCZ0	Q6ccz0 yarrowia li
609	77.5	6.9	760	2	Q960Q0	Q960q0 drosophila	682	76.5	6.8	304	2	Q8AWZ8	Q8awz8 bacillus ch
610	77.5	6.9	806	2	Q960Q0	Q960q0 drosophila	683	76.5	6.8	304	2	Q9BRD2	Q9brd2 homo sapien
611	77.5	6.9	951	1	SFR8_HUMAN	SFR8c0 homo sapien	684	76.5	6.8	308	2	Q6UJMS	Q6ujms diploactyl
612	77.5	6.9	982	2	Q6CGV5	Q6cgv5 yarrowia li	685	76.5	6.8	345	2	Q6UJMS	Q6ujms diploactyl
613	77.5	6.9	1050	2	Q16436	Q16436 caenorhabdi	686	76.5	6.8	349	2	Q9UF43	Q9uf43 homo sapien
614	77.5	6.9	1118	2	Q6CX19	Q6cx19 kluyveromyc	687	76.5	6.8				
615	77.5	6.9	1127	2	Q9C608	Q9c608 arabidopsis	688	76.5	6.8				

689	76.5	6.8	357	2	Q8NJZ0	Q8njz0 bionectria	762	76	6.8	468	2	O55279	O55279 avian adeno
690	76.5	6.8	358	2	Q6CCM7	Q6ccm7 yarrowia li	763	76	6.8	508	2	Q8GYU2	Q8gyu2 arabidopsis
691	76.5	6.8	385	1	Q9NHU9	Q9nhu9 drosophila	764	76	6.8	509	2	Q6UXI9	Q6uxi9 homo sapien
692	76.5	6.8	433	2	Q9K6G1	Q9k6g1 bacillus ha	765	76	6.8	532	2	O0I972	O0i972 caenorhabdi
693	76.5	6.8	452	2	Q6SYY7	Q6syy7 candida alb	766	76	6.8	532	2	Q7PAE0	Q7pae0 rickettsia
694	76.5	6.8	457	2	Q86AK1	Q86ak1 dictyosteli	767	76	6.8	549	2	Q9M1B1	Q9m1b1 arabidopsis
695	76.5	6.8	490	2	Q753Y1	Q753y1 ashbya gos	768	76	6.8	569	2	Q9SL10	Q9sl10 arabidopsis
696	76.5	6.8	505	2	Q14395	Q14395 homo sapien	769	76	6.8	576	2	O06604	O06604 saccharomyc
697	76.5	6.8	520	2	Q6CTM5	Q6ctm5 kluyveromyc	770	76	6.8	595	2	Q7R2J1	Q7r2j1 giardia lam
698	76.5	6.8	542	2	Q59145	Q59145 aeromonas s	771	76	6.8	612	2	Q7NY06	Q7ny06 chromobacte
699	76.5	6.8	623	2	O17562	O17562 caenorhabdi	772	76	6.8	622	2	Q6V6D8	Q6v6d8 drosophila
700	76.5	6.8	634	1	HWPI_CANAL	HWPI_CANAL	773	76	6.8	622	2	Q6V6E2	Q6v6e2 drosophila
701	76.5	6.8	653	1	LRR4_HUMAN	LRR4_HUMAN	774	76	6.8	622	2	Q6V6E4	Q6v6e4 drosophila
702	76.5	6.8	658	1	SHK1_SCHPO	SHK1_SCHPO	775	76	6.8	623	2	O57602	O57602 ictalurus p
703	76.5	6.8	676	2	Q9VB94	Q9vb94 drosophila	776	76	6.8	625	2	Q6V6E1	Q6v6e1 drosophila
704	76.5	6.8	695	2	Q802U4	Q802u4 brachydanio	777	76	6.8	653	2	Q73TB8	Q73tb8 mycobacteri
705	76.5	6.8	703	2	Q75YM4	Q75ym4 streptococc	778	76	6.8	679	2	Q69HN9	Q69hn9 mycobacteri
706	76.5	6.8	718	2	Q23447	Q23447 caenorhabdi	779	76	6.8	686	2	Q50194	Q50194 mycobacteri
707	76.5	6.8	750	2	Q39307	Q39307 equid herpe	780	76	6.8	725	2	Q7PP40	Q7pp40 anopheles g
708	76.5	6.8	862	2	Q8K0T1	Q8k0t1 mus muscula	781	76	6.8	725	2	Q6JAD6	Q6jad6 zea mays lm
709	76.5	6.8	907	2	Q6CTD8	Q6ctd8 kluyveromyc	782	76	6.8	768	2	Q8J2T4	Q8j2t4 grifola fro
710	76.5	6.8	1011	2	Q9NHZ9	Q9nhz9 helicoverpa	783	76	6.8	812	2	Q86AW3	Q86aw3 dictyosteli
711	76.5	6.8	1023	2	Q7M009	Q7m009 simian cyto	784	76	6.8	922	2	Q95U05	Q95u05 drosophila
712	76.5	6.8	1201	2	Q8EZH2	Q8ezh2 leptospira	785	76	6.8	954	2	Q7PMB9	Q7pmb9 anopheles g
713	76.5	6.8	1223	2	Q68FE6	Q68fe6 mus muscula	786	76	6.8	981	2	Q6QI9	Q6qig9 xenopus lae
714	76.5	6.8	1259	2	Q72MU1	Q72mu1 leptospira	787	76	6.8	1067	2	Q6BUL7	Q6bul7 debaromyce
715	76.5	6.8	1262	2	Q80T73	Q80t73 mus muscula	788	76	6.8	1194	2	Q6C4Z0	Q6c4z0 yarrowia li
716	76.5	6.8	1266	2	Q6FR84	Q6fr84 candida gla	789	76	6.8	1228	2	Q44334	Q44334 agrobacteri
717	76.5	6.8	1600	2	Q9XE34	Q9xe34 oryza sativ	790	76	6.8	1240	1	YQ3_CAEEL	Q9550 caenorhabdi
718	76.5	6.8	1672	1	PMPB_CHLMU	PMPB_CHLMU	791	76	6.8	1263	2	Q8T0M2	Q8tom2 drosophila
719	76.5	6.8	1674	2	Q80Z18	Q80z18 mus muscula	792	76	6.8	1360	2	Q9TYK4	Q9tyk4 caenorhabdi
720	76.5	6.8	1696	2	Q6Q0Y9	Q6q0y9 oryza sativ	793	76	6.8	1392	2	Q9SDG9	Q9sdg9 oryza sativ
721	76.5	6.8	2335	2	Q7YXR5	Q7yyr5 cryptospori	794	76	6.8	1423	2	Q6CRU1	Q6crul kluyveromyc
722	76.5	6.8	3088	2	Q6CH72	Q6ch72 streptomyce	795	76	6.8	1426	2	Q9X3P6	Q9x3p6 caidicellul
723	76.5	6.8	3176	2	Q6V712	Q6v712 equine arte	796	76	6.8	1462	2	Q9V5Q8	Q9v5q8 drosophila
724	76.5	6.8	3176	2	Q6V7J1	Q6v7j1 equine arte	797	76	6.8	1489	2	O23302	O23302 arabidopsis
725	76.5	6.8	4736	2	Q7VYT9	Q7vty9 mytilus gal	798	76	6.8	1689	2	Q911R1	Q911r1 crimean-con
726	76	6.8	167	2	Q14883	Q14883 homo sapien	799	76	6.8	1789	2	Q8T145	Q8t145 dictyosteli
727	76	6.8	243	2	Q25335	Q25335 leishmania	800	76	6.8	5376	1	ZAN_MOUSE	Q88799 mus musculu
728	76	6.8	269	2	Q9VLN8	Q9vln8 drosophila	801	75.5	6.7	127	2	O61035	O61035 trypanosoma
729	76	6.8	301	2	Q924F9	Q924f9 geomys burs	802	75.5	6.7	169	2	Q870Y2	Q870y2 neurospora
730	76	6.8	309	2	Q7S0P9	Q7s0p9 neurospora	803	75.5	6.7	193	2	Q8XTI3	Q8xti3 ralstonia s
731	76	6.8	313	2	Q8BEJ1	Q8bej1 skunkpox vi	804	75.5	6.7	194	2	Q9Y9W0	Q9y9w0 aeropyrum p
732	76	6.8	340	2	Q82ZX8	Q82zx8 salmoneila	805	75.5	6.7	228	2	Q8HZB6	Q8hzb6 gorilla gor
733	76	6.8	345	2	Q8WDI1	Q8wdi1 anolis sagr	806	75.5	6.7	232	2	Q69EV5	Q69ev5 streptococc
734	76	6.8	345	2	Q690T5	Q690t5 anolis sagr	807	75.5	6.7	232	2	Q69EV7	Q69ev7 streptococc
735	76	6.8	345	2	Q690T7	Q690t7 anolis sagr	808	75.5	6.7	232	2	Q69EV8	Q69ev8 streptococc
736	76	6.8	345	2	Q690U0	Q690u0 anolis sagr	809	75.5	6.7	232	2	Q69EX1	Q69ex1 streptococc
737	76	6.8	345	2	Q690U1	Q690u1 anolis sagr	810	75.5	6.7	260	2	O27007	O27007 methanobact
738	76	6.8	345	2	Q690U3	Q690u3 anolis sagr	811	75.5	6.7	273	2	P87519	P87519 bovine herp
739	76	6.8	345	2	Q690W5	Q690w5 anolis sagr	812	75.5	6.7	273	2	Q99CZ0	Q99cz0 bovine herp
740	76	6.8	345	2	Q690W9	Q690w9 anolis sagr	813	75.5	6.7	275	2	Q8DLX5	Q8dlx5 synechococc
741	76	6.8	345	2	Q691G5	Q691g5 anolis sagr	814	75.5	6.7	282	2	Q8L8N4	Q8l8n4 arabidopsis
742	76	6.8	345	2	Q691G8	Q691g8 anolis sagr	815	75.5	6.7	299	2	Q8Z2P6	Q8z2p6 pyrobaculum
743	76	6.8	345	2	Q691Q6	Q691q6 anolis sagr	816	75.5	6.7	300	2	Q95XH5	Q95xh5 caenorhabdi
744	76	6.8	345	2	Q691T7	Q691t7 anolis sagr	817	75.5	6.7	306	2	Q88V34	Q88v34 lactobacill
745	76	6.8	345	2	Q691U4	Q691u4 anolis sagr	818	75.5	6.7	321	2	Q9XUL7	Q9xul7 caenorhabdi
746	76	6.8	345	2	Q692A0	Q692a0 anolis sagr	819	75.5	6.7	329	2	Q6FIA0	Q6fia0 homo sapien
747	76	6.8	345	2	Q692A2	Q692a2 anolis sagr	820	75.5	6.7	329	2	Q9NWV8	Q9nwv8 homo sapien
748	76	6.8	345	2	Q692A3	Q692a3 anolis sagr	821	75.5	6.7	330	2	Q8GAR7	Q8gar7 dictyosteli
749	76	6.8	359	2	Q43656	Q43656 homo sapien	822	75.5	6.7	346	2	Q9TFU7	Q9tfu7 teratoscinc
750	76	6.8	368	1	VE2_HPV45	P36794 human papil	823	75.5	6.7	385	2	Q8T8L4	Q8t8l4 drosophila
751	76	6.8	370	2	Q9FN39	Q9fn39 arabidopsis	824	75.5	6.7	385	2	Q9N666	Q9n666 drosophila
752	76	6.8	372	2	Q8CQM2	Q8cqm2 staphylococ	825	75.5	6.7	385	2	Q9NHU6	Q9nhu6 drosophila
753	76	6.8	374	2	Q8EC31	Q8ec31 shewanella	826	75.5	6.7	385	2	Q9NHU7	Q9nhu7 drosophila
754	76	6.8	389	1	ADHA_CLOAB	Q04944 clostridium	827	75.5	6.7	397	2	Q702W7	Q702w7 human herpe
755	76	6.8	415	2	Q641C6	Q641c6 xenopus lae	828	75.5	6.7	397	2	Q702X1	Q702x1 human herpe
756	76	6.8	428	2	Q86DA4	Q86da4 caenorhabdi	829	75.5	6.7	420	2	Q8N7W9	Q8n7w9 homo sapien
757	76	6.8	429	2	Q7JMU4	Q7jmu4 caenorhabdi	830	75.5	6.7	430	1	PO23_RAT	P42571 rattus norv
758	76	6.8	431	1	YMR7_CAEEL	P34474 caenorhabdi	831	75.5	6.7	464	2	Q90WQ6	Q90wq6 oncorhynch
759	76	6.8	441	2	Q72NAG	Q72na6 leptospira	832	75.5	6.7	468	1	VASI_BOVIN	P40682 bos taurus
760	76	6.8	441	2	Q8FB95	Q8fb95 leptospira	833	75.5	6.7	476	2	Q6C1S9	Q6c1s9 humicola in
761	76	6.8	452	2	Q9ADQ9	Q9adq9 staphylococ	834	75.5	6.7	478	2	O61122	O61122 dictyosteli

835	75.5	6.7	481	2	Q9VWK3	Q9vbk3 drosophila	908	75	6.7	474	2	O46597	O46597 cercopithec
836	75.5	6.7	492	2	Q94HR9	Q94hr9 aradidopsis	909	75	6.7	491	1	YC70 CORGL	P42331 corynebacte
837	75.5	6.7	496	1	CWL6 BACSU	Q02114 bacillus su	910	75	6.7	532	2	O6P7V2	O6p7v2 mus musculu
838	75.5	6.7	511	1	VGLC HHV11	P10228 human herpe	911	75	6.7	542	2	O8P22	O8p22 xanthomonas
839	75.5	6.7	511	2	O8UYA4	Q8uya4 human herpe	912	75	6.7	554	1	CHIT MANSE	P36362 manduca sex
840	75.5	6.7	511	2	O8UYE2	Q8uye2 human herpe	913	75	6.7	554	2	O8CCJ9	Q8ccj9 mus musculu
841	75.5	6.7	511	2	O8UYF2	Q8uyf2 human herpe	914	75	6.7	604	2	O13845	O13845 schizosacch
842	75.5	6.7	511	2	O8U265	Q8uz65 human herpe	915	75	6.7	605	2	Q7PST0	Q7pst0 anopheles g
843	75.5	6.7	511	2	O8U268	Q8uz68 human herpe	916	75	6.7	612	2	Q9NVJ6	Q9nvj6 homo sapien
844	75.5	6.7	511	2	O8U269	Q8uz69 human herpe	917	75	6.7	630	2	O6NUN6	O6nun6 homo sapien
845	75.5	6.7	511	2	O8U270	Q8uz70 human herpe	918	75	6.7	634	2	O20710	O20710 caenorhabdi
846	75.5	6.7	511	2	O8U271	Q8uz71 human herpe	919	75	6.7	634	2	O20710	O20710 caenorhabdi
847	75.5	6.7	511	2	O9W1W3	Q9wiw3 human herpe	920	75	6.7	686	2	O9H6X0	O9h6x0 homo sapien
848	75.5	6.7	534	2	Q72BB2	Q72bb2 desulfovibr	921	75	6.7	686	2	O9N384	O9n384 homo sapien
849	75.5	6.7	547	1	MUI3 RAT	P97881 rattus norv	922	75	6.7	702	2	O8I221	O8i221 homo sapien
850	75.5	6.7	550	2	Q70KA7	Q70ka7 gordonia we	923	75	6.7	717	2	O6PST6	O6pst6 spodoptera
851	75.5	6.7	559	1	NUPL MOUSE	Q8k2k6 mus musculu	924	75	6.7	725	2	O8JJP6	O8jjp6 porcine lym
852	75.5	6.7	609	2	O9A6T7	Q9ast7 caulobacter	925	75	6.7	737	1	KNS1 YEAST	P32350 saccharomyc
853	75.5	6.7	639	2	O8TFL3	Q8tfl3 methanobact	926	75	6.7	746	2	O9V515	O9v515 drosophila
854	75.5	6.7	650	2	O8EYE4	Q8eye4 leptospira	927	75	6.7	768	1	AMY1_SACDI	P29760 saccharomyc
855	75.5	6.7	665	2	Q97G25	Q97g25 clostridium	928	75	6.7	793	2	O8YAG7	O8yag7 listeria mo
856	75.5	6.7	736	2	Q8COR7	Q8cor7 mus musculu	929	75	6.7	796	2	O9LQ09	O9lq09 aradidopsis
857	75.5	6.7	783	2	O63158	Q63158 rattus norv	930	75	6.7	805	1	HIFA_XENLA	O91a89 xenopus lae
858	75.5	6.7	784	2	O6C185	Q6ci85 yarrowia li	931	75	6.7	808	2	O6SL88	O6sl88 oryza sativ
859	75.5	6.7	817	2	O6PGX9	Q6pgx9 brachydanio	932	75	6.7	904	2	O8IWC1	O8iwc1 homo sapien
860	75.5	6.7	864	1	YC18 HUMAN	Q9ulh2 homo sapien	933	75	6.7	908	2	O6CST7	O6cst7 kluyveromyc
861	75.5	6.7	877	2	Q9H3Q6	Q9h3q6 homo sapien	934	75	6.7	919	2	O8I4J3	O8i4j3 caenorhabdi
862	75.5	6.7	877	2	Q8O7I5	Q8o7i5 human immun	935	75	6.7	924	2	O20189	O20189 caenorhabdi
863	75.5	6.7	878	2	Q9H3Q7	Q9h3q7 homo sapien	936	75	6.7	925	2	O9U7E8	O9u7e8 caenorhabdi
864	75.5	6.7	932	1	RENC_MACMU	Q8sqd27 macaca mula	937	75	6.7	933	2	O6ZM25	O6zm25 homo sapien
865	75.5	6.7	942	2	O7WYN3	Q7wyn3 acetivibrio	938	75	6.7	945	2	O8I4J4	O8i4j4 caenorhabdi
866	75.5	6.7	957	2	O14651	O14651 homo sapien	939	75	6.7	991	2	O6UDF7	O6udf7 chlamydia t
867	75.5	6.7	964	2	Q6CDQ6	Q6cdq6 yarrowia li	940	75	6.7	993	2	O84FV2	O84fv2 chlamydia h
868	75.5	6.7	1020	2	Q688J1	Q688j1 oryza sativ	941	75	6.7	1023	2	O86XN9	O86xn9 homo sapien
869	75.5	6.7	1045	2	O86T37	Q86t37 homo sapien	942	75	6.7	1171	2	O6ZQ63	O6zq63 mus musculu
870	75.5	6.7	1217	2	O9UKM9	Q9ukw9 homo sapien	943	75	6.7	1191	2	O68FH6	O68fh6 mus musculu
871	75.5	6.7	1320	2	O86TC9	Q86tc9 homo sapien	944	75	6.7	1198	2	O8IWE1	O8iwe1 homo sapien
872	75.5	6.7	1388	2	Q9Y4W4	Q9y4w4 homo sapien	945	75	6.7	1198	2	O76E12	O76e12 homo sapien
873	75.5	6.7	1391	2	Q8N3L4	Q8n3l4 homo sapien	946	75	6.7	1200	2	O8BGF7	O8bgf7 m mus muscu
874	75.5	6.7	1414	2	O8O222	Q8o222 mus musculu	947	75	6.7	1206	2	O75189	O75189 homo sapien
875	75.5	6.7	1444	2	O94KE2	Q94ke2 aradidopsis	948	75	6.7	1227	2	O8T872	O8t872 dictyosteli
876	75.5	6.7	1464	2	O871F7	Q871f7 neurospora	949	75	6.7	1259	2	O869X4	O869x4 dictyosteli
877	75.5	6.7	1532	2	Q9LUW1	Q9luw1 aradidopsis	950	75	6.7	1264	2	O6ZU65	O6zu65 homo sapien
878	75.5	6.7	1825	2	Q748I6	Q748i6 geobacter s	951	75	6.7	1301	2	O7L1Z7	O7l1z7 homo sapien
879	75.5	6.7	2055	2	Q7S659	Q7s659 neurospora	952	75	6.7	1329	2	O9HCE3	O9hce3 homo sapien
880	75.5	6.7	2151	2	Q9VPL6	Q9vpl6 drosophila	953	75	6.7	1343	2	O960V6	O960v6 drosophila
881	75.5	6.7	2151	2	O9VLL3	Q9yll3 drosophila	954	75	6.7	1343	2	O9W2G5	O9w2g5 drosophila
882	75.5	6.7	2850	2	O8OT03	Q8ot03 mus musculu	955	75	6.7	1475	2	O8LSQ1	O8leq1 oryza sativ
883	75.5	6.7	3222	2	Q9VPL9	Q9vpl9 drosophila	956	75	6.7	1490	1	CRK7_HUMAN	Q9nyv4 homo sapien
884	75	6.7	94	2	Q14886	Q14886 homo sapien	957	75	6.7	2180	2	O9VAS8	O9vas8 drosophila
885	75	6.7	168	2	Q9NL63	Q9nl63 sarcophaga	958	75	6.7	3375	1	UN52 CAEEL	O06561 caenorhabdi
886	75	6.7	201	2	O6WAZ6	O6waz6 trypanosoma	959	74.5	6.6	23015	2	O8IQI8	O8iqi8 drosophila
887	75	6.7	253	2	O6DT07	Q6dt07 helicobacte	960	74.5	6.6	177	2	O7TLX3	O7tlx3 choristoneu
888	75	6.7	275	2	O8T4R0	Q8t4r0 aedes aegypt	961	74.5	6.6	199	2	O6C3G4	O6c3g4 yarrowia li
889	75	6.7	310	2	O58861	O58861 pyrococcus	962	74.5	6.6	236	1	SUR2_RALSO	O03919 raietonia s
890	75	6.7	315	2	O6DST9	Q6dst9 aradidopsis	963	74.5	6.6	262	2	O9TZA1	O9tza1 caenorhabdi
891	75	6.7	318	2	O96B22	Q96b22 homo sapien	964	74.5	6.6	271	2	O6NVE7	O6nve7 brachydanio
892	75	6.7	328	2	O00446	O00446 homo sapien	965	74.5	6.6	292	2	O7QDX6	O7qdx6 anopheles g
893	75	6.7	333	2	O92K36	Q92k36 rhizobium m	966	74.5	6.6	342	2	O9TXW7	O9txw7 caenorhabdi
894	75	6.7	337	2	O6FUQ8	Q6fuq8 candida gla	967	74.5	6.6	345	2	O6OUJ1	O6ujr1 streptococc
895	75	6.7	344	2	O691Z8	Q691z8 anolis sagr	968	74.5	6.6	346	2	O8SHB2	O8shb2 rhampholeon
896	75	6.7	345	2	O690W1	Q690w1 anolis sagr	969	74.5	6.6	385	2	O8T8L3	O8t8l3 drosophila
897	75	6.7	345	2	O690X0	Q690x0 anolis sagr	970	74.5	6.6	385	2	O9NHU5	O9nhu5 drosophila
898	75	6.7	345	2	O691G9	Q691g9 anolis sagr	971	74.5	6.6	385	2	O9NHU8	O9nhu8 drosophila
899	75	6.7	345	2	O691M1	Q691m1 anolis sagr	972	74.5	6.6	385	2	O9NHV1	O9nhv1 drosophila
900	75	6.7	345	2	O691R1	Q691r1 anolis sagr	973	74.5	6.6	392	2	O7S0T1	O7s0t1 neurospora
901	75	6.7	345	2	O691U7	Q691u7 anolis sagr	974	74.5	6.6	397	2	O702Y5	O702y5 human herpe
902	75	6.7	345	2	O692A8	Q692a8 anolis sagr	975	74.5	6.6	404	2	O9LVB0	O9lvb0 aradidopsis
903	75	6.7	424	2	O8N4A9	Q8n4a9 pyrobaculum	976	74.5	6.6	407	1	LMP1_CRIGR	P49129 cricetus
904	75	6.7	436	2	O8N4A9	Q8n4a9 caenorhabdi	977	74.5	6.6	421	2	O6Z4B1	O6z4b1 caenorhabdi
905	75	6.7	468	1	ALS2_CANAL	O74e57 candida alb	978	74.5	6.6	431	2	O9EZP5	O9ezf5 streptococc
906	75	6.7	468	2	Q7URQ0	Q7urq0 candida alb	979	74.5	6.6	440	2	O8C6J0	O8c6j0 mus musculu
907	75	6.7	469	2	Q7JJ48	Q7jj48 cercopithec	980	74.5	6.6	450	2	O8C935	O8c935 mus musculu

981	74.5	6.6	467	2	Q6C5E7	Q6C5E7	Yarrowia li	1054	74	6.6	435	2	O45484	O45484	caenorhabdi
982	74.5	6.6	469	2	Q82940	Q82940	nitrosomona	1055	74	6.6	437	2	Q9EZF7	Q9EZF7	streptococc
983	74.5	6.6	474	2	Q7JP78	Q7JP78	caenorhabdi	1056	74	6.6	441	1	END2_HUMAN	END2_HUMAN	homo sapien
984	74.5	6.6	475	2	Q22794	Q22794	arabidopsis	1057	74	6.6	451	2	Q82DJ2	Q82DJ2	streptomyce
985	74.5	6.6	482	2	Q20858	Q20858	caenorhabdi	1058	74	6.6	458	2	O16285	O16285	caenorhabdi
986	74.5	6.6	484	2	Q872J7	Q872J7	neurospora	1059	74	6.6	464	2	Q8MN43	Q8MN43	dictyosteli
987	74.5	6.6	507	2	Q8R4H1	Q8R4H1	mus musculus	1060	74	6.6	467	2	Q8GM73	Q8GM73	streptococc
988	74.5	6.6	507	2	Q6P5D7	Q6P5D7	mus musculus	1061	74	6.6	472	2	O8PLF5	O8PLF5	xanthomonas
989	74.5	6.6	511	2	Q8U2P63	Q8U2P63	human herpe	1062	74	6.6	490	2	Q6V6N2	Q6V6N2	drosophila
990	74.5	6.6	530	2	Q8BLS0	Q8BLS0	m mus muscu	1063	74	6.6	490	2	Q6V6N6	Q6V6N6	drosophila
991	74.5	6.6	540	2	Q9X4R5	Q9X4R5	streptococc	1064	74	6.6	505	2	Q8TWN8	Q8TWN8	methanopyru
992	74.5	6.6	567	1	CHT3_CANAL	CHT3_CANAL	canida alb	1065	74	6.6	515	2	Q8Y941	Q8Y941	listeria mo
993	74.5	6.6	567	2	Q6FR51	Q6FR51	canida alb	1066	74	6.6	518	2	O16283	O16283	caenorhabdi
994	74.5	6.6	588	2	Q9VGA8	Q9VGA8	drosophila	1067	74	6.6	538	2	Q967D0	Q967D0	geodia cydo
995	74.5	6.6	606	2	Q8ES22	Q8ES22	caenorhabdi	1068	74	6.6	542	1	SCWB_YEAST	SCWB_YEAST	saccharomyc
996	74.5	6.6	612	2	Q9FS24	Q9FS24	vigna ungui	1069	74	6.6	543	2	Q7YZ30	Q7YZ30	cryptospori
997	74.5	6.6	626	2	Q6UDE6	Q6UDE6	schizophyll	1070	74	6.6	551	2	Q815U4	Q815U4	bagillus ce
998	74.5	6.6	635	2	Q9LDJ5	Q9LDJ5	lycopersico	1071	74	6.6	578	2	Q63ZX6	Q63ZX6	mus musculus
999	74.5	6.6	636	2	Q66HZ5	Q66HZ5	brachydanio	1072	74	6.6	581	2	Q7SGW5	Q7SGW5	neurospora
1000	74.5	6.6	678	2	Q92K48	Q92K48	rhizobium m	1073	74	6.6	586	2	Q08118	Q08118	saccharomyc
1001	74.5	6.6	709	2	O16783	O16783	caenorhabdi	1074	74	6.6	600	1	PFCK_CHLCV	PFCK_CHLCV	chlamydophi
1002	74.5	6.6	751	2	Q7S5B7	Q7S5B7	neurospora	1075	74	6.6	601	2	Q9T0K6	Q9T0K6	arabidopsis
1003	74.5	6.6	806	2	Q7RXW7	Q7RXW7	neurospora	1076	74	6.6	601	2	Q6V6S0	Q6V6S0	drosophila
1004	74.5	6.6	812	2	O52504	O52504	thermotoga	1077	74	6.6	602	2	Q8W4K6	Q8W4K6	arabidopsis
1005	74.5	6.6	813	2	O87964	O87964	thermotoga	1078	74	6.6	647	2	Q7S5I2	Q7S5I2	neurospora
1006	74.5	6.6	841	2	O94002	O94002	canida alb	1079	74	6.6	666	2	Q7QXK0	Q7QXK0	giardia lam
1007	74.5	6.6	849	2	P87107	P87107	saccharomyc	1080	74	6.6	691	2	Q6BNQ7	Q6BNQ7	debaromyce
1008	74.5	6.6	860	1	CH12_COCIM	CH12_COCIM	coccidioides	1081	74	6.6	725	2	Q8CV93	Q8CV93	mus musculus
1009	74.5	6.6	896	1	MUTS_LACPL	MUTS_LACPL	lactobacilli	1082	74	6.6	783	2	Q7SA55	Q7SA55	ashbya goss
1010	74.5	6.6	909	1	LDL1_XENLA	LDL1_XENLA	xenopus lae	1083	74	6.6	794	2	Q61P23	Q61P23	photobacter
1011	74.5	6.6	910	2	O9D4H6	O9D4H6	m mus muscu	1084	74	6.6	809	2	Q7SDN1	Q7SDN1	neurospora
1012	74.5	6.6	998	1	EPB3_HUMAN	EPB3_HUMAN	homo sapien	1085	74	6.6	835	2	Q7R2W3	Q7R2W3	giardia lam
1013	74.5	6.6	998	2	Q7Z740	Q7Z740	homo sapien	1086	74	6.6	860	1	ENV_HV2BE	ENV_HV2BE	human immun
1014	74.5	6.6	1009	2	Q6CTH0	Q6CTH0	kluyveromyc	1087	74	6.6	873	2	Q9NYU3	Q9NYU3	homo sapien
1015	74.5	6.6	1032	2	Q6XLI7	Q6XLI7	rattus norv	1088	74	6.6	906	2	Q97YQ1	Q97YQ1	sulfolobus
1016	74.5	6.6	1074	2	Q8COP8	Q8COP8	mus musculus	1089	74	6.6	1047	2	Q24019	Q24019	drosophila
1017	74.5	6.6	1075	1	FLOS_YEAST	FLOS_YEAST	saccharomyc	1090	74	6.6	1100	2	Q9VUE7	Q9VUE7	drosophila
1018	74.5	6.6	1089	2	Q86KP4	Q86KP4	dictyosteli	1091	74	6.6	1226	2	Q9NZB6	Q9NZB6	homo sapien
1019	74.5	6.6	1091	2	Q7SDT8	Q7SDT8	neurospora	1092	74	6.6	1248	2	Q8AUP9	Q8AUP9	oryza sativ
1020	74.5	6.6	1100	1	TCG1_MOUSE	TCG1_MOUSE	mus musculus	1093	74	6.6	1342	2	Q9GPP6	Q9GPP6	drosophila
1021	74.5	6.6	1126	2	Q9EQJ9	Q9EQJ9	mus musculus	1094	74	6.6	1342	2	Q9VPZ7	Q9VPZ7	drosophila
1022	74.5	6.6	1170	2	Q69ZE1	Q69ZE1	mus musculus	1095	74	6.6	1355	2	Q86AM1	Q86AM1	dictyosteli
1023	74.5	6.6	1209	2	Q7SZF4	Q7SZF4	brachydanio	1096	74	6.6	1371	2	Q8BV57	Q8BV57	mus musculus
1024	74.5	6.6	1233	1	MUSA_HUMAN	MUSA_HUMAN	homo sapien	1097	74	6.6	1378	2	Q8SQI2	Q8SQI2	sarcophaga
1025	74.5	6.6	1388	1	CAIE_HUMAN	CAIE_HUMAN	homo sapien	1098	74	6.6	1455	2	Q7RYI6	Q7RYI6	neurospora
1026	74.5	6.6	1720	2	Q81486	Q81486	plasmodium	1099	74	6.6	1469	2	Q7S353	Q7S353	neurospora
1027	74.5	6.6	1790	2	Q81816	Q81816	aplysia cal	1100	74	6.6	2071	2	Q8GZY7	Q8GZY7	oryza sativ
1028	74.5	6.6	1838	1	CA15_HUMAN	CA15_HUMAN	homo sapien	1101	74	6.6	2414	1	P300_HUMAN	P300_HUMAN	homo sapien
1029	74.5	6.6	1838	2	Q15094	Q15094	homo sapien	1102	74	6.6	4060	2	Q91H28	Q91H28	gill-associ
1030	74.5	6.6	1969	2	Q7SEZ5	Q7SEZ5	neurospora	1103	74	6.6	4498	2	Q9W2Z3	Q9W2Z3	drosophila
1031	74.5	6.6	2888	1	ZEPI_MOUSE	ZEPI_MOUSE	mus musculus	1104	73.5	6.5	143	2	O15776	O15776	trypanosoma
1032	74	6.6	147	1	IR13_HCMVA	IR13_HCMVA	human cytom	1105	73.5	6.5	166	2	Q94J61	Q94J61	oryza sativ
1033	74	6.6	147	2	Q7M575	Q7M575	human cytom	1106	73.5	6.5	217	2	Q6FM83	Q6FM83	candida gla
1034	74	6.6	172	2	Q8WTL2	Q8WTL2	caenorhabdi	1107	73.5	6.5	225	2	P89669	P89669	san miguel
1035	74	6.6	192	2	O02817	O02817	oryctolagus	1108	73.5	6.5	286	2	O8CB51	O8CB51	mus musculus
1036	74	6.6	218	2	Q9XCK5	Q9XCK5	streptococc	1109	73.5	6.5	290	1	LECR_CLALU	LECR_CLALU	cladraetis
1037	74	6.6	223	2	O02255	O02255	caenorhabdi	1110	73.5	6.5	304	2	Q9QNN4	Q9QNN4	lymphocyctic
1038	74	6.6	267	2	Q6CLX9	Q6CLX9	kluyveromyc	1111	73.5	6.5	304	2	Q9QNN5	Q9QNN5	lymphocyctic
1039	74	6.6	340	2	Q88140	Q88140	pseudomonas	1112	73.5	6.5	304	2	Q9QNN6	Q9QNN6	lymphocyctic
1040	74	6.6	345	2	Q690W7	Q690W7	anolis sagr	1113	73.5	6.5	304	2	Q9QNN7	Q9QNN7	lymphocyctic
1041	74	6.6	345	2	Q690X9	Q690X9	anolis sagr	1114	73.5	6.5	304	2	Q9QNN8	Q9QNN8	lymphocyctic
1042	74	6.6	345	2	Q691U5	Q691U5	anolis sagr	1115	73.5	6.5	304	2	Q9QNN9	Q9QNN9	lymphocyctic
1043	74	6.6	358	2	Q8FQU1	Q8FQU1	corynebacte	1116	73.5	6.5	304	2	Q9QNP0	Q9QNP0	lymphocyctic
1044	74	6.6	364	2	Q96D42	Q96D42	homo sapien	1117	73.5	6.5	304	2	Q9QNP1	Q9QNP1	lymphocyctic
1045	74	6.6	367	2	Q7YUQ8	Q7YUQ8	trypanosoma	1118	73.5	6.5	304	2	Q9QNP2	Q9QNP2	lymphocyctic
1046	74	6.6	369	2	Q7YUQ3	Q7YUQ3	trypanosoma	1119	73.5	6.5	304	2	Q9QNP3	Q9QNP3	lymphocyctic
1047	74	6.6	392	2	O89HN7	O89HN7	bradyrhizob	1120	73.5	6.5	304	2	Q9QNP4	Q9QNP4	lymphocyctic
1048	74	6.6	397	2	Q97GX2	Q97GX2	clostridium	1121	73.5	6.5	336	2	O9HF70	O9HF70	candida dub
1049	74	6.6	408	2	Q6UDF5	Q6UDF5	psittacid h	1122	73.5	6.5	336	2	Q6W762	Q6W762	homo sapien
1050	74	6.6	418	2	Q21941	Q21941	caenorhabdi	1123	73.5	6.5	337	2	Q872L8	Q872L8	neurospora
1051	74	6.6	418	2	Q90410	Q90410	brachydanio	1124	73.5	6.5	338	2	O43420	O43420	homo sapien
1052	74	6.6	431	1	MNS1_MACFA	MNS1_MACFA	macaca fasc	1125	73.5	6.5	358	2	Q8YNI5	Q8YNI5	anabaena sp
1053	74	6.6	435	2	Q7S3T5	Q7S3T5	neurospora	1126	73.5	6.5	365	1	PMA2_MOUSE	PMA2_MOUSE	mus musculus

1127	73.5	367	2	Q9P018	Q9p018 homo sapien	1200	73.5	6.5	1689	2	Q8JS22	Q8jazz2 crimean-con
1128	73.5	369	2	Q96V15	Q96v15 pneumocysti	1201	73.5	6.5	1752	2	Q86XQ7	Q86xq7 dictyosteli
1129	73.5	371	2	Q25333	Q25333 leishmania	1202	73.5	6.5	1761	2	Q86XN2	Q86xn2 homo sapien
1130	73.5	385	2	Q9NHV0	Q9nhv0 drosophila	1203	73.5	6.5	1937	2	Q9VT17	Q9vt17 drosophila
1131	73.5	385	2	Q9NHV2	Q9nhv2 drosophila	1204	73.5	6.5	2081	2	Q8HJ37	Q8hj37 thermoplas
1132	73.5	385	2	Q9NHV3	Q9nhv3 drosophila	1205	73.5	6.5	2232	2	Q8IFX6	Q8ifx6 caenorhabdi
1133	73.5	389	2	Q6GXX1	Q6gxx1 swine hepat	1206	73.5	6.5	2338	2	Q759S3	Q759s3 ashbya goss
1134	73.5	407	2	Q865F6	Q865f6 macaca neme	1207	73.5	6.5	2527	2	Q9V7F2	Q9v7f2 drosophila
1135	73.5	415	2	Q7X148	Q7x148 oryza sativ	1208	73.5	6.5	3176	1	CA36_HUMAN	P12111 homo sapien
1136	73.5	447	2	Q63348	Q63348 rattus norv	1209	73	6.5	143	2	Q61028	Q61028 trypanosoma
1137	73.5	451	2	Q95144	Q95144 cercopithe	1210	73	6.5	172	2	Q7PRG9	Q7prg9 anopheles g
1138	73.5	460	2	Q02321	Q02321 phanerocha	1211	73	6.5	256	2	Q6L3V7	Q6l3v7 solanum dem
1139	73.5	464	2	Q9C247	Q9c247 neurospora	1212	73	6.5	260	2	Q90274	Q90274 brachydanio
1140	73.5	476	2	Q6AYP5	Q6ayp5 rattus norv	1213	73	6.5	327	2	Q844J7	Q844j7 lactobacill
1141	73.5	484	1	GUX_CELFI	P07986 cellulomona	1214	73	6.5	327	2	Q25334	Q25334 leishmania
1142	73.5	485	2	Q59277	Q59277 cellulomona	1215	73	6.5	335	2	Q14652	Q14652 homo sapien
1143	73.5	510	2	Q6M375	Q6m375 bdellovibri	1216	73	6.5	340	2	Q8W763	Q8w763 homo sapien
1144	73.5	511	1	VGJC_HHV1K	P28986 human herpe	1217	73	6.5	343	2	Q6GJP6	Q6gjp6 staphylococ
1145	73.5	534	2	Q8KJ12	Q8kj12 streptococc	1218	73	6.5	345	2	Q9VJ23	Q9vj23 drosophila
1146	73.5	534	2	Q9YI56	Q9yi56 gallus gall	1219	73	6.5	345	2	Q690U4	Q690u4 anolis sagr
1147	73.5	537	2	Q96UK5	Q96uk5 coccidioid	1220	73	6.5	345	2	Q690W4	Q690w4 anolis sagr
1148	73.5	542	2	Q18637	Q18637 caenorhabdi	1221	73	6.5	345	2	Q891H0	Q891h0 anolis sagr
1149	73.5	558	2	Q6M2G6	Q6m2g6 homo sapien	1222	73	6.5	345	2	Q891N0	Q891n0 anolis sagr
1150	73.5	565	2	Q6ND51	Q6nd51 rhodospseudo	1223	73	6.5	345	2	Q691T6	Q691t6 anolis sagr
1151	73.5	566	2	Q96M23	Q96m23 homo sapien	1224	73	6.5	345	2	Q692B8	Q692b8 anolis sagr
1152	73.5	575	1	CH61_CUCMA	Q05045 cucurbita m	1225	73	6.5	365	2	Q8T110	Q8t110 battonella
1153	73.5	594	2	Q75UN9	Q75un9 haliotis di	1226	73	6.5	385	2	Q8T8I7	Q8t8i7 drosophila
1154	73.5	594	2	Q86M37	Q86m37 haliotis di	1227	73	6.5	385	2	Q8T8I9	Q8t8i9 drosophila
1155	73.5	595	1	TNR8_HUMAN	P28908 homo sapien	1228	73	6.5	395	2	Q8CAU7	Q8cau7 yarrowia li
1156	73.5	601	2	Q97YX7	Q97yx7 sulfolobus	1229	73	6.5	417	2	Q9VLA9	Q9vla9 drosophila
1157	73.5	602	2	Q9V1P0	Q9v1p0 drosophila	1230	73	6.5	418	2	Q43421	Q43421 homo sapien
1158	73.5	608	2	Q6NP13	Q6np13 drosophila	1231	73	6.5	441	2	Q89H15	Q89h15 homo sapien
1159	73.5	626	2	Q8Y5N1	Q8y5n1 listeria mo	1232	73	6.5	459	2	Q9P3J7	Q9p3j7 neurospora
1160	73.5	664	2	Q96PV8	Q96pv8 homo sapien	1233	73	6.5	461	2	Q9P3J7	P37563 bacillus su
1161	73.5	670	1	YFGG_SCHPO	Q13854 schizosacch	1234	73	6.5	472	1	YACA_BACSU	P10064 bos taurus
1162	73.5	677	2	Q9FNB7	Q9fnb7 arabidopsis	1235	73	6.5	492	1	GAA3_BOVIN	Q63p57 burkholderi
1163	73.5	679	2	Q8GY46	Q8gy46 arabidopsis	1236	73	6.5	495	2	Q63P57	Q63p57 burkholderi
1164	73.5	708	2	Q9CCY4	Q9ccy4 mycobacteri	1237	73	6.5	507	2	Q9HA16	Q9ha16 homo sapien
1165	73.5	720	2	Q8N6M6	Q8n6m6 homo sapien	1238	73	6.5	528	1	FIT1_YEAST	Q04433 saccharomyc
1166	73.5	720	2	Q8NLF6	Q8nlf6 corynebacte	1239	73	6.5	530	2	Q8FT30	Q8ft30 candida gla
1167	73.5	733	2	Q618T9	Q618t9 cucumis sat	1240	73	6.5	533	2	Q9BTQ8	Q9btq8 homo sapien
1168	73.5	734	2	Q35930	Q35930 mus musculu	1241	73	6.5	544	1	GP10_DICDI	Q06885 dictyosteli
1169	73.5	754	2	Q6DFX1	Q6dfx1 mus musculu	1242	73	6.5	550	2	Q9RY21	Q9ry21 deinococcus
1170	73.5	794	2	O18742	O18742 bos taurus	1243	73	6.5	582	2	Q24160	Q24160 drosophila
1171	73.5	806	2	Q28874	Q28874 archaeoglob	1244	73	6.5	600	1	P8CK_CHLPN	Q82755 chlamydia p
1172	73.5	820	2	O18743	O18743 bos taurus	1245	73	6.5	637	2	Q80ZE7	Q80ze7 rattus norv
1173	73.5	825	2	Q873Y0	Q873y0 aspergillus	1246	73	6.5	639	1	CZAP_HUMAN	Q9Y5K6 homo sapien
1174	73.5	829	2	Q7RW40	Q7rw40 neurospora	1247	73	6.5	645	2	Q7PWE4	Q7pwe4 anopheles g
1175	73.5	835	2	O53129	O53129 mycobacteri	1248	73	6.5	652	2	Q83364	Q83364 murine leuk
1176	73.5	835	2	O57075	O57075 bombyx mori	1249	73	6.5	656	2	Q76184	Q76184 mus musculu
1177	73.5	838	2	Q9VQA9	Q9vqa9 drosophila	1250	73	6.5	681	1	VGP_MABVP	P35254 marburg vir
1178	73.5	866	2	O39781	Q9781 equid herpe	1251	73	6.5	681	2	Q71VM1	Q71vml lake victor
1179	73.5	880	1	PH7F_DROME	Q9v9a8 drosophila	1252	73	6.5	709	2	Q86A80	Q86a80 dictyosteli
1180	73.5	905	2	O18741	O18741 bos taurus	1253	73	6.5	711	2	Q86A07	Q86a07 dictyosteli
1181	73.5	907	2	Q8AWX1	Q8awx1 xenopus tro	1254	73	6.5	715	2	Q6DTM7	Q6dtm7 candida gla
1182	73.5	939	2	Q69ZZ9	Q69zz9 mus musculu	1255	73	6.5	719	2	Q6DJ90	Q6dj90 xenopus tro
1183	73.5	943	1	YL61_SCHPO	Q8tf99 schizosacch	1256	73	6.5	728	2	O19182	O19182 caenorhabdi
1184	73.5	968	2	Q6BEV7	Q6bev7 caenorhabdi	1257	73	6.5	741	2	Q7QVE9	Q7qve9 giardia lam
1185	73.5	976	2	Q9A531	Q9a531 caulobacter	1258	73	6.5	748	2	Q9Y6E1	Q9y6e1 homo sapien
1186	73.5	989	2	Q9M1E4	Q9mie4 arabidopsis	1259	73	6.5	771	2	Q22783	Q22783 caenorhabdi
1187	73.5	1004	1	YD83_SCHPO	Q10408 schizosacch	1260	73	6.5	776	2	Q6ZVF9	Q6zvf9 homo sapien
1188	73.5	1010	2	Q9U6W2	Q9u6w2 heliothis v	1261	73	6.5	777	2	Q82ID3	Q82id3 streptomyce
1189	73.5	1016	2	O17718	Q17718 caenorhabdi	1262	73	6.5	780	2	Q6DFV2	Q6dfv2 mus musculu
1190	73.5	1017	2	Q6Y096	Q6y096 legionella	1263	73	6.5	781	2	Q7RVJ3	Q7rvj3 neurospora
1191	73.5	1033	2	Q6Q121	Q6qi21 aspergillus	1264	73	6.5	782	1	SP4_MOUSE	Q62445 mus musculu
1192	73.5	1120	2	Q9VUK6	Q9vuk6 drosophila	1265	73	6.5	784	2	Q9H5A0	Q9h5a0 homo sapien
1193	73.5	1124	2	Q810N9	Q810n9 caenorhabdi	1266	73	6.5	801	2	Q6P2S1	Q6p2e1 homo sapien
1194	73.5	1258	2	Q86IA2	Q86ia2 dictyosteli	1267	73	6.5	802	2	O81VE4	O8ive4 homo sapien
1195	73.5	1316	2	Q9HLF6	Q9hlf6 thermoplas	1268	73	6.5	803	2	Q9P2W4	Q9p2w4 homo sapien
1196	73.5	1366	2	Q86AM2	Q86am2 dictyosteli	1269	73	6.5	824	2	Q7KU28	Q7ku28 drosophila
1197	73.5	1385	2	Q8EF73	Q8ef73 shewanella	1270	73	6.5	825	2	Q9LZA6	Q9lza6 arabidopsis
1198	73.5	1487	2	Q7SEY2	Q7sey2 neurospora	1271	73	6.5	827	2	Q61WN3	Q61wn3 ustilago ma
1199	73.5	1625	2	Q6MVD4	Q6mvd4 neurospora	1272	73	6.5	852	2	Q8IGN7	Q8ign7 drosophila

1273	73	6.5	852	2	Q89607	Q89607 human immun	1346	72.5	6.4	567	2	Q6L3J1	Q6L3j1 solanum dem
1274	73	6.5	878	2	Q9GZ22	Q9gzz2 homo sapien	1347	72.5	6.4	575	2	Q48592	Q48592 arabidopsis
1275	73	6.5	884	2	Q8UKP5	Q8ukp5 agrobacteri	1348	72.5	6.4	575	2	Q39117	Q39117 arabidopsis
1276	73	6.5	918	1	IL6B_HUMAN	P40189 homo sapien	1349	72.5	6.4	627	2	Q6UN14	Q6un14 leishmania
1277	73	6.5	941	2	Q7D410	Q7d410 agrobacteri	1350	72.5	6.4	631	2	P88938	P88938 human herpe
1278	73	6.5	943	2	Q8X0B4	Q8x0b4 neurospora	1351	72.5	6.4	648	2	O14760	O14760 homo sapien
1279	73	6.5	993	2	Q82JC5	Q92jc5 rickettsia	1352	72.5	6.4	673	2	Q7T5C3	Q7t5c3 cercopithe
1280	73	6.5	1016	1	ENG1_SCHPO	Q9ut45 schizosacch	1353	72.5	6.4	685	2	O40935	O40935 human herpe
1281	73	6.5	1104	2	Q9VQP6	Q9vqp6 drosophila	1354	72.5	6.4	691	2	O92608	O92608 human herpe
1282	73	6.5	1163	2	Q8F613	Q8f613 leptospira	1355	72.5	6.4	698	2	Q8UKG8	Q8ukg8 heliothis z
1283	73	6.5	1171	2	Q89DP3	Q89dp3 bradyrhizob	1356	72.5	6.4	708	2	Q73H41	Q73h41 wolbachia p
1284	73	6.5	1204	2	Q7KU29	Q7ku29 drosophila	1357	72.5	6.4	720	2	Q6FEP2	Q6fep2 acinetobact
1285	73	6.5	1225	2	Q72Q54	Q72q54 leptospira	1358	72.5	6.4	729	2	Q9ZU22	Q9zu22 arabidopsis
1286	73	6.5	1233	2	Q9VZA8	Q9vza8 drosophila	1359	72.5	6.4	736	2	Q758X9	Q758x9 ashbya goss
1287	73	6.5	1235	2	Q24315	Q24315 drosophila	1360	72.5	6.4	748	2	Q7PRX2	Q7prx2 anopheles g
1288	73	6.5	1237	2	Q8SSS5	Q8ss85 dictyosteli	1361	72.5	6.4	748	2	Q6R7E1	Q6r7e1 ostreid her
1289	73	6.5	1369	1	NFAS_CHICK	Q42414 gallus gall	1362	72.5	6.4	750	2	Q6NX46	Q6nx46 homo sapien
1290	73	6.5	1439	2	Q75BH9	Q75bh9 ashbya goss	1363	72.5	6.4	753	2	Q80T27	Q80t27 rattus norv
1291	73	6.5	1502	2	Q81S10	Q8is10 dictyosteli	1364	72.5	6.4	762	2	O86AG3	O86ag3 dictyosteli
1292	73	6.5	1583	2	O6C398	Q6c398 yarrowia li	1365	72.5	6.4	764	1	HTR2_HALSA	P71410 halobacteri
1293	73	6.5	1709	2	Q86L43	Q86l43 dictyosteli	1366	72.5	6.4	785	2	Q80T28	Q80t28 rattus norv
1294	73	6.5	1770	2	Q9X3P5	Q9x3p5 caldicellul	1367	72.5	6.4	791	2	Q66VC3	Q66vc3 equid herpe
1295	73	6.5	2179	1	POUG_HRV14	P03303 h genome po	1368	72.5	6.4	795	2	Q80T26	Q80t26 rattus norv
1296	73	6.5	2468	2	Q912M3	Q9i2m3 pseudomonas	1369	72.5	6.4	797	1	VGLX_BHV1B	P28968 equine herp
1297	73	6.5	8545	1	ANCI_CAEEL	Q9n4m4 caenorhabdi	1370	72.5	6.4	797	1	O6DLE0	Q6dle0 equid herpe
1298	73	6.5	8545	2	O6TME3	Q6imp3 caenorhabdi	1371	72.5	6.4	800	1	ASNT_RAT	P41739 rattus norv
1299	72.5	6.4	123	2	O61027	O61027 trypanosoma	1372	72.5	6.4	800	2	Q80T29	Q80t29 rattus norv
1300	72.5	6.4	123	2	P90602	P90602 trypanosoma	1373	72.5	6.4	826	2	Q8V0L5	Q8v0l5 equid herpe
1301	72.5	6.4	229	2	Q6M463	Q6m463 corynebacte	1374	72.5	6.4	829	1	CADG_HUMAN	Q75309 homo sapien
1302	72.5	6.4	233	2	Q8WP51	Q8np51 corynebacte	1375	72.5	6.4	849	2	Q94EF5	Q94ef5 oryza sativ
1303	72.5	6.4	236	1	SLR1_RALSO	P58590 ralstonia s	1376	72.5	6.4	859	2	O8IWC2	O8iwc2 homo sapien
1304	72.5	6.4	253	2	O8EGT2	Q8egt2 streptococ	1377	72.5	6.4	866	2	O6S6W0	Q6s6w0 equid herpe
1305	72.5	6.4	263	2	Q91367	Q91367 brachydanio	1378	72.5	6.4	867	2	O39782	O39782 equid herpe
1306	72.5	6.4	311	2	Q8SV78	Q8sv78 drosophila	1379	72.5	6.4	907	1	VGP3_BBV	P03200 epstein-bar
1307	72.5	6.4	313	2	Q8VCV1	Q8vcv1 mus musculu	1380	72.5	6.4	907	2	Q66537	Q66537 human herpe
1308	72.5	6.4	321	2	Q9XUL6	Q9xul6 caenorhabdi	1381	72.5	6.4	907	2	Q777F0	Q777f0 human herpe
1309	72.5	6.4	332	2	Q8V0L9	Q8v0l9 equid herpe	1382	72.5	6.4	927	2	Q6FXK6	Q6fxk6 candida gla
1310	72.5	6.4	333	2	Q9XJU2	Q99ju2 mus musculu	1383	72.5	6.4	930	2	O9YBL5	O9ybl5 aeropyrum p
1311	72.5	6.4	333	2	Q8C5Q8	Q8c5q8 mus musculu	1384	72.5	6.4	967	2	O8Y8G0	O8y8g0 candida alb
1312	72.5	6.4	337	2	P95738	P95738 staphylococ	1385	72.5	6.4	974	1	EPB3_XENLA	EPB3 xenopus lae
1313	72.5	6.4	337	2	Q9R968	Q9r968 staphylococ	1386	72.5	6.4	974	2	Q6DFG4	Q6dfg4 xenopus lae
1314	72.5	6.4	337	2	Q8VOM1	Q8v0m1 equid herpe	1387	72.5	6.4	992	2	Q7TT14	Q7tt14 mus musculu
1315	72.5	6.4	338	2	Q9CLF8	Q9clf8 pasteurella	1388	72.5	6.4	1002	1	RBMC_MOUSE	RBMc mouse
1316	72.5	6.4	342	2	Q8VOL8	Q8vol8 equid herpe	1389	72.5	6.4	1016	2	O6Y087	O6y087 legionella
1317	72.5	6.4	344	2	Q6AXV5	Q6axv5 rattus norv	1390	72.5	6.4	1021	1	BUB1_YEAST	BuB1 yeast
1318	72.5	6.4	356	2	Q8VOL7	Q8v0l7 equid herpe	1391	72.5	6.4	1060	2	Q86AN6	Q86an6 dictyosteli
1319	72.5	6.4	357	2	Q8VOM2	Q8v0m2 equid herpe	1392	72.5	6.4	1138	2	Q6PHT6	Q6pht6 mus musculu
1320	72.5	6.4	362	2	Q7NSJ3	Q7nsj3 chromobacte	1393	72.5	6.4	1149	2	O6PCL1	O6pcl1 xenopus lae
1321	72.5	6.4	372	2	Q8VOM3	Q8v0m3 equid herpe	1394	72.5	6.4	1150	2	O9HBC4	O9hbc4 homo sapien
1322	72.5	6.4	374	2	Q8VOL6	Q8v0l6 equid herpe	1395	72.5	6.4	1180	2	O8CHH4	O8chh4 lactococcus
1323	72.5	6.4	382	2	Q9XWQ0	Q9xwq0 caenorhabdi	1396	72.5	6.4	1243	2	O6JXK6	O6jkk6 heliothis z
1324	72.5	6.4	383	2	Q702X5	Q702x5 human herpe	1397	72.5	6.4	1284	2	Q8RQU9	Q8rqu9 bacillus gi
1325	72.5	6.4	388	2	Q966V2	Q966v2 halocynthia	1398	72.5	6.4	1490	2	O9U485	O9u485 drosophila
1326	72.5	6.4	389	2	Q8VOM0	Q8v0m0 equid herpe	1399	72.5	6.4	1666	2	Q8MXG2	Q8mxg2 caenorhabdi
1327	72.5	6.4	395	2	Q702Z0	Q702z0 human herpe	1400	72.5	6.4	1737	2	Q9TW28	Q9tw28 dictyosteli
1328	72.5	6.4	402	2	O46226	O46226 caenorhabdi	1401	72.5	6.4	1749	2	O81LM5	O8ilm5 plasmodium
1329	72.5	6.4	436	2	Q91656	Q91656 xenopus lae	1402	72.5	6.4	1761	2	Q81091	Q8i091 plasmodium
1330	72.5	6.4	442	2	Q758Q5	Q758q5 ashbya goss	1403	72.5	6.4	1811	2	Q9QXM9	Q9qxm9 mus musculu
1331	72.5	6.4	452	2	Q7R2X5	Q7r2x5 giardia lam	1404	72.5	6.4	1817	2	Q8TIS9	Q8tis9 methanosarc
1332	72.5	6.4	463	1	MFGM_MOUSE	P21956 mus musculu	1405	72.5	6.4	1854	2	Q7ZA78	Q7za78 candida alb
1333	72.5	6.4	466	2	O6A720	O6a720 propionibac	1406	72.5	6.4	1949	2	Q8MXG3	Q8mxg3 caenorhabdi
1334	72.5	6.4	487	2	Q75JY9	Q75jy9 dictyosteli	1407	72.5	6.4	1975	2	O6Y8G2	O6y8g2 candida alb
1335	72.5	6.4	497	2	Q8WY24	Q8wy24 homo sapien	1408	72.5	6.4	1986	2	Q9QXN0	Q9qxn0 mus musculu
1336	72.5	6.4	498	1	VGLY_LYCVA	P09991 lymphocytic	1409	72.5	6.4	2031	2	Q6Y8G1	Q6y8g1 candida alb
1337	72.5	6.4	518	2	Q72VV7	Q72vv7 leptospira	1410	72.5	6.4	2066	2	Q9DDV8	Q9ddv8 xenopus lae
1338	72.5	6.4	518	2	Q8F9H6	Q8f9h6 leptospira	1411	72.5	6.4	2297	2	Q9HGK6	Q9hgk6 candida alb
1339	72.5	6.4	523	2	Q707A2	Q7q7a2 anopheles g	1412	72.5	6.4	3033	2	Q99IB8	Q99ib8 hepatitis c
1340	72.5	6.4	540	1	CH60_STRCV	Q8kjl8 streptococ	1413	72.5	6.4	5017	2	O6HKW5	O6hkw5 bacillus th
1341	72.5	6.4	540	1	CH60_STRGN	Q8vts8 streptococ	1414	72	6.4	155	2	Q6GE28	Q6ge28 staphylococ
1342	72.5	6.4	548	2	Q8LBM5	Q8lbm5 arabidopsis	1415	72	6.4	158	2	Q9VF17	Q9vfi7 drosophila
1343	72.5	6.4	559	2	O96046	Q96046 drosophila	1416	72	6.4	159	2	Q9YG42	Q9yg42 aeropyrum p
1344	72.5	6.4	563	2	Q72Y40	Q72y40 bacillus ce	1417	72	6.4	171	1	CASK_TRAJA	Q29137 tragulus ja
1345	72.5	6.4	563	2	Q81XF7	Q81xf7 bacillus an	1418	72	6.4	180	2	Q82S04	Q82s04 nitrosomona

1419	72	6.4	182	2	Q17742	Q17742 caenorhabdi
1420	72	6.4	195	2	Q9GKU2	Q9GKU2 macaca fasc
1421	72	6.4	199	1	TNF4_RAT	Q9ZP23 rattus norv
1422	72	6.4	236	2	O55704	O55704 chilo iride
1423	72	6.4	246	2	O14762	O14762 homo sapien
1424	72	6.4	248	2	Q9BPR7	Q9BPR7 bombyx mori
1425	72	6.4	249	2	Q61111	Q61111 drosophila
1426	72	6.4	252	2	Q94UD6	Q94UD6 oryza sativ
1427	72	6.4	269	2	Q813X7	Q813X7 plasmodium
1428	72	6.4	271	2	Q81SH2	Q81SH2 aedes aegypt
1429	72	6.4	275	2	Q8T4Q8	Q8T4Q8 aedes aegypt
1430	72	6.4	275	2	Q9GFP9	Q9GFP9 aedes aegypt
1431	72	6.4	275	2	Q87R16	Q87R16 vibrio para
1432	72	6.4	281	2	Q81SH0	Q81SH0 aedes aegypt
1433	72	6.4	282	2	Q9FSR0	Q9FSR0 oryza sativ
1434	72	6.4	300	1	JAM1_MOUSE	Q88792 mus musculu
1435	72	6.4	300	2	Q8VC39	Q88792 mus musculu
1436	72	6.4	312	2	Q7SFT3	Q7SFT3 neurospora
1437	72	6.4	321	2	Q8S5S4	Q8S5S4 oryza sativ
1438	72	6.4	324	2	Q61735	Q61735 mus musculu
1439	72	6.4	326	2	Q9NFX5	Q9NFX5 ceratitis c
1440	72	6.4	329	2	Q7RX34	Q7RX34 neurospora
1441	72	6.4	345	2	Q691G7	Q691G7 anolis sagr
1442	72	6.4	345	2	Q691M5	Q691M5 anolis sagr
1443	72	6.4	345	2	Q691M6	Q691M6 anolis sagr
1444	72	6.4	345	2	Q691N7	Q691N7 anolis sagr
1445	72	6.4	345	2	Q691U0	Q691U0 anolis sagr
1446	72	6.4	345	2	Q691U2	Q691U2 anolis sagr
1447	72	6.4	345	2	Q691V5	Q691V5 anolis sagr
1448	72	6.4	354	2	Q6PNA3	Q6PNA3 triticum ae
1449	72	6.4	363	2	Q8U043	Q8U043 pyrococcus
1450	72	6.4	369	2	Q9C275	Q9C275 neurospora
1451	72	6.4	369	2	Q7YUQ1	Q7YUQ1 trypanosoma
1452	72	6.4	369	2	Q7YUQ2	Q7YUQ2 trypanosoma
1453	72	6.4	373	2	Q6DE66	Q6DE66 xenopus lae
1454	72	6.4	375	2	Q7TFG9	Q7TFG9 rhesus cyto
1455	72	6.4	382	2	Q81217	Q81217 plasmodium
1456	72	6.4	385	2	Q25331	Q25331 leishmania
1457	72	6.4	399	2	Q62C41	Q62C41 burkholderi
1458	72	6.4	401	2	Q99XV1	Q99XV1 streptococc
1459	72	6.4	406	1	LMF1_MOUSE	P11438 mus musculu
1460	72	6.4	406	2	Q8VH34	Q8VH34 mus musculu
1461	72	6.4	431	2	Q8KAQ7	Q8KAQ7 chlorobium
1462	72	6.4	432	2	Q6A5A0	Q6A5A0 caenorhabdi
1463	72	6.4	432	2	Q7Y0E4	Q7Y0E4 oryza sativ
1464	72	6.4	447	2	Q6V6D1	Q6V6D1 drosophila
1465	72	6.4	449	2	Q6CWX6	Q6CWX6 kluyveromyc
1466	72	6.4	463	2	Q6YHB1	Q6YHB1 ambystoma t
1467	72	6.4	463	2	Q8QQA0	Q8QQA0 epizootic h
1468	72	6.4	469	2	Q7URP8	Q7URP8 candida alb
1469	72	6.4	473	2	Q7JJ47	Q7JJ47 cercopithe
1470	72	6.4	478	2	Q4E598	Q4E598 cercopithe
1471	72	6.4	480	2	Q9VWD5	Q9VWD5 drosophila
1472	72	6.4	481	2	Q13900	Q13900 schizosacch
1473	72	6.4	482	2	Q9XY38	Q9XY38 acanthamoeb
1474	72	6.4	543	2	Q8SSX3	Q8SSX3 suberites d
1475	72	6.4	556	2	Q6DEK7	Q6DEK7 brachydanio
1476	72	6.4	561	2	Q751W4	Q751W4 ashbya gos
1477	72	6.4	563	2	Q8P900	Q8P900 xanthomonas
1478	72	6.4	569	1	STF7_SCHPO	Q10136 schizosacch
1479	72	6.4	592	2	O53538	O53538 mycobacteri
1480	72	6.4	592	2	Q7VEM4	Q7VEM4 mycobacteri
1481	72	6.4	594	2	Q7RX45	Q7RX45 neurospora
1482	72	6.4	601	2	Q6V6S4	Q6V6S4 drosophila
1483	72	6.4	602	2	Q86JM6	Q86JM6 dictyosteli
1484	72	6.4	619	2	Q76P26	Q76P26 dictyosteli
1485	72	6.4	631	2	Q6MZY6	Q6MZY6 homo sapien
1486	72	6.4	636	2	Q6GL09	Q6GL09 xenopus tro
1487	72	6.4	688	1	SLP2_CLOTH	Q08953 clostridium
1488	72	6.4	714	2	Q7U5X6	Q7U5X6 synectococc
1489	72	6.4	733	2	Q7RX10	Q7RX10 neurospora
1490	72	6.4	777	2	Q86JF9	Q86JF9 dictyosteli
1491	72	6.4	780	2	Q9LK78	Q9LK78 arabidopsis
1492	72	6.4	781	2	Q96JM7	Q96JM7 homo sapien
1493	72	6.4	782	2	Q8GX37	Q8GX37 arabidopsis
1494	72	6.4	783	2	O91331	O91331 cercopithe
1495	72	6.4	807	2	Q9VC14	Q9VC14 drosophila
1496	72	6.4	807	2	Q70LC2	Q70LC2 acidianus f
1497	72	6.4	828	2	Q9BQ15	Q9BQ15 homo sapien
1498	72	6.4	847	2	Q6ZQ82	Q6ZQ82 mus musculu
1499	72	6.4	854	2	Q8UNL0	Q8UNL0 human immun
1500	72	6.4	858	2	Q81VES	Q81VES homo sapien

ALIGNMENTS

RESULT 1

Q9UNF4 PRELIMINARY; PRT; 322 AA.

ID Q9UNF4; AC Q9UNF4; DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE Hyaluronic acid receptor (XLKD1).

GN Name=HAR; ORFNames=UNQ230;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Winkelmann J.C., Basu S., Ozdemir E., Blough R.I.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yaneura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA Godowski P.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RT bioinformatics assessment.";

RL Genome Res. 13:2265-2270(2003).

DR EMBL; AF127670; AAD49220.2; -.

DR EMBL; AY358925; AAQ89284.1; -.

DR HSSP; P98066; 107B.

DR GO; GO:0005540; F:hyaluronic acid binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR000538; Link.

DR Pfam; PF00193; Xlink; 1.

DR PRINTS; PR01265; LINKMODULE.

DR ProDom; PD000918; Link; 1.

DR PROSITE; PS00963; LINK_2; 1.

KW Receptor.

SQ SEQUENCE 322 AA; 35213 MW; 8B4D6D623F52D559 CRC64;

Query Match 100.0%; Score 1125; DB 2; Length 322;

Best Local Similarity 100.0%; Pred. No: 3.8e-90;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKECRLGLSLAGKQVET 60

Db 17 TRLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKECRLGLSLAGKQVET 76

QY 61 ALKASFCTCSYGVWDGDFWVLSRISPNPKCGKNGVGLWKPVSQFAAYCYNSSDTWT 120

Db 77 ALKASFCTCSYGVWDGDFWVLSRISPNPKCGKNGVGLWKPVSQFAAYCYNSSDTWT 136

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QY 121 NSCIPETITKDPINFNTOTATOTTEFIIVSDTSYVASPYSTIPAPTTTPPAPASTSIPRR 180
    |||||
Db 137 NSCIPETITKDPINFNTOTATOTTEFIIVSDTSYVASPYSTIPAPTTTPPAPASTSIPRR 196
    |||||
QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAAFKNEAAGFG 218
    |||||
Db 197 KKLICVTEVFMTSTMTSTETEPFVENKAAAFKNEAAGFG 234
    |||||

RESULT 2
Q8TC18
ID Q8TC18 PRELIMINARY; PRT; 322 AA.
AC Q8TC18;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Extracellular link domain containing 1.
GN Name=XLKD1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore S.I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026231; AAH26231.1; -.
DR HSSP; P98066; 107B.
DR Genew; HGNC:14687; XLKD1.
DR GO; GO:0005540; F.hyaluronic acid binding; IEA.
DR GO; GO:0007155; P.cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Link; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS0963; LINK 2; 1.
SQ SEQUENCE 322 AA; 35183 MW; 0B1EDBD76CE4610A CRC64;

Query Match 98.8%; Score 1111; DB 2; Length 322;
Best Local Similarity 99.5%; Pred. No. 6.4e-89;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRLLVQSLRAEELSIOVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQDVET 60
    |||||
Db 17 TRLLVQSLRAEELSIOVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQDVET 76
    |||||

QY 61 ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
    |||||
Db 77 ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
    |||||

RESULT 3
Q9Y5Y7
ID Q9Y5Y7 PRELIMINARY; PRT; 322 AA.
AC Q9Y5Y7;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA Jackson D.G.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
RL receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801(1999).
DR EMBL; AF118108; AAD42764.1; -.
DR HSSP; P98066; 107B.
DR GO; GO:0005887; C.integral to plasma membrane; TAS.
DR GO; GO:0005624; C.membrane fraction; TAS.
DR GO; GO:0004872; F.receptor activity; TAS.
DR GO; GO:0006928; P.cell motility; TAS.
DR GO; GO:0007160; P.cell-matrix adhesion; TAS.
DR GO; GO:0009653; P.morphogenesis; TAS.
DR GO; GO:0009611; P.response to wounding; TAS.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS0963; LINK_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35238 MW; 0BBEA56729CEBFF7 CRC64;

Query Match 98.3%; Score 1106; DB 2; Length 322;
Best Local Similarity 98.6%; Pred. No. 1.8e-88;
Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRLLVQSLRAEELSIOVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQDVET 60
    |||||
Db 17 TRLLVQSLRAEELSIOVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQDVET 76
    |||||

QY 61 ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
    |||||
Db 77 ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
    |||||

RESULT 4
Q6UCB8

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Db 77 ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
    |||||
QY 121 NSCIPETITKDPINFNTOTATOTTEFIIVSDTSYVASPYSTIPAPTTTPPAPASTSIPRR 180
    |||||
Db 137 NSCIPETITKDPINFNTOTATOTTEFIIVSDTSYVASPYSTIPAPTTTPPAPASTSIPRR 196
    |||||
QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAAFKNEAAGFG 218
    |||||
Db 197 KKLICVTEVFMTSTMTSTETEPFVENKAAAFKNEAAGFG 234
    |||||

RESULT 3
Q9Y5Y7
ID Q9Y5Y7 PRELIMINARY; PRT; 322 AA.
AC Q9Y5Y7;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA Jackson D.G.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
RL receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801(1999).
DR EMBL; AF118108; AAD42764.1; -.
DR HSSP; P98066; 107B.
DR GO; GO:0005887; C.integral to plasma membrane; TAS.
DR GO; GO:0005624; C.membrane fraction; TAS.
DR GO; GO:0004872; F.receptor activity; TAS.
DR GO; GO:0006928; P.cell motility; TAS.
DR GO; GO:0007160; P.cell-matrix adhesion; TAS.
DR GO; GO:0009653; P.morphogenesis; TAS.
DR GO; GO:0009611; P.response to wounding; TAS.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS0963; LINK_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35238 MW; 0BBEA56729CEBFF7 CRC64;

Query Match 98.3%; Score 1106; DB 2; Length 322;
Best Local Similarity 98.6%; Pred. No. 1.8e-88;
Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRLLVQSLRAEELSIOVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQDVET 60
    |||||
Db 17 TRLLVQSLRAEELSIOVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQDVET 76
    |||||

QY 61 ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
    |||||
Db 77 ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
    |||||

RESULT 4
Q6UCB8

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ID Q6UC88 PRELIMINARY; PRT; 322 AA.
AC Q6UC88;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Call surface retention sequence binding protein-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;
RA Huang S.-S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,
RA Huang J.S.;
RT "Cloning, expression, characterization and role in autocrine cell
RT growth of cell surface retention sequence binding protein-1.";
RL J. Biol. Chem. 278:43855-43869(2003).
DR EMBL; AY372937; AAQ85130.1; -.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPRO00538; Link.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK 1; UNKNOWN_1.
DR PROSITE; PS0963; LINK 2; 1.
SQ SEQUENCE 322 AA; 35561 MW; 4901DA1BF92648AE CRC64;

Query Match 63.9%; Score 719; DB 2; Length 322;
Best Local Similarity 63.3%; Pred. No. 1.3e-54;
Matches 138; Conservative 31; Mismatches 49; Indels 0; Gaps 0;

QY 1 TRLVQGSRLARAEISIQVSCRIMGTLVSKKANQQLNFTEAKACRLGLSLAGKDQVET 60
DB 17 TRLVQGSRLARAEISIQVSCRIMGTLVSKKANQQLNFTEAKACRLGLSLAGKDQVET 76
QY 61 ALKASFTCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCVNSDWT 120
DB 77 ARKFGFTCSYGVWKNQFVVISRISPNPKCGKNGVGLIWRSLSRHRSYCHNSDDIW 136
QY 121 NSCIPEIITTKDPIFNQTATOTTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPRR 180
DB 137 NSCLPEIITTDPLFNTEATATVTKLWVSDTHSELSDTGPDPVITTVAPPLASTSTPRK 196
QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFG 218
DB 197 RKLCITEAFMDTSAVATERESDIQNRPAFKNEAVGFG 234

RESULT 5
Q99NE4 PRELIMINARY; PRT; 318 AA.
ID Q99NE4;
AC Q99NE4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Hyaluronan receptor precursor.
DE product:extra cellular link domain-containing 1, full insert
GN Name=Xikdi; Synonyms=LYVE-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c; TISSUE=Digestive tract;
RX MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA Banerji S.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein is a lymph-specific
RT receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801(1999).
RN [2]
```

```
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c; TISSUE=Digestive tract;
RX MEDLINE=21276443; PubMed=11278811; DOI=10.1074/jbc.M011004200;
RA Prevo R., Banerji S., Ferguson D.J.P., Clasper S., Jackson D.G.;
RT "Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic
RT endothelium.";
RL J. Biol. Chem. 276:19420-19430(2001).
DR EMBL; AJ311501; CAC33082.1; -.
DR HSSP; P98066; 107B.
DR MGD; MGI:2136348; Xlkdl.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR InterPro; IPRO00538; Link.
DR Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK 1; UNKNOWN_1.
DR PROSITE; PS0963; LINK 2; 1.
KW Receptor; Signal.
FT SIGNAL 1 23
FT CHAIN 24 318
FT SEQUENCE 318 AA; 34641 MW; 1248974A16113330 CRC64;

Query Match 59.5%; Score 669; DB 2; Length 318;
Best Local Similarity 61.0%; Pred. No. 3e-50;
Matches 133; Conservative 28; Mismatches 53; Indels 4; Gaps 3;

QY 1 TRLVQGSRLARAEISIQVSCRIMGTLVSKKANQQLNFTEAKACRLGLSLAGKDQVET 60
DB 17 TRHPVQGDVLVDLIS-TCRIMGVALVGNKNQPNFTEAKACRLGLTLASRDQVES 75
QY 61 ALKASFTCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCVNSDWT 120
DB 76 AQKSGFTCSYGVWGEQFVVISRISPNPKCGKNGVGLIWNAPSSQKFKAYCHNSDWT 135
QY 121 NSCIPEIITTKDPIFNQTATOTTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPRR 180
DB 136 NSCIPEIITTFYPLVDQ--TPATEFVSSSAYLASSPDSTTPVSATT-RAPPLTSMARK 192
QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFG 218
DB 193 TKKICITEVTEPITMATETEAFAVSGAAPKNEAGFG 230

RESULT 6
Q8BHC0 PRELIMINARY; PRT; 318 AA.
ID Q8BHC0;
AC Q8BHC0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Extra cellular link domain-containing 1 (Mus musculus adult male lung
DE cDNA, RIKEN full-length enriched library, clone:1200012G08
DE product:extra cellular link domain-containing 1, full insert
DE sequence).
GN Name=Xikdi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RX MEDLINE=2328257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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SQ SEQUENCE 201 AA; 22219 MW; BAAF34E7EACBBAB3 CRC64;
Query Match 46.3%; Score 520.5; DB 2; Length 201;
Best Local Similarity 64.3%; Pred. No. 1.7e-37;
Matches 101; Conservative 20; Mismatches 33; Indels 3; Gaps 2;

QY 65 SPETCSYGVGVGVFVVISRISPNKCGKGVGLWKPVSROFAAYCYNSSDTWTNSCI 124
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 SPETCSYGVGVGVGVFVVISRISPNKCGKGVGLWKPVSROFAAYCYNSSDTWTNSCI 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 125 PIIITTKDPIFNQTQTATOTTEFIVSDTYSVAS--PYSTI-PAPITTPAPASTSPRK 181
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 PIIIPNDTFNTAPYTTETVNDRTSSSTGSSVMETVTTSLPLATSPKR 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 182 KLICVTEVFMETSTMSTETEPFVNKAAPKNEAAGFG 218
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 KLICITEAPMETSTISTETELVIENRTAFKNEAIGFG 157
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
Q6GM56 PRELIMINARY; PRT; 441 AA.
AC Q6GM56;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE LOC443701 protein (Fragment).
GN Name=LOC443701;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=23188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RL Klein S., Gerhard D.S.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074228; AAF74228.1;
GO; GO:0016020; C:membrane; IEA.
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DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PRO0658; CD44.
DR PRINTS; PRO1265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS00963; LINK_2; 1.
FT NON_TER 1
SQ SEQUENCE 441 AA; 49207 MW; DF9AA596D506D1A1 CRC64;

Query Match 21.4%; Score 241; DB 2; Length 441;
Best Local Similarity 34.3%; Pred. No. 1.2e-12;
Matches 57; Conservative 19; Mismatches 70; Indels 20; Gaps 3;

QY 18 VSCRIMGITLVSKKANQOLNFTAEKACRLGLSLAGKDQVETALKASPETCSYGVGDG 77
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
32 ISCRFGVHFVEKNDYSLNQEDAVKLCGLMTTITIASVAQLBIDFGFETCRYGWIEDR 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 78 FVVISRISPNKCGKGVGLWKPVSROFAAYCYNSSDTWTNSCIPPI----- 127
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
92 -VLIPIRIKPNPICAAANYTGITGLNNESLRVDVVCYNASSETDKSLPVLNLTDFSHN 150
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 128 -ITTKDPIFNQTQTATOTTEFIVSDTYSVASPYSTIPAPITTPAP 172
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 TIDSVDPLDTQIQNSDKSGYQGSV-----TDPAPAMITPDP 188
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
Q6P8A2 PRELIMINARY; PRT; 437 AA.
AC Q6P8A2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Hypothetical protein MGC75816.
GN Name=MGC75816;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RL Klein S., Gerhard D.S.;
```

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RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061327; AAH61327.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR PRINTS; PR00658; CD44.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; Link; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS0963; LINK_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 437 AA; 49108 MW; 7088441D0E138C10 CRC64;

Query Match 20.1%; Score 226; DB 2; Length 437;
Best Local Similarity 34.1%; Pred. No. 2.5e-11;
Matches 61; Conservative 18; Mismatches 78; Indels 22; Gaps 4;

QY 18 VSCRWGTGLVSKKANQQLNFTAEACELLGLSLAGKQDVETALKASFETCSYWGVDG 77
DB 24 ISCRFGVPHVEKYDRYALNREDAIKLCHELNNTTIANLTLMETIAQDIGFETCRYGWIEDR 83

QY 78 FVVISRISPNPKCGKNGVGLIWKVPVGRQPAAYCVNSGSDTWTNSCIP-----E 126
DB 84 -VVIPRIKPNPCAAANYGIFLGNDSRLRYDAYCYNASETDKSCPEVLLNETDLSHK 142

QY 127 IITTKDPIFNQTATQTTFEIVSDSTYSVASPYSTIPAP-----TTTPPA-PAST 175
DB 143 TIDSVDPTLDTQNPRFTQNSKSGDVTDPGAMITPDPGQWDWDIQTGTTDHPGDPFST 201

RESULT 10
CD44 RAT
ID CD44 RAT STANDARD; PRT; 503 AA.
AC P26051; Q99021;
DT 01-MAY-1992 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD44 antigen precursor (phagocytic glycoprotein I) (PGP-I) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-
GN Name=CD44;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BDIX; TISSUE=Pancreas;
RX MEDLINE=91191552; PubMed=1707342; DOI=10.1016/0092-8674(91)90403-L;
RA Guentert U., Hofmann M., Rudy W., Reber S., Zoeller M., Haussmann I.,
RA Matzku S., Wenzel A., Ponta H., Herrlich P.;
RT "A new variant of glycoprotein CD44 confers metastatic potential to
RT rat carcinoma cells.";
RL Cell 65:13-24 (1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stevens J.W., Midura R.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RL [3]
RP SULFATION OF TYR-288.
RX PubMed=962903;
RA Slesman J.P., Rahmsdorf U., Steffen A., Ponta H., Herrlich P.;
RT "CD44 variant exon v5 encodes a tyrosine that is sulphated.";
RL CC
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=2; Synonyms=Long, Meta-1;
IsoId=P26051-1; Sequence=Displayed;
Name=1; Synonyms=Short;
IsoId=P26051-2; Sequence=VSP 005330;
-!- PTM: N-glycosylated (By similarity).
-!- PTM: O-glycosylated; contains Chondroitin sulfate glycans which
can be more or less sulfated (By similarity).
-!- PTM: Phosphorylated; activation of PKC results in the
dephosphorylation of Ser-467 (constitutive phosphorylation site),
and the phosphorylation of Ser-433 (By similarity).
-!- SIMILARITY: Contains 1 Link domain.

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or send an email to license@isb-sib.ch).
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EMBL; M61875; AAA53532.1; -.
DR EMBL; M61874; AAA53534.1; -.
DR EMBL; U52179; AAA97915.1; -.
DR EMBL; U46957; AAA92920.1; -.
DR FIR; B38745; B38745.
DR HSSP; P98066; I7SG.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; XLink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR PROSITE; PS01241; LINK_1; 1.
DR PROSITE; PS0963; LINK_2; 1.
KW Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;
KW Proteoglycan; Pyrrolidone carboxylic acid; Receptor; Signal;
KW Sulfation; Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 503
FT DOMAIN 22 410 CD44 antigen.
FT TRANSMEM 411 431 Extracellular (Potential).
FT DOMAIN 432 503 Potential.
FT DOMAIN 35 124 Cytoplasmic (Potential).
FT DOMAIN 154 162 Link.
FT DOMAIN 228 410 Arg/Lys-rich (basic).
FT MOD_RES 22 22 Stem.
FT MOD_RES 56 122 Pyrrolidone carboxylic acid (Probable).
FT DISULFID 56 122 By similarity.
FT DISULFID 80 100 By similarity.
FT MOD_RES 288 288 Sulfotyrosine (in isoform 2).
FT MOD_RES 433 433 Phosphoserine (by PKC) (By similarity).
FT MOD_RES 467 467 Phosphoserine (By similarity).
FT CARBOHYD 28 28 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 103 103 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 124 124 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 274 274 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 306 306 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 224 385 IATTPWSAHGNTQQRQRTQWNPISHPVLIQTTRMTDID
RNTTSAGHNTQEPFPFNHNYODEBTATTTWADP
NSTTEAATQKEKFNENQKGNPTSPEDSHVTEGTASA
HNNPSSQRMVTTQSDVSWTDFDFFDISHPMGQHGTESK
--> SDGSSMDPRGGFDVTTHGSELA (in isoform
1).
/FTId=VSP 005330.
R -> S (in Ref. 2).
CC CONFLICT 74 74
CC SEQUENCE 503 AA; 55945 MW; FB489D009BD4EE22 CRC64;
Query Match 19.0%; Score 213.5; DB 1; Length 503;

```



```
Best Local Similarity 32.1%; Pred. No. 3.6e-10;
Matches 51; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 4 LVQSLRAEELSIOVSCRMGITLVSKKANQOQLNFTFEAKACRLGLSLAGKQDVETALK 63
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 15 LLQLSLAQOQIDLNITCRVAGVPHVEKNGRYSISRTEADLCFAFNTLPTWQAQMEALR 74
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 64 ASPTCSYGVWGDGFVVISRISPNPKCGKNGVGLWKPVSQFAAYCNSSDTWTNSC 123
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 75 KGFETCRYGFI-EGHVIPRIHPNAICAAANTGVILLASNTSHYDTYCFNASAPLEEDC 133
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 124 IPEIITTKDPIENTQTATQTFEIVSDST-YSVASPYST 161
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 134 -----TSVTDLPNSPDGVPVTITIVNRDGRYSKKGEYRT 167
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 11
O08779 PRELIMINARY; PRT; 780 AA.
AC O08779;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD44 protein.
GN Name-CD44;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BDX; TISSUE=Pancreas;
RA Hofmann M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U96138; AAB54002.1; -.
DR HSP; P98056; 107B.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
DR PROSITE; PS0963; LINK; 2; 1.
SQ SEQUENCE 780 AA; 85917 MW; CC4D35AB1EA7377C CRC64;

Query Match 19.0%; Score 213.5; DB 2; Length 780;
Best Local Similarity 32.1%; Pred. No. 6.2e-10;
Matches 51; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 4 LVQSLRAEELSIOVSCRMGITLVSKKANQOQLNFTFEAKACRLGLSLAGKQDVETALK 63
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 15 LLQLSLAQOQIDLNITCRVAGVPHVEKNGRYSISRTEADLCFAFNTLPTWQAQMEALR 74
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 64 ASPTCSYGVWGDGFVVISRISPNPKCGKNGVGLWKPVSQFAAYCNSSDTWTNSC 123
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 75 KGFETCRYGFI-EGHVIPRIHPNAICAAANTGVILLASNTSHYDTYCFNASAPLEEDC 133
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 124 IPEIITTKDPIENTQTATQTFEIVSDST-YSVASPYST 161
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 134 -----TSVTDLPNSPDGVPVTITIVNRDGRYSKKGEYRT 167
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 12
O07059 PRELIMINARY; PRT; 364 AA.
AC O07059;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
```

```
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glycoprotein CD44s (CD44 protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lumbar spine;
RA Stevens J.W.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Burtfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065147; AAC17117.1; -.
DR EMBL; BC061531; AAB61531.1; -.
DR HSP; P98066; 107B.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRODOM; PD000918; Link; 1.
DR PROSITE; PS01241; LINK; 1.
DR PROSITE; PS0963; LINK; 2; 1.
SQ SEQUENCE 364 AA; 39725 MW; BA249776C4419AA7 CRC64;

Query Match 18.8%; Score 211.5; DB 2; Length 364;
Best Local Similarity 32.1%; Pred. No. 3.7e-10;
Matches 51; Conservative 24; Mismatches 77; Indels 7; Gaps 3;

QY 4 LVQSLRAEELSIOVSCRMGITLVSKKANQOQLNFTFEAKACRLGLSLAGKQDVETALK 63
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 15 LLQLSLAQOQIDLNITCRVAGVPHVEKNGRYSISRTEADLCFAFNTLPTWQAQMEALR 74
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 64 ASPTCSYGVWGDGFVVISRISPNPKCGKNGVGLWKPVSQFAAYCNSSDTWTNSC 123
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 75 KGFETCRYGFI-EGHVIPRIHPNAICAAANTGVILLASNTSHYDTYCFNASAPLEEDC 133
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 124 IPEIITTKDPIENTQTATQTFEIVSDST-YSVASPYST 161
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 134 -----TSVTDLPNSPDGVPVTITIVNRDGRYSKKGEYRT 167
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
```

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RESULT 13
Q98SR5 PRELIMINARY; PRT; 265 AA.
AC Q98SR5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE T cell antigen CD44 isoform b.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Pekin;
RA Chan S.W.S., Warr G.W., Middleton D.L., Higgins D.A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF32869; AAK18277.1; -.
DR HSSP; P98066; 107B.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS0963; LINK 2; 1.
SQ SEQUENCE 265 AA; 29215 MW; 77C176E0A98D081 CRC64;

Query Match 18.8%; Score 211; DB 2; Length 265;
Best Local Similarity 28.4%; Pred. No. 2.8e-10;
Matches 62; Conservative 31; Mismatches 93; Indels 32; Gaps 5;

QY 13 ELSIQVSCRIMGITLVSKANQQLNFTKEAKCRLLGLSLAGKQVETALKASFETCSYG 72
Db 21 ETQFNVSCRYRGVHFVEKNGRYSLTRTEAADLCRALNSTLSTLEQLEKAHELGFETCRYG 80

QY 73 WYGDGFVVISRPNPKCGKNGVGLWKVPVSRQFAAYCYNSSDWTNNSCIP----- 125
Db 81 FV-VGVIVIPRNPYHLCAANTGIYKLSANTTGRYDAYCYNATETRDKACEPIERDTS 139

QY 126 -----EIITTKDP-----IFNTQTATQTTEFIVSDTYSVASPYSTIPAPTT 174
Db 140 FLSNGEIVIDNEDGSRYNADGTRHSGDSSTSGVDENVVSGSGSHDTPVDTSIRRSPPS 199

QY 175 -----TSIPR-----RKKLICVTEVFMETSTWSTE 199
Db 200 YYGSVTFVPHLSDHSGGGEKFFPVTNSDDEISPTSTD 237

RESULT 14
Q90ZL8 PRELIMINARY; PRT; 398 AA.
AC Q90ZL8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE T cell antigen CD44 isoform a.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Pekin;
RA Chan S.W.S., Warr G.W., Middleton D.L., Higgins D.A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029553; AAK40246.1; -.
DR HSSP; P98066; 107B.

Query Match 18.6%; Score 209.5; DB 2; Length 398;
Best Local Similarity 30.1%; Pred. No. 6.1e-10;
Matches 52; Conservative 27; Mismatches 75; Indels 19; Gaps 3;

QY 13 ELSIQVSCRIMGITLVSKANQQLNFTKEAKCRLLGLSLAGKQVETALKASFETCSYG 72
Db 21 ETQFNVSCRYRGVHFVEKNGRYSLTRTEAADLCRALNSTLSTLEQLEKAHELGFETCRYG 80

QY 73 WYGDGFVVISRPNPKCGKNGVGLWKVPVSRQFAAYCYNSSDWTNNSCIP----- 125
Db 81 FV-VGVIVIPRNPYHLCAANTGIYKLSANTTGRYDAYCYNATETRDKACEPIERDTS 139

QY 126 -----EIITTKDP-----IFNTQTATQTTEFIVSDTYSVASPYSTIPAPTT 167
Db 140 FLSNGEIVIDNEDGSRYNADGTRHSGDSSTSGVDENVVSGSGSHDTPVDTS 192

RESULT 15
CD44_MOUSE STANDARD; PRT; 778 AA.
AC P15379; Q05732; Q61395; Q62060; Q62061; Q62062; Q62063; Q62408;
AC Q62409; Q64296; Q99J14; Q9QYX8;
DT 01-APR-1990 (Rel. 14, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-
DE 24).
GN Name=Cd44;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 4; 6; 7 AND 12).
RC STRAIN=DBA/2; TISSUE=Lung;
RX MEDLINE=93107170; PubMed=1469058; DOI=10.1083/jcb.119.6.1711;
RA He Q., Lesley J., Hyman R., Ishihara K., Kincade P.W.;
RT "Molecular isoforms of murine CD44 and evidence that the membrane
RT proximal domain is not critical for hyaluronate recognition.";
RL J. Cell Biol. 119:1711-1719(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RX MEDLINE=90038499; PubMed=2681416;
RA Zhou D.F.H., Ding J.F., Picker L.J., Bargatze R.F., Butcher E.C.,
RA Goeddel D.V.;
RT "Molecular cloning and expression of Pgp-1. The mouse homolog of the
RT human H-CAM (Hermes) lymphocyte homing receptor.";
RL J. Immunol. 143:3390-3395(1989).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RX MEDLINE=90046829; PubMed=2682651;
RA Nottenburg C., Rees G., St John T.;
RT "Isolation of mouse CD44 cDNA: structural features are distinct from
RT the primate cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8521-8525(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20318634; PubMed=10859330;
RA Wittig B.M., Johansson B., Zoeller M., Schwaerzler C., Guenther U.;

```

RT "Abrogation of experimental colitis correlates with increased
RT apoptosis in mice deficient for CD44 variant exon 7 (CD44v7).";
RL J. Exp. Med. 191:2053-2064(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 13)
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uddin T.B., Toehyuk S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchan J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 13)
RX STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKensie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wegner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [7]
RP SEQUENCE OF 8-778 FROM N.A. (ISOFORM 13).
RX MEDLINE=90094420; PubMed=2403559;
RA Wolffe E.J., Gause W.C., Palfrey C.M., Holland S.M., Steinberg A.D.,
RA August J.T.,
RT "The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell
RT surface antigen and proteoglycan core/link proteins.";
RL J. Biol. Chem. 265:341-347(1990).
RN [8]
RP SEQUENCE OF 224-637 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).
RX STRAIN=GR;
MEDLINE=933219085; PubMed=8464707;
RA Toelig C., Hofmann M., Herrlich P., Ponta H.,
RT "Splicing choice from ten variant exons establishes CD44

RT variability.";
RL Nucleic Acids Res. 21:1225-1229(1993).
RN [9]
RP SEQUENCE OF 224-637 FROM N.A. (ISOFORM 9).
RX STRAIN=BALB/c;
MEDLINE=93286043; PubMed=8509359;
RA Screation G.R., Bell M.V., Bell J.I., Jackson D.G.,
RT "The identification of a new alternative exon with highly restricted
RT tissue expression in transcripts encoding the mouse Pgp-1 (CD44)
RT homing receptor. Comparison of all 10 variable exons between mouse,
RT human, and rat.";
RL J. Biol. Chem. 268:12235-12238(1993).
RN [10]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11).
RX STRAIN=Swiss Webster;
MEDLINE=96355396; PubMed=8702806; DOI=10.1074/jbc.271.34.20603;
RA Yu Q., Toole B.P.,
RT "A new alternatively spliced exon between v9 and v10 provides a
RT molecular basis for synthesis of soluble CD44.";
RL J. Biol. Chem. 271:20603-20607(1996).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=13;
CC Name=1;
CC IsoId=P15379-14; Sequence=Displayed;
CC Name=2;
CC IsoId=P15379-7; Sequence=VSP_007329;
CC Name=3;
CC IsoId=P15379-8; Sequence=VSP_007330;
CC Name=4; Synonyms=M2;
CC IsoId=P15379-4; Sequence=VSP_007331;
CC Name=5;
CC IsoId=P15379-9; Sequence=VSP_007332;
CC Name=6; Synonyms=M3;
CC IsoId=P15379-5; Sequence=VSP_005326;
CC Name=7; Synonyms=M4;
CC IsoId=P15379-6; Sequence=VSP_005327;
CC Name=8;
CC IsoId=P15379-10; Sequence=VSP_007330, VSP_007334;
CC Name=9;
CC IsoId=P15379-11; Sequence=VSP_007332, VSP_007335;
CC Name=10;
CC IsoId=P15379-12; Sequence=VSP_007336, VSP_007337;
CC Name=11;
CC IsoId=P15379-13; Sequence=VSP_007338, VSP_007339;
CC Name=12; Synonyms=M1;
CC IsoId=P15379-3; Sequence=VSP_005328;
CC Name=13; Synonyms=M0;
CC IsoId=P15379-2; Sequence=VSP_005329, VSP_007333;
CC -!- PTM: N-glycosylated (By similarity).
CC -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which
CC can be more or less sulfated (By similarity).
CC -!- PTM: Phosphorylated; activation of PKC results in the
CC dephosphorylation of Ser-742 (constitutive phosphorylation site),
CC and the phosphorylation of Ser-708 (By similarity).
CC -!- POLYMORPHISM: Two allelic forms of this glycoprotein, PGP-1.1 and
CC PGP-1.2, have been reported. The expressed product is PGP-1.1 (Ly-
CC 24.1).
CC -!- SIMILARITY: Contains 1 Link domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X66084; CAA46883.1; --.

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DR EMBL; X66083; CAA46882.1; -
DR EMBL; X66082; CAA46881.1; -
DR EMBL; X66081; CAA46880.1; -
DR EMBL; M30655; AAA39922.1; -
DR EMBL; M27129; AAA37406.1; -
DR EMBL; M27130; AAA37407.1; -
DR EMBL; AJ251594; CAB61888.1; -
DR EMBL; BC005676; AAH05676.1; -
DR EMBL; AK045226; BAC32269.1; -
DR EMBL; J05163; AAA39923.1; -
DR EMBL; X69724; CAA49380.1; -
DR EMBL; LI3611; AAA37145.1; -

Query Match      18.6%; Score 209.5; DB 1; Length 778;
Best Local Similarity 32.7%; Pred. No. 1.4e-09;
Matches 52; Conservative 25; Mismatches 75; Indels 7; Gaps 3;

QY 4 LVQGSIRAEELSIQVSCRIMGITLVSKKANQQLNFTAEKACRLILGLSLAGKQVETALK 63
Db 14 LLQLSLAHQQIDILNVTCTRVAGVFHVEKNGRYSISRTEAADLCOAFNSTLPTWDQMKLALS 73
QY 64 ASFETCSYGVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDWTWNSC 123
Db 74 KGFETCRYGFI-EGNVVPIRIHPNAICAAAHHTGVYILVTSNTSHYDTYCFNASAPPEDC 132
QY 124 IPEIITTKDPPIENTQTATOTTEFIVSDST-YSVASPYST 161
Db 133 -----TSVTDLNPSFDGVPVTITIVNRDGTTRYSKKGEYRT 166
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Search completed: October 5, 2005, 17:31:52
Job time : 114.256 secs

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OM protein - protein search, using sw model

Run on: October 5, 2005, 17:16:37 ; Search time 20.5889 Seconds
(without alignments)
1018.766 Million cell updates/sec

Title: US-10-063-510-6_COPY_17_234

Perfect score: 1125
Sequence: 1 TRLLVQGSURABELSIQVSC.....ETEPFVENKAAPKNEAGFG 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR 79:*

1: piri:*

2: piri2:*

3: piri3:*

4: piri4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213.5	19.0	503	B38745	cell adhesion mole
2	209.5	18.6	363	A37009	CD44 homolog membr
3	207	18.4	362	A35616	T-cell surface gly
4	203.5	18.1	362	A30901	lymphocyte adhesio
5	202	18.0	742	A47195	lymphocyte homing
6	199.5	17.7	493	S13530	CD44E protein, epi
7	198.5	17.6	365	A34424	CD44 membrane glyc
8	198.5	17.6	426	JH0518	lymphocyte homing
9	197	17.5	361	JH0417	cell adhesion mole
10	196.5	17.5	699	I37369	epican - human
11	196	17.4	395	I77371	CD44R5 - human
12	194	17.2	351	S45305	CD44 antigen precu
13	194	17.2	366	A53286	cell-surface glyco
14	183.5	16.3	359	S24240	lymphocyte surface
15	145.5	12.9	3562	A47171	chondroitin sulfat
16	145	12.9	277	A41735	hyaluronate-bindin
17	144	12.8	275	JC6506	tumor necrosis fac
18	143	12.7	2109	I50421	aggrecan precursor
19	137	12.2	276	A47290	TSG-6 homolog PS4
20	131.5	11.7	2124	A28452	proteoglycan core
21	131	11.6	2132	A55182	aggrecan precursor
22	130.5	11.6	883	S27653	brevican precursor
23	130.5	11.6	2415	A39086	aggrecan precursor
24	128	11.4	2327	T42630	aggrecan - bovine
25	127.5	11.3	883	S49126	brevican precursor
26	120.5	10.7	912	A54423	brevican precursor
27	118	10.5	1340	A39808	proteoglycan core
28	116	10.3	2397	A55535	versican precursor
29	115	10.2	370	S29139	aggrecan - pig (fr

30	115	10.2	1643	2	T14274	versican precursor
31	115	10.2	3381	2	T42389	versican precursor
32	112.5	10.0	340	2	JC7505	brain link protein
33	111	9.9	2409	1	A60979	versican precursor
34	109.5	9.7	1257	2	S28764	neurocan precursor
35	109	9.7	1069	2	T42681	hypothetical prote
36	108	9.6	354	1	LKHU	proteoglycan link
37	107	9.5	355	1	LKCH	proteoglycan link
38	107	9.5	371	2	A53908	brevican precursor
39	107	9.5	408	1	LKRT2	proteoglycan link
40	107	9.5	1268	2	S2781	neurocan - mouse
41	105.5	9.4	113	2	A5885	chondroitin sulfat
42	104.5	9.3	862	2	S43922	versican - pig-tai
43	104	9.2	354	1	S04243	proteoglycan link
44	104	9.2	354	1	S42938	proteoglycan link
45	102	9.1	739	2	T21769	hypothetical prote
46	101.5	9.0	380	2	T28081	hypothetical prote
47	101	9.0	708	2	T19474	hypothetical prote
48	100	8.9	378	2	I46268	brevican precursor
49	97	8.6	390	1	Q0BE77	glycoprotein I pre
50	96	8.5	796	2	T21460	hypothetical prote
51	92.5	8.2	851	2	T22696	hypothetical prote
52	92	8.2	846	2	T21700	hypothetical prote
53	91	8.1	645	2	T29818	hypothetical prote
54	91	8.1	747	2	T34329	hypothetical prote
55	90	8.0	388	2	S36500	E2 protein - human
56	90	8.0	402	2	S73773	dihydrolipoamide a
57	89.5	8.0	411	2	A33664	96K lysosomal memb
58	89.5	8.0	518	2	T49778	hypothetical prote
59	89	7.9	307	1	GSFF3	salivary glue prot
60	89	7.9	416	1	A31959	lysosome-associate
61	89	7.9	429	1	JC5861	endo-1,4-beta-xyla
62	89	7.9	517	2	T20658	probable zinc meta
63	88.5	7.9	770	2	T22808	hypothetical prote
64	88.5	7.9	1101	2	S15271	endoglucanase C 15
65	88	7.8	456	2	T31483	hypothetical prote
66	88	7.8	602	2	AD2067	hypothetical prote
67	88	7.8	1229	2	T25697	hypothetical prote
68	87.5	7.8	1085	2	S40476	Ca(2+) -sensing rec
69	87	7.7	235	2	PC2022	mucin like protein
70	87	7.7	721	2	B50487	hypothetical prote
71	87	7.7	1506	2	T30886	integumentary muc
72	86.5	7.7	400	1	A28172	spasmolysin precu
73	86.5	7.7	477	2	S53362	mucin 5AC (clone J
74	86.5	7.7	768	2	T00073	hypothetical prote
75	86.5	7.7	909	1	ORXLL2	LDL receptor 2 pre
76	86.5	7.7	1007	2	T24643	hypothetical prote
77	86.5	7.7	2616	2	A57096	nudel protein prec
78	85.5	7.6	786	2	T16509	hypothetical prote
79	85.5	7.6	895	2	T02597	Mutator-like trans
80	85.5	7.6	1367	1	S48478	glucan 1,4-alpha-g
81	85	7.6	265	2	T33695	hypothetical prote
82	85	7.6	449	2	T33257	hypothetical prote
83	85	7.6	569	2	A11347	hypothetical prote
84	85	7.6	627	2	G86860	serine/threonine p
85	85	7.6	660	2	JW0067	chitinase (EC 3.2.
86	85	7.6	1016	2	H71460	probable outer mem
87	85	7.6	1162	2	T21557	hypothetical prote
88	84.5	7.5	752	2	E72616	probable membrane
89	84.5	7.5	1161	2	S77180	hypothetical prote
90	84	7.5	262	2	S76772	AP2-containing DNA
91	84	7.5	335	2	H96667	mucin JUL7 - human
92	84	7.5	543	2	S35047	mucin FIM-C.1 - Af
93	84	7.5	662	2	A45155	hypothetical prote
94	84	7.5	927	2	T24031	mannan endo-1,4-be
95	84	7.5	1331	2	A48954	amylopullulanase P
96	84	7.5	1362	2	A75207	xylanase - Caldice
97	84	7.5	1779	2	T31085	mucin-like glycop
98	84	7.5	1832	2	T11113	mucin 2 precursor,
99	84	7.5	3020	2	A43932	mucin - rhesus mac
100	83.5	7.4	216	2	I51920	mucin 5AC (clone J
101	83.5	7.4	279	2	S53363	protein M01E10.2 [
102	83.5	7.4	1286	2	A88396	

103	83	7.4	409	2	S44346	RAD23 protein homo	176	77.5	6.9	514	2	J01317	activin receptor p
104	83	7.4	605	2	S48940	hypothetical prote	177	77.5	6.9	592	2	T34446	hypothetical prote
105	83	7.4	977	2	T18232	hypothetical prote	178	77.5	6.9	1050	2	T31853	hypothetical prote
106	82.5	7.3	383	1	S15624	E2 protein - huma	179	77.5	6.9	1127	2	E86386	probable mutator-1
107	82.5	7.3	726	2	S67044	Nfil protein - yea	180	77.5	6.9	2761	2	T21064	hypothetical prote
108	82.5	7.3	825	2	S62042	probable membrane	181	77	6.8	350	2	E75341	peptidyl-prolyl ci
109	82.5	7.3	1206	2	S24407	formin isoform IV	182	77	6.8	453	2	F75206	maltose-binding pe
110	82.5	7.3	1407	2	T18381	latrophilin-2 (spl	183	77	6.8	598	2	T22610	hypothetical prote
111	82.5	7.3	1420	2	T18385	latrophilin-2 (spl	184	77	6.8	639	2	T33166	hypothetical prote
112	82.5	7.3	1422	2	T18383	latrophilin-2, spl	185	77	6.8	771	2	JC7388	M83 protein - huma
113	82.5	7.3	1435	2	T18387	latrophilin-2 (spl	186	77	6.8	1092	1	JN0635	neural cell adhesi
114	82.5	7.3	1450	2	T18382	latrophilin-2 (spl	187	77	6.8	1513	2	A54895	mucin 2, intestina
115	82.5	7.3	1463	2	T18386	latrophilin-2 (spl	188	77	6.8	187	2	T30826	nascent polypeptid
116	82.5	7.3	1465	2	T18384	latrophilin-2 (spl	189	76.5	6.8	2187	2	T30826	hypothetical prote
117	82.5	7.3	1468	2	S11515	latrophilin-2 (spl	190	76.5	6.8	349	2	T43457	hypothetical prote
118	82.5	7.3	1478	2	T18388	formin - mouse	191	76.5	6.8	433	2	H84120	hypothetical prote
119	82	7.3	389	2	T33340	hypothetical prote	192	76.5	6.8	505	2	B46629	mucin 6, gastric (
120	82	7.3	463	2	T38444	hypothetical prote	193	76.5	6.8	542	2	T139540	chitinase (EC 3.2.
121	82	7.3	476	2	A46118	myosin-binding pro	194	76.5	6.8	623	2	T18892	hypothetical prote
122	82	7.3	693	2	T19551	mucin-like protein	195	76.5	6.8	658	2	T39500	serine/threonine-s
123	82	7.3	973	2	A97522	ribonuclease E, RN	196	76.5	6.8	658	2	S60170	protein kinase Pak
124	82	7.3	977	2	AC2741	ribonuclease E (im	197	76.5	6.8	718	2	T29708	hypothetical prote
125	81.5	7.2	386	2	B71212	protein containing	198	76.5	6.8	750	2	T42614	probable envelope
126	81.5	7.2	584	2	T19061	hypothetical prote	199	76.5	6.8	1023	2	JC4013	major acidic nucle
127	81.5	7.2	860	2	AG1612	DNA mismatch repai	200	76	6.8	1672	2	C81675	polymorphic membra
128	81.5	7.2	1216	2	P88473	protein F40H6.5 [i	201	76	6.8	167	2	A33532	mucin SMUC-40 - hu
129	81.5	7.2	1513	2	T23681	hypothetical prote	202	76	6.8	243	2	B41710	promastigote surfa
130	81.5	7.2	1777	2	T23469	hypothetical prote	203	76	6.8	340	2	AH0940	probable ABC trans
131	81.5	7.2	3175	1	RRWVEV	genome polyprotein	204	76	6.8	368	2	S36564	E2 protein - human
132	81	7.2	225	2	S53649	ribosomal protein	205	76	6.8	382	2	B88561	protein F58A4.7b [
133	81	7.2	967	2	S66852	hypothetical prote	206	76	6.8	389	2	A47013	butanol dehydrogen
134	81	7.2	1128	2	A49960	bud emergence prot	207	76	6.8	389	2	E97305	NADH-dependent but
135	81	7.2	1537	2	S53465	flocculation prote	208	76	6.8	532	2	T28784	hypothetical prote
136	81	7.2	1609	2	S25345	probable membrane	209	76	6.8	549	2	T49298	hypothetical prote
137	80.5	7.2	148	1	S07723	immediate-early se	210	76	6.8	569	2	B84470	zonalactin - mouse
138	80.5	7.2	391	1	S15617	E2 protein - human	211	76	6.8	576	2	S59829	hypothetical prote
139	80.5	7.2	441	2	T31482	hypothetical prote	212	76	6.8	592	2	T16725	hypothetical prote
140	80.5	7.2	742	2	T33514	hypothetical prote	213	76	6.8	1251	2	T21389	hypothetical prote
141	80.5	7.2	798	2	T32448	hypothetical prote	214	76	6.8	1360	2	T33922	hypothetical prote
142	80.5	7.2	896	2	T22061	hypothetical prote	215	76	6.8	1489	2	G71406	probable retroviro
143	80.5	7.2	2225	2	T26063	hypothetical prote	216	75.5	6.7	430	1	A46216	transcription fact
144	80	7.1	725	2	A41258	a-agglutinin core	217	75.5	6.7	468	2	A55116	vacuolar ATPase (E
145	80	7.1	881	2	S56032	probable membrane	218	75.5	6.7	496	2	B41322	N-acetylmuramoyl-L
146	79.5	7.1	354	2	T46324	microfilament shea	219	75.5	6.7	511	1	VGBEF4	glycoprotein C - h
147	79.5	7.1	860	2	AC1250	DNA mismatch repai	220	75.5	6.7	609	2	G87496	peptidase, M23/M37
148	79.5	7.1	3570	2	T45025	mucin MUC5B, trach	221	75.5	6.7	665	2	G97213	probable membrane-
149	79	7.0	249	2	G84781	hypothetical prote	222	75.5	6.7	737	1	S64767	probable serine/th
150	79	7.0	339	2	T25562	hypothetical prote	223	75.5	6.7	793	2	AH1094	probable peptidogl
151	79	7.0	352	2	T51659	myb-related trans	224	75.5	6.7	796	2	E96654	hypothetical prote
152	79	7.0	359	2	T13478	hypothetical prote	225	75.5	6.7	940	2	D89723	protein F39D8.1b [
153	79	7.0	410	1	B31959	lysosome-associate	226	75.5	6.7	945	2	T21998	hypothetical prote
154	79	7.0	410	1	JC4317	lysosome-associate	227	75.5	6.7	3375	2	T19821	hypothetical prote
155	79	7.0	575	2	T21775	hypothetical prote	228	75	6.7	262	2	T33597	hypothetical prote
156	78.5	7.0	164	2	I53641	mucin SAC - human	229	75	6.7	388	2	T16861	hypothetical prote
157	78.5	7.0	232	2	A60095	larval glue protei	230	75	6.7	407	2	T26938	hypothetical prote
158	78.5	7.0	294	2	A37232	mucin, tracheal (A	231	75	6.7	475	2	E84745	probable splicing
159	78.5	7.0	322	2	A53715	apomucin precursor	232	75	6.7	482	2	T22754	hypothetical prote
160	78.5	7.0	567	2	A57088	nucleoporin-like p	233	75	6.7	709	2	T28712	hypothetical prote
161	78.5	7.0	577	2	G89430	protein K02E2.3 [i	234	75	6.7	860	2	JC4566	chitinase (EC 3.2.
162	78.5	7.0	825	2	T29634	hypothetical prote	235	75	6.6	909	1	QRXLL1	LDL receptor 1 pre
163	78.5	7.0	1420	2	T17158	CL2AB protein - ra	236	75	6.6	998	2	S37627	protein-tyrosine k
164	78.5	7.0	1435	2	T46611	CL2AB protein - ra	237	75	6.6	1075	2	S48992	flocculation prote
165	78.5	7.0	1452	2	T17157	CL2BB protein - ra	238	75	6.6				
166	78.5	7.0	1463	2	T17159	CL2AC protein - ra	239	74.5	6.6				
167	78.5	7.0	1467	2	T17160	CL2BA protein - ra	240	74.5	6.6				
168	78.5	7.0	1478	2	T17185	CL2BC protein - ra	241	74.5	6.6				
169	78.5	7.0	1487	2	T14324	alpha-latrototoxin r	242	74.5	6.6				
170	78	6.9	253	2	S76719	hypothetical prote	243	74.5	6.6				
171	78	6.9	293	2	G87018	probable membrane	244	74.5	6.6				
172	78	6.9	430	2	B84684	hypothetical prote	245	74.5	6.6				
173	78	6.9	530	2	A45690	transactivator EBN	246	74.5	6.6				
174	78	6.9	1091	1	IUCHNL	neural cell adhesi	247	74.5	6.6				
175	78	6.9	1955	1	AGCH	agrin precursor -	248	74.5	6.6				

249	74.5	6.6	1388	2	A53317	collagen alpha 1(X	322	72.5	6.4	797	1	VBEX1	glycoprotein x pre
250	74.5	6.6	1838	1	CGHU1V	collagen alpha 1(V	323	72.5	6.4	867	2	T45463	membrane glycoprot
251	74.5	6.6	2688	2	I49477	alpha-A-crystallin	324	72.5	6.4	907	1	QOBZ21	membrane antigen g
252	74	6.6	147	2	S09762	hypothetical prote	325	72.5	6.4	930	2	B72537	hypothetical prote
253	74	6.6	223	2	T21930	hypothetical prote	326	72.5	6.4	1021	2	S64506	protein kinase BUS
254	74	6.6	384	2	T21929	hypothetical prote	327	72.5	6.4	1180	2	E86719	hypothetical prote
255	74	6.6	397	2	E97176	N-terminal domain	328	72.5	6.4	1367	2	A59235	unconventional myo
256	74	6.6	417	2	T20327	hypothetical prote	329	72.5	6.4	1367	2	T33216	hypothetical prote
257	74	6.6	418	2	T16713	hypothetical prote	330	72	6.4	159	2	F72758	hypothetical prote
258	74	6.6	515	2	AD1162	flagellar motor sw	331	72	6.4	182	2	T30078	hypothetical prote
259	74	6.6	518	2	G84961	protein F59A7.8 [i	332	72	6.4	199	2	JE0351	OX40 ligand protei
260	74	6.6	542	2	S64030	probable membrane	333	72	6.4	236	2	T03041	hypothetical prote
261	74	6.6	586	2	S66697	probable membrane	334	72	6.4	246	2	PC4397	hypothetical prote
262	74	6.6	600	2	T06292	hypothetical prote	335	72	6.4	324	2	S36646	mucin 3 T10 - huma
263	74	6.6	906	2	G90281	conserved hypotet	336	72	6.4	405	2	A60534	integrin-associate
264	74	6.6	1047	2	A55617	transcript precurs	337	72	6.4	481	2	T38149	P2B/LAMP-1 precurs
265	74	6.6	2414	2	A54277	transcription adap	338	72	6.4	482	2	A44997	pre-mrna splicing
266	73.5	6.5	263	2	T38003	hypothetical ser-t	339	72	6.4	576	2	T38293	merozoite surface
267	73.5	6.5	290	2	S66355	lectin-related sto	340	72	6.4	592	2	D70863	hypothetical serin
268	73.5	6.5	358	2	AD2378	hypothetical prote	341	72	6.4	688	2	T18263	hypothetical prote
269	73.5	6.5	371	2	S20075	promastigote surfa	342	72	6.4	1176	2	T49482	S-layer protein -
270	73.5	6.5	447	2	A39321	mucin - rat (fragm	343	72	6.4	1203	2	T17415	hypothetical prote
271	73.5	6.5	451	2	S71754	cellular hepatitis	344	72	6.4	1367	2	S51959	mycelial surface a
272	73.5	6.5	484	1	A24994	cellulose 1,4-beta	345	72	6.4	1419	2	T30531	hypothetical prote
273	73.5	6.5	511	1	VBBIK	glycoprotein C - h	346	72	6.4	1489	2	T31108	agglutinin-like ad
274	73.5	6.5	542	2	T19952	hypothetical prote	347	72	6.4	1723	2	H86557	cyst germination s
275	73.5	6.5	575	2	S29315	chaperonin 60 - cu	348	72	6.4	1723	2	E72067	polymorphic membra
276	73.5	6.5	595	2	A42086	CD30 antigen precu	349	72	6.4	1732	2	C81601	polymorphic membra
277	73.5	6.5	601	2	H90270	hypothetical prote	350	72	6.4	2526	2	T20531	hypothetical prote
278	73.5	6.5	626	2	AB1328	probable peptidogl	351	72	6.4	2722	2	T20532	hypothetical prote
279	73.5	6.5	708	2	F87245	penicillin-binding	352	72	6.4	2738	2	E88320	protein F07A11.6 [
280	73.5	6.5	806	2	E69424	hypothetical prote	353	72	6.4	2971	2	T08026	hypothetical prote
281	73.5	6.5	866	2	T45462	membrane glycoprot	354	71.5	6.4	141	2	A38196	non-structural hyp
282	73.5	6.5	905	2	T02205	Lu-ECAM-1 protein	355	71.5	6.4	152	2	T15170	hypothetical prote
283	73.5	6.5	976	2	A87576	peptidase, M16 fam	356	71.5	6.4	152	2	T28759	hypothetical prote
284	73.5	6.5	989	2	T47503	hypothetical prote	357	71.5	6.4	162	2	C84948	NADH2 dehydrogenas
285	73.5	6.5	1004	2	T38074	hypothetical prote	358	71.5	6.4	281	2	T49537	hypothetical prote
286	73.5	6.5	1016	2	T19006	ankyrin related pr	359	71.5	6.4	305	2	AB2149	hypothetical prote
287	73.5	6.5	2232	2	T34434	hypothetical prote	360	71.5	6.4	313	2	AH0734	probable bacteriop
288	73.5	6.5	3176	2	CGHU3A	collagen alpha 3(V	361	71.5	6.4	363	2	T25278	hypothetical prote
289	73	6.5	260	2	I50109	gastrulation prote	362	71.5	6.4	477	2	T32938	hypothetical prote
290	73	6.5	327	2	S20074	promastigote surfa	363	71.5	6.4	496	2	E90181	hypothetical prote
291	73	6.5	481	2	T51044	related to spore c	364	71.5	6.4	499	2	A12449	hypothetical prote
292	73	6.5	486	2	S66097	cell-cycle protein	365	71.5	6.4	540	2	H98086	hypothetical prote
293	73	6.5	492	1	CHBOA3	gamma-aminobutyric	366	71.5	6.4	540	2	G95222	chaperonin GroEL [
294	73	6.5	528	2	S69589	hypothetical prote	367	71.5	6.4	675	2	T47378	chaperonin, 60 kDa
295	73	6.5	550	2	C75557	hypothetical prote	368	71.5	6.4	755	2	T20950	probable transposa
296	73	6.5	600	2	E72027	phosphoenolpyruvat	369	71.5	6.4	822	2	JC4076	hypothetical prote
297	73	6.5	600	2	A86597	phosphoenolpyruvat	370	71.5	6.4	882	2	T01168	dextranase (EC 3.2
298	73	6.5	639	2	T13151	adaptor protein CM	371	71.5	6.4	1042	2	T48801	hypothetical prote
299	73	6.5	681	2	S33316	structural protein QM	372	71.5	6.4	1166	2	S37692	hypothetical prote
300	73	6.5	728	2	T20561	hypothetical prote	373	71.5	6.4	1557	2	D41214	probable tumor sup
301	73	6.5	771	2	T34376	hypothetical prote	374	71.5	6.4	1630	2	C41214	protein-tyrosine-p
302	73	6.5	781	2	T49472	hormone-sensitive	375	71	6.3	98	2	S53367	protein-tyrosine-p
303	73	6.5	814	2	T33140	hypothetical prote	376	71	6.3	240	2	T33698	mucin 5AC (clone M
304	73	6.5	825	2	T48431	hypothetical prote	377	71	6.3	292	2	S24169	hypothetical prote
305	73	6.5	884	2	AE3166	ATP-dependent DNA	378	71	6.3	304	2	T15922	mucin - rat
306	73	6.5	918	2	A36337	membrane glycoprot	379	71	6.3	343	2	S75435	hypothetical prote
307	73	6.5	993	2	F97717	hypothetical prote	380	71	6.3	349	2	T05857	hypothetical prote
308	73	6.5	1016	2	T41720	hypothetical prote	381	71	6.3	378	2	S00842	leukosialin precur
309	73	6.5	1235	2	T13710	protein-tyrosine k	382	71	6.3	379	1	S71571	alcohol dehydrogen
310	73	6.5	2179	1	GNNYH4	genome polyprotein	383	71	6.3	384	2	A41710	promastigote surfa
311	73	6.5	2468	2	A83412	hypothetical prote	384	71	6.3	410	1	S68153	cellulase (EC 3.2.
312	72.5	6.4	263	2	I51225	snail protein - z	385	71	6.3	415	2	A35560	lysosomal membrane
313	72.5	6.4	321	2	T26153	hypothetical prote	386	71	6.3	416	2	T20448	hypothetical prote
314	72.5	6.4	382	2	T27058	hypothetical prote	387	71	6.3	534	2	G97703	hypothetical prote
315	72.5	6.4	463	1	A3647M	milk fat globule m	388	71	6.3	626	1	NBHUIA	platelet glycoprot
316	72.5	6.4	498	1	VGXPLM	surface glycoprote	389	71	6.3	727	2	A88131	protein F10G7.9 [i
317	72.5	6.4	560	2	T32661	hypothetical prote	390	71	6.3	738	2	I40719	isocitrate dehydro
318	72.5	6.4	575	2	S39484	DNA-binding protei	391	71	6.3	739	1	A34873	transcription facc
319	72.5	6.4	648	2	PC4395	mucin 3 - human (f	392	71	6.3	791	2	T39924	hypothetical prote
320	72.5	6.4	729	2	G96559	hypothetical prote	393	71	6.3	1014	1	A29725	NAD ADP-ribosyltra
321	72.5	6.4	765	1	T44946	transducer protein	394	71	6.3	1241	2	S01827	period clock prote

395	71	6.3	1272	2	S26180	neurofascin - chic	468	69.5	6.2	558	2	A98199	translocated intim
396	71	6.3	1367	2	T33819	hypothetical prote	469	69.5	6.2	558	2	E86045	probable transloca
397	71	6.3	1595	2	T31082	endo-1,4-beta-xyla	470	69.5	6.2	621	2	T20307	hypothetical prote
398	71	6.3	1993	2	AF1450	probable peptidogl	471	69.5	6.2	640	2	T25367	hypothetical prote
399	70.5	6.3	118	2	S49913	cryptogein - Phyto	472	69.5	6.2	672	2	T20310	hypothetical prote
400	70.5	6.3	128	2	A35690	mucin 3 (clone SIB	473	69.5	6.2	736	2	T19366	hypothetical prote
401	70.5	6.3	168	2	A31196	prespore-specific	474	69.5	6.2	832	2	AF2089	hypothetical prote
402	70.5	6.3	172	2	F49247	merozoite surface	475	69.5	6.2	852	2	T46091	hypothetical prote
403	70.5	6.3	174	2	E49247	merozoite surface	476	69.5	6.2	863	2	T40290	hypothetical prote
404	70.5	6.3	255	2	E46606	MHC SLA-DQ alpha c	477	69.5	6.2	993	2	AE1905	outer membrane sec
405	70.5	6.3	275	2	T21933	hypothetical prote	478	69.5	6.2	1051	2	JC4091	glycoprotein A - P
406	70.5	6.3	308	2	T29756	hypothetical prote	479	69.5	6.2	1071	2	T22327	hypothetical prote
407	70.5	6.3	321	2	T19259	hypothetical prote	480	69.5	6.2	1118	2	A48292	mucin, tracheobron
408	70.5	6.3	330	2	S28102	rlx protein - Stap	481	69.5	6.2	1212	2	T13804	shs protein - frui
409	70.5	6.3	350	2	A10139	UTP-hexose-1-phosp	482	69.5	6.2	1785	2	A45546	major merozoite su
410	70.5	6.3	385	2	F70591	probable kefB prot	483	69.5	6.2	2717	2	A34203	DNA-binding protei
411	70.5	6.3	431	1	S35541	transcription fact	484	69	6.1	171	2	T31478	hypothetical prote
412	70.5	6.3	427	2	C88883	protein JG8.10 (im	485	69	6.1	217	2	S01358	salivary glue prot
413	70.5	6.3	431	1	JC2002	transcription fact	486	69	6.1	255	2	T22429	hypothetical prote
414	70.5	6.3	478	2	A32555	major merozoite su	487	69	6.1	258	2	S23106	pria protein - shi
415	70.5	6.3	496	2	T30976	hypothetical prote	488	69	6.1	284	2	T42367	a-aggutinin core
416	70.5	6.3	534	2	T39903	serine-rich protei	489	69	6.1	299	2	S44554	citrate transport
417	70.5	6.3	562	2	A85042	hypothetical prote	490	69	6.1	338	2	F69437	hypothetical prote
418	70.5	6.3	610	2	S35049	mucin JERS7 - huma	491	69	6.1	356	2	S73315	protoporphyrin IX
419	70.5	6.3	616	2	T29234	hypothetical prote	492	69	6.1	382	2	A28067	lysosomal membrane
420	70.5	6.3	674	2	S74506	ribonuclease E - S	493	69	6.1	412	1	AJBORS	argininosuccinate
421	70.5	6.3	893	2	T18271	hypothetical prote	494	69	6.1	416	2	T34279	hypothetical prote
422	70.5	6.3	910	1	S73361	dnaU homolog prote	495	69	6.1	420	2	AB2426	hypothetical prote
423	70.5	6.3	968	2	T00353	hypothetical prote	496	69	6.1	483	2	G86902	dextranucrase (BC
424	70.5	6.3	1032	2	T18293	guanylate kinase-i	497	69	6.1	511	2	I50114	early growth respo
425	70.5	6.3	1123	2	T18270	hypothetical prote	498	69	6.1	530	2	S62439	hypothetical serin
426	70.5	6.3	1131	2	T15787	hypothetical prote	499	69	6.1	608	2	A46312	gag polyprotein -
427	70.5	6.3	1742	2	T17120	cellulase (EC 3.2.	500	69	6.1	652	2	S50210	surface layer prot
428	70.5	6.3	3054	1	GNEVEV	genome polyprotein	501	69	6.1	658	2	T41309	hypothetical threo
429	70.5	6.3	3069	2	H70656	fatty-acid synthas	502	69	6.1	670	2	F84540	hypothetical prote
430	70	6.2	147	2	JC7938	type II antifreeze	503	69	6.1	790	2	T34293	hypothetical prote
431	70	6.2	209	2	AB2218	hypothetical prote	504	69	6.1	814	2	T49207	receptor kinase-li
432	70	6.2	311	2	H96002	probable sugar kin	505	69	6.1	850	1	MMHUE4	erythrocyte membra
433	70	6.2	329	2	S38082	pathogenesis-relat	506	69	6.1	854	1	QRHYLD	LDL receptor precu
434	70	6.2	340	2	C90894	probable LACI-type	507	69	6.1	1169	2	S38181	flooducation prote
435	70	6.2	340	2	F85723	probable LACI-type	508	69	6.1	1199	2	A40670	nuclear envelope p
436	70	6.2	340	2	G64905	sugar-binding prot	509	69	6.1	1904	2	T13256	tail-host specific
437	70	6.2	357	2	F72245	hydrolase, ama/hip	510	69	6.1	2035	2	A40718	host cell factor C
438	70	6.2	358	2	A88082	protein T05A8.7 li	511	69	6.1	2067	2	A42854	probable spindle p
439	70	6.2	408	2	A45712	glycoprotein Ila -	512	69	6.1	2282	2	T42717	DNA-binding protei
440	70	6.2	497	2	T53195	hypothetical prote	513	69	6.1	2481	2	D90011	FmB protein limpo
441	70	6.2	542	2	B47022	chitinase (EC 3.2.	514	69	6.1	26926	1	I38344	titin, cardiac mus
442	70	6.2	613	2	B90294	hypothetical prote	515	68.5	6.1	204	2	S51232	gibberellin-respon
443	70	6.2	767	1	JU0474	glucan 1,4-alpha-g	516	68.5	6.1	213	2	A86228	hypothetical prote
444	70	6.2	778	1	ALBYG	glucan 1,4-alpha-g	517	68.5	6.1	218	2	AH1837	hypothetical prote
445	70	6.2	835	2	F45140	cell surface-assoc	518	68.5	6.1	246	2	A47805	hypothetical prote
446	70	6.2	1048	1	S61388	dotA protein - leg	519	68.5	6.1	246	2	D51186	probable outer mem
447	70	6.2	1213	2	A41724	limb deformity (ld	520	68.5	6.1	246	2	C86033	probable outer mem
448	70	6.2	1726	2	A39401	merozoite surface	521	68.5	6.1	261	2	T30170	hypothetical prote
449	70	6.2	3507	1	T34513	hypothetical prote	522	68.5	6.1	280	2	AE2031	gamma-tocopherol m
450	69.5	6.2	120	1	W4WL42	E4 protein - human	523	68.5	6.1	294	2	A12016	hypothetical prote
451	69.5	6.2	124	2	E84613	hypothetical prote	524	68.5	6.1	310	1	Y4ZQ31	300K antigen Ag231
452	69.5	6.2	150	2	T48611	agp6 protein - Ara	525	68.5	6.1	318	2	T20063	hypothetical prote
453	69.5	6.2	172	2	T21753	hypothetical prote	526	68.5	6.1	359	2	G70814	probable far prote
454	69.5	6.2	202	2	AB2378	hypothetical prote	527	68.5	6.1	369	2	T01196	transcription fact
455	69.5	6.2	299	2	G70784	probable mmp33 pro	528	68.5	6.1	382	2	T25280	hypothetical prote
456	69.5	6.2	372	2	T48660	heat shock protein	529	68.5	6.1	385	2	H97239	polyferredoxin (im
457	69.5	6.2	373	2	F81333	chaperone DnaJ Cj1	530	68.5	6.1	420	2	A88962	protein F59A7.1 li
458	69.5	6.2	400	2	T27055	hypothetical prote	531	68.5	6.1	426	2	A35641	5-aminimidazole r
459	69.5	6.2	425	1	F0MWGC	gag polyprotein -	532	68.5	6.1	435	2	C86340	protein F2D10.28 l
460	69.5	6.2	432	2	T08771	hypothetical prote	533	68.5	6.1	435	2	T25350	hypothetical prote
461	69.5	6.2	458	2	F86433	protein Ti7H7.5 li	534	68.5	6.1	498	1	VGXPLA	surface glycoprote
462	69.5	6.2	465	2	S46759	hypothetical prote	535	68.5	6.1	500	1	S60929	probable aldehyde
463	69.5	6.2	476	2	B44997	merozoite surface	536	68.5	6.1	507	2	S05542	hypothetical prote
464	69.5	6.2	514	2	A44100	cell adhesion mole	537	68.5	6.1	509	2	T48459	cytochrome P450-li
465	69.5	6.2	514	2	A31643	cell adhesion 80K	538	68.5	6.1	514	1	A47692	fumate hydratase
466	69.5	6.2	519	2	S69989	unspecific monooxy	539	68.5	6.1	533	2	B84443	hypothetical prote
467	69.5	6.2	540	1	F0MWHL	gag polyprotein -	540	68.5	6.1	553	2	A49364	59 protein, brain

541	68.5	6.1	607	2	S63395	probable membrane	614	67.5	6.0	391	2	A44063	paired box transcr
542	68.5	6.1	654	2	T33044	hypothetical prote	615	67.5	6.0	399	2	T42242	hypothetical 44.2K
543	68.5	6.1	659	2	T40383	hypothetical prote	616	67.5	6.0	433	2	S37790	probable serine/th
544	68.5	6.1	699	2	T09483	Cys-rich protein R	617	67.5	6.0	435	2	AG1028	prepilin imported
545	68.5	6.1	700	2	A54641	interspersed repea	618	67.5	6.0	476	2	T32032	hypothetical prote
546	68.5	6.1	721	2	E70766	hypothetical prote	619	67.5	6.0	476	2	T27051	hypothetical prote
547	68.5	6.1	737	2	AG2156	hypothetical prote	620	67.5	6.0	493	2	A34130	gamma-aminobutyric
548	68.5	6.1	795	2	T20609	hypothetical prote	621	67.5	6.0	527	2	T28878	hypothetical prote
549	68.5	6.1	802	2	T21315	hypothetical prote	622	67.5	6.0	530	2	T32812	hypothetical prote
550	68.5	6.1	865	2	AC1966	hypothetical prote	623	67.5	6.0	538	2	S65764	chitinase (EC 3.2.
551	68.5	6.1	942	2	T19553	hypothetical prote	624	67.5	6.0	601	2	S56144	SH3 domain binding
552	68.5	6.1	1200	1	SNP80	ice nucleation pro	625	67.5	6.0	642	2	T39607	fork head protein
553	68.5	6.1	1379	2	T45119	FIM protein (impor	626	67.5	6.0	644	2	T39607	oligopeptide-bind
554	68.5	6.1	1438	2	A48216	neurexin III-alpha	627	67.5	6.0	651	2	T21175	hypothetical prote
555	68.5	6.1	1471	2	B48218	neurexin III-alpha	628	67.5	6.0	656	1	A49358	RNA-binding protei
556	68.5	6.1	1541	2	S46686	hypothetical prote	629	67.5	6.0	670	2	T49510	fibroin-3 related
557	68.5	6.1	3122	2	T17202	DNA-directed DNA p	630	67.5	6.0	710	2	A9486	ABC transporter, b
558	68	6.0	62	2	S53366	mucin 5AC (Clone M	631	67.5	6.0	736	2	T41259	hypothetical prote
559	68	6.0	211	2	H72608	hypothetical prote	632	67.5	6.0	749	2	T50397	probable serine/th
560	68	6.0	248	2	AF1914	carbon dioxide con	633	67.5	6.0	792	2	S70305	hypothetical prote
561	68	6.0	295	2	S50316	CIN5 protein - yea	634	67.5	6.0	815	2	C84287	hypothetical prote
562	68	6.0	301	2	H70644	hypothetical prote	635	67.5	6.0	839	2	T41826	P95 orf83 - Bombyx
563	68	6.0	333	2	T15367	hypothetical prote	636	67.5	6.0	872	2	JH0561	metabolic glucosyl
564	68	6.0	339	2	AH0050	probable periplasm	637	67.5	6.0	886	2	T23807	hypothetical prote
565	68	6.0	372	2	T45628	glycerophosphodias	638	67.5	6.0	882	2	S29605	glycoprotein 350/2
566	68	6.0	378	2	S61992	SLG1 protein - yea	639	67.5	6.0	901	2	A44825	phosphoprotein, sy
567	68	6.0	380	1	S51826	alcohol dehydrogen	640	67.5	6.0	971	2	P88448	protein C45G9, 10 f
568	68	6.0	387	2	A56275	1,3-propanediol de	641	67.5	6.0	998	2	S21735	NAD ADP-ribosyltra
569	68	6.0	388	2	T43019	probable DNA-bind	642	67.5	6.0	1051	2	T51904	hypothetical prote
570	68	6.0	423	2	T4531	S-locus-specific g	643	67.5	6.0	1203	2	T04294	hypothetical prote
571	68	6.0	426	2	T48379	gene hb protein -	644	67.5	6.0	1348	2	S27812	probable epidermal
572	68	6.0	452	2	T46147	zinc finger protei	645	67.5	6.0	1348	2	A43917	probable epidermal
573	68	6.0	456	2	T38221	hypothetical serin	646	67.5	6.0	1633	2	T01879	hypothetical prote
574	68	6.0	479	2	A84588	probable tyrosine	647	67.5	6.0	1751	2	A45604	major blood-stage
575	68	6.0	500	2	A11913	apolipoprotein N-a	648	67.5	6.0	1784	2	T10532	gag-pol polyprotei
576	68	6.0	502	2	T21935	hypothetical prote	649	67.5	6.0	1896	2	B27175	hypothetical prote
577	68	6.0	515	2	B84406	TRK potassium upta	650	67.5	6.0	1897	2	T28621	hypothetical prote
578	68	6.0	537	1	F0MVM7	gag polyprotein -	651	67.5	6.0	3345	2	T13423	hypothetical prote
579	68	6.0	600	2	S56744	mucin (clone pGM7-	652	67	6.0	149	2	S12913	cystatin - fruit f
580	68	6.0	655	1	A55726	RNA-binding protei	653	67	6.0	201	1	WNBEHL	UL4 protein - huma
581	68	6.0	669	2	B70186	translation elonga	654	67	6.0	214	2	A46629	mucin 6, gastric (
582	68	6.0	679	2	S64258	hypothetical prote	655	67	6.0	232	1	WMADC2	early E1A 25K prot
583	68	6.0	709	2	S51793	diabasic processing	656	67	6.0	233	2	T22977	hypothetical prote
584	68	6.0	730	2	A75486	hypothetical prote	657	67	6.0	264	2	A49149	mesoderm developme
585	68	6.0	749	2	B86403	probable mutator-1	658	67	6.0	276	2	T51685	myb-related trans
586	68	6.0	816	2	S64439	hypothetical prote	659	67	6.0	305	2	T24283	hypothetical prote
587	68	6.0	871	2	T43427	pob1 protein - fis	660	67	6.0	319	2	T43040	hypothetical prote
588	68	6.0	916	2	T20909	hypothetical prote	661	67	6.0	398	2	AE0975	probable racemase
589	68	6.0	1016	1	J50428	NAD ADP-ribosyltra	662	67	6.0	402	2	E86185	hypothetical prote
590	68	6.0	1098	2	T08599	probable transcrip	663	67	6.0	412	2	B88736	protein F33D4.6a f
591	68	6.0	1131	2	T41144	hypothetical serin	664	67	6.0	426	2	F75394	hypothetical prote
592	68	6.0	1203	2	T51029	related to pathway	665	67	6.0	438	1	S70602	cellulose 1,4-beta
593	68	6.0	1275	2	F81158	exodeoxyribonuclea	666	67	6.0	441	2	C75076	heme biosynthesis
594	68	6.0	1275	2	T33369	hypothetical prote	667	67	6.0	443	2	T14916	mitosis-specific c
595	68	6.0	1390	2	T18883	hypothetical prote	668	67	6.0	448	2	G88639	protein C34H4.2 (i
596	68	6.0	1401	2	T30247	werner syndrome pr	669	67	6.0	466	2	S45419	hypothetical prote
597	68	6.0	1578	2	I48216	neurexin III-alpha	670	67	6.0	476	2	C39481	Ig heavy chain pre
598	68	6.0	1711	2	T31337	1,4-beta-glucanase	671	67	6.0	486	2	B39481	serum response fac
599	68	6.0	2440	2	S39162	transcription coac	672	67	6.0	494	1	A29079	lymphocyte surface
600	68	6.0	2441	2	S39161	CREB-binding prote	673	67	6.0	514	2	H70699	probable ppp prote
601	68	6.0	3191	2	T22945	hypothetical prote	674	67	6.0	536	2	H71563	hypothetical prote
602	68	6.0	3712	2	S18253	laminin alpha-1 ch	675	67	6.0	549	2	S04845	hypothetical prote
603	67.5	6.0	150	2	T52587	probable arabinoga	676	67	6.0	558	2	S57953	C4BP protein alpha
604	67.5	6.0	159	2	T31598	hypothetical prote	677	67	6.0	579	2	D84137	methy1-accepting c
605	67.5	6.0	191	2	S38117	hypothetical prote	678	67	6.0	581	2	B86408	F3H9.11 protein -
606	67.5	6.0	210	2	B88082	protein T05A8.6 (i	679	67	6.0	588	2	B70618	probable PE protei
607	67.5	6.0	256	2	H36857	B26R protein - var	680	67	6.0	610	1	I46001	C4b-binding protei
608	67.5	6.0	297	2	S55063	conserved hypothet	681	67	6.0	617	2	T15408	hypothetical prote
609	67.5	6.0	338	2	S28004	probable cell surf	682	67	6.0	620	2	A70525	hypothetical prote
610	67.5	6.0	345	2	E88103	protein w10G11.5 (683	67	6.0	634	2	T49415	hypothetical prote
611	67.5	6.0	346	2	T46916	hypothetical prote	684	67	6.0	636	2	S63131	probable membrane
612	67.5	6.0	375	2	S22137	MID2 protein - yea	685	67	6.0	644	2	F81411	probable ribonucle
613	67.5	6.0	387	2	A86302	hypothetical prote	686	67	6.0	650	2	S22835	alpha-agglutinin -

687	6.0	672	2	T32557	hypothetical prote	760	66.5	5.9	919	2	T16693	hypothetical prote
688	6.0	698	1	JX0202	long-chain-fatty-a	761	66.5	5.9	996	2	JF0237	apolipoprotein E r
689	6.0	710	2	T21339	hypothetical prote	762	66.5	5.9	1059	2	T22545	hypothetical prote
690	6.0	723	2	H85092	hypothetical prote	763	66.5	5.9	1060	2	T31763	hypothetical prote
691	6.0	732	2	T25937	hypothetical prote	764	66.5	5.9	1221	2	A10193	ribonuclease E (EC
692	6.0	784	2	S26638	SPR-1 protein - hu	765	66.5	5.9	1369	2	S70713	protein-tyrosine k
693	6.0	824	2	T23923	hypothetical prote	766	66.5	5.9	1655	2	T32633	hypothetical prote
694	6.0	826	2	G90283	hypothetical prote	767	66.5	5.9	1868	2	S48938	hypothetical prote
695	6.0	850	2	S56015	gastric mucin MUC5	768	66	5.9	162	2	T02072	probable glycine c
696	6.0	855	2	T19405	hypothetical prote	769	66	5.9	162	2	A49247	merozoite surface
697	6.0	910	2	C69456	subtilisin sendai	770	66	5.9	193	2	D72643	hypothetical prote
698	6.0	948	2	T11678	hypothetical prote	771	66	5.9	253	2	T27279	hypothetical prote
699	6.0	1140	2	D88690	protein F41H10.3 (772	66	5.9	255	2	B75309	hypothetical prote
700	6.0	1140	2	S73786	hypothetical prote	773	66	5.9	256	2	JC2398	PM33 homolog misma
701	6.0	1228	2	C98219	proline dehydrat	774	66	5.9	259	2	E82029	methionyl aminop
702	6.0	1228	2	AG3067	proline dehydrat	775	66	5.9	282	2	B90313	conserved hypothet
703	6.0	1401	2	T17452	werner syndrome pr	776	66	5.9	315	2	S74357	hypothetical prote
704	6.0	1630	2	AS3577	ascites sialoglyco	777	66	5.9	360	2	T33835	hypothetical prote
705	6.0	1804	2	H96597	hypothetical prote	778	66	5.9	367	1	W2WL11	E2 protein - human
706	6.0	1819	2	T32008	hypothetical prote	779	66	5.9	369	2	A11079	conserved hypothet
707	6.0	1900	2	S45530	probable l-phospha	780	66	5.9	375	2	S36547	E2 protein - human
708	6.0	2476	2	T34022	zonadhesin - pig	781	66	5.9	380	1	S00912	alcohol dehydrogen
709	6.0	4377	2	AS5575	ankyrin 3, long sp	782	66	5.9	383	2	E96972	riboflavin biosynt
710	66.5	5.9	128	T05635	hypothetical prote	783	66	5.9	393	1	HVRKCI	120K lysosomal mem
711	66.5	5.9	148	S50653	hypothetical prote	784	66	5.9	407	2	A30200	neurexin III beta
712	66.5	5.9	149	E71227	hypothetical prote	785	66	5.9	426	2	B53580	dermal glycoprotei
713	66.5	5.9	175	T50094	hypothetical prote	786	66	5.9	431	2	G86277	cellulose 1,4-beta
714	66.5	5.9	217	S45446	hypothetical prote	787	66	5.9	433	2	T14329	hypothetical prote
715	66.5	5.9	238	T07921	probable starch sy	788	66	5.9	459	2	T17364	hypothetical prote
716	66.5	5.9	240	S31573	hypothetical prote	789	66	5.9	463	1	P2WL13	L2 protein - human
717	66.5	5.9	254	D88560	protein F58A4.1 (l	790	66	5.9	471	1	A38979	cellulose 1,4-beta
718	66.5	5.9	263	S01360	salivary glue prot	791	66	5.9	471	1	A26160	hypothetical prote
719	66.5	5.9	319	A35163	carbonate dehydrat	792	66	5.9	482	2	S76376	hypothetical prote
720	66.5	5.9	327	H82554	conserved hypothet	793	66	5.9	584	2	JC7809	sulfakinin recepto
721	66.5	5.9	345	AH0457	UDP-N-acetylurama	794	66	5.9	599	2	G71481	probable phosphoen
722	66.5	5.9	348	T37760	UTP-hexose-1-phosp	795	66	5.9	611	2	T04510	hypothetical prote
723	66.5	5.9	348	AE0594	galactose-1-phosph	796	66	5.9	614	2	A43390	gamma-aminobutyric
724	66.5	5.9	359	S42787	serine/threonine-r	797	66	5.9	619	2	T15969	hypothetical prote
725	66.5	5.9	369	E84291	iron (III) ABC tra	798	66	5.9	627	2	T27123	hypothetical prote
726	66.5	5.9	371	AJMSQ3	glutamate-ammonia	799	66	5.9	643	2	H84305	Ht18 transducer (l
727	66.5	5.9	371	FOVCS	gag polyprotein -	800	66	5.9	645	2	T16078	hypothetical prote
728	66.5	5.9	373	AJHUQ	glutamate-ammonia	801	66	5.9	655	2	AD2422	DNA polymerase III
729	66.5	5.9	385	T38113	hypothetical serin	802	66	5.9	657	2	E96812	protein F3F9.10 (l
730	66.5	5.9	397	T22932	hypothetical prote	803	66	5.9	657	2	H71422	hypothetical prote
731	66.5	5.9	413	S48756	transcription fact	804	66	5.9	674	2	G70875	probable oxidoredu
732	66.5	5.9	452	T26827	hypothetical prote	805	66	5.9	687	2	A49636	soluble vascular e
733	66.5	5.9	458	T31631	hypothetical prote	806	66	5.9	730	2	A53064	folded gastrulatio
734	66.5	5.9	461	D72414	anthranilate synth	807	66	5.9	733	2	T01875	probable long-chai
735	66.5	5.9	506	AG1864	hypothetical prote	808	66	5.9	786	1	A47547	serine proteinase
736	66.5	5.9	507	T23375	hypothetical prote	809	66	5.9	816	2	A49151	fibroblast growth
737	66.5	5.9	516	A31270	radial spoke prote	810	66	5.9	897	2	S50550	SIN1-associated pr
738	66.5	5.9	521	S69559	hypothetical prote	811	66	5.9	978	1	RGBY13	regulatory protein
739	66.5	5.9	521	C87472	hypothetical prote	812	66	5.9	994	1	KNWVM	nonstructural prot
740	66.5	5.9	527	T16022	hypothetical prote	813	66	5.9	1039	2	T09883	hypothetical prote
741	66.5	5.9	542	JN0661	heat shock protein	814	66	5.9	1041	2	S55862	probable membrane
742	66.5	5.9	542	S32106	groEL protein - la	815	66	5.9	1273	2	S58782	SEC31 protein - ye
743	66.5	5.9	562	A41035	chitinase (EC 3.2.	816	66	5.9	1338	2	S09982	protein-tyrosine k
744	66.5	5.9	562	S50371	chitinase (EC 3.2.	817	66	5.9	1422	2	T42636	protein-tyrosine-p
745	66.5	5.9	571	H97070	membrane associate	818	66	5.9	1711	2	AB1283	peptidoglycan link
746	66.5	5.9	615	T47395	hypothetical prote	819	66	5.9	2271	2	F90073	hypothetical prote
747	66.5	5.9	637	T20981	hypothetical prote	820	66	5.9	2405	2	T08164	dynein alpha heavy
748	66.5	5.9	640	T43337	polo-like kinase-1	821	65.5	5.8	157	2	JP0075	lectin CEL-IV, C-t
749	66.5	5.9	650	I49523	tumor necrosis fac	822	65.5	5.8	198	2	A40709	ecdysone receptor
750	66.5	5.9	681	A45705	type I transmembra	823	65.5	5.8	211	1	MUKAD	lysozyme (EC 3.2.1
751	66.5	5.9	710	S67098	probable membrane	824	65.5	5.8	248	2	T40149	hypothetical prote
752	66.5	5.9	719	T33170	hypothetical prote	825	65.5	5.8	282	2	T21222	hypothetical prote
753	66.5	5.9	739	I56187	transcription fact	826	65.5	5.8	287	2	S65765	chitinase (EC 3.2.
754	66.5	5.9	811	A41054	fasciclin II, tran	827	65.5	5.8	290	2	A43897	spicule matrix pro
755	66.5	5.9	843	S44868	kinesin heavy chai	828	65.5	5.8	314	2	D96703	hypothetical prote
756	66.5	5.9	880	S44833	F54H12.5 protein -	829	65.5	5.8	316	2	G86333	hypothetical prote
757	66.5	5.9	896	S46326	clathrin assembly	830	65.5	5.8	328	2	S69715	hypothetical prote
758	66.5	5.9	913	D82885	multiple banded an	831	65.5	5.8	356	2	D86382	hypothetical prote
759	66.5	5.9	915	S36327	clathrin assembly	832	65.5	5.8	365	2	T26564	hypothetical prote

833	65.5	5.8	377	2	A48018	mucin 7 precursor,	906	65	5.8	633	2	T04835	probable serine/th
834	65.5	5.8	443	2	C88427	protein R07E5.6 [i	907	65	5.8	704	2	T15524	hypothetical prote
835	65.5	5.8	459	2	G84752	En/Spm-like transp	908	65	5.8	706	2	S33761	transferrin precu
836	65.5	5.8	460	2	T23955	hypothetical prote	909	65	5.8	708	2	T29669	hypothetical prote
837	65.5	5.8	461	2	T39862	hypothetical prote	910	65	5.8	702	2	A42166	hypothetical prote
838	65.5	5.8	463	2	T15416	hypothetical prote	911	65	5.8	742	2	G88445	protein C6E6.2 [i
839	65.5	5.8	493	2	JC5486	membrane glycoprot	912	65	5.8	770	2	A42166	ribonucleoside-dip
840	65.5	5.8	497	2	D81723	conserved hypotet	913	65	5.8	775	1	WMBE19	cyclin F - human
841	65.5	5.8	516	2	T24644	hypothetical prote	914	65	5.8	786	2	A55501	conserved hypotet
842	65.5	5.8	526	2	C84552	hypothetical prote	915	65	5.8	792	2	F90566	ribonuclease (impo
843	65.5	5.8	540	2	T19956	hypothetical prote	916	65	5.8	817	2	F86742	hypothetical prote
844	65.5	5.8	541	2	T44725	chaperonin 60K [im	917	65	5.8	859	2	T29630	probable insectici
845	65.5	5.8	575	2	S29316	chaperonin 60 - cu	918	65	5.8	874	2	A10281	probable lipoxigen
846	65.5	5.8	575	2	T34280	hypothetical prote	919	65	5.8	876	2	T05943	TBP-associated fac
847	65.5	5.8	588	2	A25902	65K antigen - Myco	920	65	5.8	921	2	A45183	transcription init
848	65.5	5.8	592	2	S43529	coiled-coil protei	921	65	5.8	955	2	F84914	hypothetical prote
849	65.5	5.8	594	2	S62597	hypothetical prote	922	65	5.8	973	2	B86547	polymorphic oute
850	65.5	5.8	604	1	JP0001	glucan 1,4-alpha-g	923	65	5.8	995	2	C81593	polymorphic membra
851	65.5	5.8	628	2	F84219	Htr16 transducer [924	65	5.8	1088	1	IJXLNL	neural cell adhesi
852	65.5	5.8	631	2	T32761	hypothetical prote	925	65	5.8	1095	2	PC1114	SKCDC25 protein -
853	65.5	5.8	642	1	T44253	transducer protein	926	65	5.8	1096	2	H86237	protein F14N23.29
854	65.5	5.8	649	2	JQ0103	hypothetical 70K p	927	65	5.8	1097	2	T49187	hypothetical prote
855	65.5	5.8	667	2	T15710	hypothetical prote	928	65	5.8	1124	2	F17119	hypothetical prote
856	65.5	5.8	679	2	T13703	hypothetical prote	929	65	5.8	1139	1	E64234	cytadherence-acces
857	65.5	5.8	713	2	T44447	neuregulin-3 limpo	930	65	5.8	1146	2	S46837	hypothetical prote
858	65.5	5.8	746	2	G02838	enhancer-of-zeste	931	65	5.8	1156	2	T43326	germline RNA helic
859	65.5	5.8	759	2	T44142	DR1 protein (impor	932	65	5.8	1172	2	T12759	hypothetical prote
860	65.5	5.8	784	2	AH2560	hypothetical prote	933	65	5.8	1216	2	B30580	hypothetical prote
861	65.5	5.8	790	1	FQMVHZ	gag-kit polyprotei	934	65	5.8	1314	2	H86327	protein F18O14.25
862	65.5	5.8	815	2	H84199	dihydropterate sy	935	65	5.8	1459	2	T32271	hypothetical prote
863	65.5	5.8	821	2	S39983	eps8 protein - mou	936	65	5.8	1566	2	T20058	hypothetical prote
864	65.5	5.8	826	2	T46060	hypothetical prote	937	65	5.8	1605	2	T13435	DNA-directed RNA p
865	65.5	5.8	841	2	B71212	hypothetical prote	938	65	5.8	1642	2	T19130	hypothetical prote
866	65.5	5.8	841	2	F90070	Clumping factor B	939	65	5.8	1895	2	T15881	hypothetical prote
867	65.5	5.8	877	2	F90070	Clumping factor B	940	65	5.8	2311	1	TVCHSR	myoblast city prot
868	65.5	5.8	894	2	T13029	beta-adaptin homol	941	65	5.8	69	2	D72852	kinase-related pro
869	65.5	5.8	905	2	T23908	hypothetical prote	942	65	5.8	69	2	D72852	actin rearrangemen
870	65.5	5.8	1043	2	F97302	hypothetical prote	943	65	5.7	117	2	AB0028	50S ribosomal prot
871	65.5	5.8	1161	2	A27069	lethal (2) giant 1	944	65	5.7	134	2	T24968	hypothetical prote
872	65.5	5.8	1306	2	S25370	MSB2 protein - yea	945	65	5.7	153	2	S67294	hypothetical prote
873	65.5	5.8	1442	1	B48148	protein-tyrosine-p	946	65	5.7	204	2	S67295	probable membrane
874	65.5	5.8	1524	2	S68553	surface layer prot	947	65	5.7	220	2	I50588	fibroblast growth
875	65.5	5.8	1650	2	S28721	hypothetical prote	948	65	5.7	226	2	T28268	hypothetical prote
876	65.5	5.8	1829	2	T24583	hypothetical prote	949	65	5.7	226	2	T28268	hypothetical prote
877	65.5	5.8	3124	2	A40020	collagen alpha 1(X	950	65	5.7	227	2	T50033	casual polysacch
878	65.5	5.8	7576	2	T17428	FK506 polyketide s	951	65	5.7	292	2	JC4741	mosquitocidal toxi
879	65	5.8	179	2	T26929	hypothetical prote	952	65	5.7	313	2	A34677	secretory pathway
880	65	5.8	194	2	B73642	hypothetical prote	953	65	5.7	322	2	AH2192	hypothetical prote
881	65	5.8	244	2	D90783	probable outer mem	954	65	5.7	322	2	AH2192	hypothetical prote
882	65	5.8	244	2	F85643	outer membrane pre	955	65	5.7	336	2	S67570	hypothetical prote
883	65	5.8	271	2	B96773	hypothetical prote	956	65	5.7	336	2	T15837	hypothetical prote
884	65	5.8	275	2	T48436	hypothetical prote	957	65	5.7	341	2	C83578	hypothetical prote
885	65	5.8	282	2	T26397	hypothetical prote	958	65	5.7	345	2	T12344	hypothetical prote
886	65	5.8	284	2	A97203	2-oxoacid ferredox	959	65	5.7	349	2	T42965	NADH2 dehydrogenas
887	65	5.8	332	2	T31928	hypothetical prote	960	65	5.7	354	2	S59521	glycoprotein - ate
888	65	5.8	348	2	AD3264	electron transfer	961	65	5.7	378	2	A33271	mucin Sac - mouse
889	65	5.8	373	2	AG3191	amide hydrolase [i	962	65	5.7	385	2	AC2857	manganese peroxida
890	65	5.8	380	1	S53307	alcohol dehydrogen	963	65	5.7	385	2	AC2857	conserved hypotet
891	65	5.8	392	2	T49471	mucin (muc3) relat	964	65	5.7	397	2	B69378	hypothetical prote
892	65	5.8	393	2	A49008	paired box transcr	965	65	5.7	402	2	D69530	probable acyl-CoA
893	65	5.8	402	2	T20595	hypothetical prote	966	65	5.7	416	2	S65110	chitinase (EC 3.2.
894	65	5.8	434	2	S62168	hypothetical prote	967	65	5.7	420	1	AJBYRS	argininosuccinate
895	65	5.8	459	2	T17358	NADH2 dehydrogenas	968	65	5.7	424	1	VBEE9	glycoprotein gp63
896	65	5.8	465	2	T34984	probable integral	969	65	5.7	425	1	A26431	nerve growth facto
897	65	5.8	473	2	G90401	flagella-related p	970	65	5.7	446	2	T07907	hydroxyproline-ric
898	65	5.8	503	2	S63257	probable membrane	971	65	5.7	471	2	T15155	hypothetical prote
899	65	5.8	516	2	JE0134	mannan endo-1,4-be	972	65	5.7	485	2	T37550	hypothetical coile
900	65	5.8	585	2	JC5013	2,4-chlorocatechol	973	65	5.7	491	2	G86297	F309.8 protein - A
901	65	5.8	608	2	S05341	probable reverse t	974	65	5.7	512	2	E59437	F02569.2 protein [
902	65	5.8	609	2	S36569	E1 protein - human	975	65	5.7	519	1	S69988	unspecific monooxy
903	65	5.8	611	2	E86388	probable chaperoni	976	65	5.7	532	2	B35621	spore germination
904	65	5.8	618	2	A10171	probable exported	977	65	5.7	568	2	A34891	ig heavy chain pre
905	65	5.8	619	2	A43361	Ets-related transcr	978	65	5.7	568	2	I58106	gene DMR-N9 protei
			627	2	S37954	RNA polymerase I t							

979	64.5	5.7	570	2	H97244	membrane associate	1052	64	5.7	562	2	S69055	TTAGGG repeat-bind
980	64.5	5.7	574	2	E82282	probable chitinase	1053	64	5.7	562	2	T49386	hypothetical prote
981	64.5	5.7	577	2	A60501	thrombomodulin pre	1054	64	5.7	580	2	T20716	hypothetical prote
982	64.5	5.7	587	2	S21139	amine oxidase (cop	1055	64	5.7	583	2	S67571	hypothetical prote
983	64.5	5.7	590	2	S69556	hypothetical prote	1056	64	5.7	586	2	S44850	K12H4.1 protein -
984	64.5	5.7	593	2	S49525	glycoprotein G - s	1057	64	5.7	589	2	A10684	hypothetical prote
985	64.5	5.7	623	2	A48123	cell cycle regulat	1058	64	5.7	646	2	JC5583	85K SH3 domain-con
986	64.5	5.7	631	2	H70754	probable abc trans	1059	64	5.7	664	2	T48258	kinesin-like prote
987	64.5	5.7	648	2	A32576	beta-glucuronidase	1060	64	5.7	716	2	G01627	androgen receptor
988	64.5	5.7	680	2	S26764	major coat protein	1061	64	5.7	745	2	T03119	hypothetical prote
989	64.5	5.7	680	2	T19939	hypothetical prote	1062	64	5.7	750	2	T10864	transcription acti
990	64.5	5.7	690	2	H86464	hypothetical prote	1063	64	5.7	756	2	T27642	hypothetical prote
991	64.5	5.7	757	2	F96518	protein T2E6.10 [i	1064	64	5.7	768	2	A29066	DNA ligase (ATP) (
992	64.5	5.7	760	1	S07896	transcription fact	1065	64	5.7	801	2	A37353	membrane protein 4
993	64.5	5.7	770	1	S30293	transcription fact	1066	64	5.7	825	1	GUHQ	beta-glucosidase (
994	64.5	5.7	802	2	T32448	hypothetical prote	1067	64	5.7	894	2	B96557	probable receptor
995	64.5	5.7	833	2	F75621	arylesterase/monox	1068	64	5.7	1104	2	S59310	probable membrane
996	64.5	5.7	854	1	WMBP12	gene 12 protein -	1069	64	5.7	1115	2	S64101	PAN2 protein - yea
997	64.5	5.7	920	1	PXK2P	H+-exporting ATPas	1070	64	5.7	1132	2	B82538	ribonuclease E Xp2
998	64.5	5.7	1032	2	G89427	protein T08D2.3 [i	1071	64	5.7	1217	2	T25894	hypothetical prote
999	64.5	5.7	1032	2	S65341	probable membrane	1072	64	5.7	1280	2	E55031	alkaline amylopull
1000	64.5	5.7	1033	2	T37715	actin-interacting	1073	64	5.7	1282	2	JE0120	glycoprotein A - m
1001	64.5	5.7	1079	2	A86220	protein F22O13.29	1074	64	5.7	1328	2	T43060	agrin - electric r
1002	64.5	5.7	1117	2	S63399	probable membrane	1075	64	5.7	1445	1	A48148	protein-tyrosine-p
1003	64.5	5.7	1125	2	B41206	microtubule-associ	1076	64	5.7	1547	2	T28657	blackjack protein,
1004	64.5	5.7	1152	2	AC1347	probable peptidogl	1077	64	5.7	1607	2	T02837	long chain fatty a
1005	64.5	5.7	1160	2	A27868	lethal (2) giant 1	1078	64	5.7	1671	2	S71628	sensory transducti
1006	64.5	5.7	1200	2	T17404	hyalin - sea urchi	1079	64	5.7	1859	1	A34092	DNA-directed RNA p
1007	64.5	5.7	1205	2	S64819	probable membrane	1080	64	5.7	1862	2	T29959	DNA-directed RNA p
1008	64.5	5.7	1249	2	A56511	myosin I myoA - Em	1081	64	5.7	1870	2	D88486	protein F20H11.2 [
1009	64.5	5.7	1277	2	S70306	hypothetical prote	1082	64	5.7	1975	2	B81192	hemagglutinin/hemo
1010	64.5	5.7	1477	2	AG3009	polyketide synthet	1083	64	5.7	1995	2	G81044	hemagglutinin/hemo
1011	64.5	5.7	1489	2	G98274	hypothetical prote	1084	64	5.7	2055	2	T30259	multiple PDZ domai
1012	64.5	5.7	1501	2	C84512	probable retroelem	1085	64	5.7	2274	2	T30258	adenomatous polyop
1013	64.5	5.7	1505	2	S26765	genome polyprotein	1086	64	5.7	2292	1	GNVYEB	genome polyprotein
1014	64.5	5.7	1842	2	T43409	probable fatty-ac	1087	64	5.7	2292	1	GNVYED	capsid polyprotein
1015	64.5	5.7	1842	2	T38781	fatty acid synthas	1088	64	5.7	2292	2	S55401	genomic polyprotein
1016	64	5.7	131	2	T25705	hypothetical prote	1089	64	5.7	6805	2	S20901	titin - rabbit (fr
1017	64	5.7	171	2	H86413	hypothetical prote	1090	63.5	5.6	101	2	E72458	hypothetical prote
1018	64	5.7	230	2	T33364	hypothetical prote	1091	63.5	5.6	149	2	A71074	probable methyalm
1019	64	5.7	234	2	E72456	hypothetical prote	1092	63.5	5.6	166	1	C65000	NADH2 dehydrogenas
1020	64	5.7	259	2	C81008	methionine aminope	1093	63.5	5.6	166	2	B85869	NADH dehydrogenase
1021	64	5.7	268	2	S63630	acid proteinase (E	1094	63.5	5.6	166	2	A91025	NADH dehydrogenase
1022	64	5.7	279	2	E82689	conserved hypothet	1095	63.5	5.6	185	2	S20593	alcohol dehydrogen
1023	64	5.7	298	2	D95354	probable epimerase	1096	63.5	5.6	197	2	C49247	merozoite surface
1024	64	5.7	303	2	S40973	hypothetical prote	1097	63.5	5.6	197	2	T19892	hypothetical prote
1025	64	5.7	309	2	S40749	hypothetical prote	1098	63.5	5.6	205	2	S55670	hypothetical prote
1026	64	5.7	314	1	HNVZVW	hemagglutinin prec	1099	63.5	5.6	255	2	I47093	MHC OVAR-DQ-ALPHA-
1027	64	5.7	314	1	JQ1793	hemagglutinin prec	1100	63.5	5.6	275	2	S09774	hypothetical prote
1028	64	5.7	354	2	F65092	hypothetical prote	1101	63.5	5.6	284	2	T28018	hypothetical prote
1029	64	5.7	360	2	S12850	protein TPX - Ther	1102	63.5	5.6	289	2	T41305	hypothetical prote
1030	64	5.7	364	1	EDBESP	immediate-early pr	1103	63.5	5.6	296	2	I40258	outer surface prot
1031	64	5.7	376	2	AG0455	thiamin biosynthes	1104	63.5	5.6	296	2	I40267	outer surface prot
1032	64	5.7	384	2	S36529	E2 protein - human	1105	63.5	5.6	296	2	I40256	outer surface prot
1033	64	5.7	393	2	S62335	I71-7 protein - fr	1106	63.5	5.6	296	2	I40250	outer surface prot
1034	64	5.7	394	2	T23078	hypothetical prote	1107	63.5	5.6	296	2	I40260	outer surface prot
1035	64	5.7	395	2	H75457	hypothetical prote	1108	63.5	5.6	309	2	A00144	hypothetical prote
1036	64	5.7	413	2	AG0632	glucose-1-phosphat	1109	63.5	5.6	312	2	D71363	hypothetical prote
1037	64	5.7	416	2	S68822	neurotensin recept	1110	63.5	5.6	322	2	E82505	conserved hypothet
1038	64	5.7	417	2	T24618	hypothetical prote	1111	63.5	5.6	327	2	I55459	Fra-2 - rat
1039	64	5.7	417	2	T24618	hypothetical prote	1112	63.5	5.6	341	2	F71042	hypothetical prote
1040	64	5.7	428	2	D86003	hypothetical prote	1113	63.5	5.6	357	2	A37440	red-sensitive visu
1041	64	5.7	428	2	F91157	probable membrane	1114	63.5	5.6	366	2	T27912	hypothetical prote
1042	64	5.7	438	1	HVRKCS	Ig mu chain C regi	1115	63.5	5.6	373	1	AJMSQ	glutamate-ammonia
1043	64	5.7	461	1	HVRKCO	Ig mu chain C regi	1116	63.5	5.6	378	2	A12180	hypothetical prote
1044	64	5.7	461	1	D96647	hypothetical prote	1117	63.5	5.6	412	1	AJMSRS	argininosuccinate
1045	64	5.7	471	2	S46739	hypothetical prote	1118	63.5	5.6	412	1	AJRTSR	argininosuccinate
1046	64	5.7	473	2	T45954	hypothetical prote	1119	63.5	5.6	423	2	T01559	probable WRKY-type
1047	64	5.7	519	2	T45764	hypothetical prote	1120	63.5	5.6	427	2	T00465	hypothetical prote
1048	64	5.7	543	1	QFMSL	neurofilament trip	1121	63.5	5.6	432	2	T25471	hypothetical prote
1049	64	5.7	554	2	T45840	GTPase activating	1122	63.5	5.6	445	2	I38521	inwardly rectifyin
1050	64	5.7	560	2	S50392	hypothetical prote	1123	63.5	5.6	445	2	S45713	potassium channel
1051	64	5.7	561	2	T41097	RNA binding protei	1124	63.5	5.6	446	2	S66268	inward rectifier p

1125	63.5	5.6	451	2	F97230	probable maltodext	1198	63	5.6	139	2	T05847	hypothetical prote
1126	63.5	5.6	462	2	S05050	retinoic acid nucl	1199	63	5.6	154	2	C71162	hypothetical prote
1127	63.5	5.6	484	2	T20451	hypothetical prote	1200	63	5.6	190	2	T26357	hypothetical prote
1128	63.5	5.6	498	2	H85040	hypothetical prote	1201	63	5.6	204	2	AG2437	hypothetical prote
1129	63.5	5.6	509	2	A35016	cystathionine gamm	1202	63	5.6	204	2	S49031	cadmium-induced pr
1130	63.5	5.6	512	2	S21171	activin receptor S	1203	63	5.6	259	2	T09317	glycoprotein - hum
1131	63.5	5.6	541	2	S40245	heat shock protein	1204	63	5.6	266	2	T30919	hypothetical prote
1132	63.5	5.6	542	2	H89780	60 KD chaperonin [1205	63	5.6	291	2	G81407	hypothetical prote
1133	63.5	5.6	546	2	D83759	hypothetical prote	1206	63	5.6	292	2	B89807	exotoxin 9 [import
1134	63.5	5.6	560	2	D83759	methyl-accepting c	1207	63	5.6	309	2	E70319	phosphoribosylanth
1135	63.5	5.6	630	2	A39344	tumor-associated m	1208	63	5.6	309	2	T17557	procyclin homolog
1136	63.5	5.6	631	2	I52257	episialin - mouse	1209	63	5.6	321	2	T50966	hypothetical prote
1137	63.5	5.6	649	2	T04606	protein kinase hom	1210	63	5.6	326	2	S15749	transforming prote
1138	63.5	5.6	651	2	C56653	membrane glycoprot	1211	63	5.6	326	2	I48351	fos-related antige
1139	63.5	5.6	653	2	A13404	transposase BME112	1212	63	5.6	326	2	G69366	homoserine dehydro
1140	63.5	5.6	675	2	D85065	receptor protein k	1213	63	5.6	346	2	H84512	hypothetical prote
1141	63.5	5.6	688	2	T23108	hypothetical prote	1214	63	5.6	348	2	D87097	conserved hypotet
1142	63.5	5.6	694	2	S68442	Grb2-associated bi	1215	63	5.6	348	2	JQ0431	hypothetical prote
1143	63.5	5.6	699	2	C43674	US4 protein - huma	1216	63	5.6	361	2	T19395	transforming prote
1144	63.5	5.6	702	2	E69498	hypothetical prote	1217	63	5.6	371	1	TVXLT1	transforming prote
1145	63.5	5.6	708	2	H64631	outer membrane pro	1218	63	5.6	375	2	T33797	hypothetical prote
1146	63.5	5.6	713	2	B86315	F2H15.20 protein -	1219	63	5.6	376	2	S11558	probable cell wall
1147	63.5	5.6	761	2	T00940	hypothetical prote	1220	63	5.6	380	2	T32944	hypothetical prote
1148	63.5	5.6	761	2	T03719	probable thyroid r	1221	63	5.6	382	1	WZVZ16	hypothetical 35.5K
1149	63.5	5.6	764	2	A84328	Htr2 transducer (i	1222	63	5.6	396	1	C64907	chloramphenicol re
1150	63.5	5.6	767	1	WMBEP6	ribonucleoside-dip	1223	63	5.6	396	2	H85721	probable resistanc
1151	63.5	5.6	774	2	T23109	hypothetical prote	1224	63	5.6	396	2	G90895	hypothetical prote
1152	63.5	5.6	777	2	C86454	hypothetical prote	1225	63	5.6	402	2	S42367	lag-2 protein - Ca
1153	63.5	5.6	782	2	S04047	finger protein zfy	1226	63	5.6	427	2	E83711	hypothetical prote
1154	63.5	5.6	799	2	H71255	probable cell divi	1227	63	5.6	443	2	E82046	proteinase HslVU,
1155	63.5	5.6	808	2	T23129	hypothetical prote	1228	63	5.6	451	2	T15718	hypothetical prote
1156	63.5	5.6	826	2	T46061	hypothetical prote	1229	63	5.6	482	2	A12094	hypothetical prote
1157	63.5	5.6	854	1	WMBP22	gene 12 protein -	1230	63	5.6	486	2	AF1575	acetaldehyde dehyd
1158	63.5	5.6	861	2	S77409	hypothetical prote	1231	63	5.6	486	2	AC1222	probable permease
1159	63.5	5.6	865	2	A47282	calcium-binding pr	1232	63	5.6	487	2	S40820	hypothetical serin
1160	63.5	5.6	880	2	D89756	protein T3E7.2b [1233	63	5.6	509	2	T50398	transducin homolog
1161	63.5	5.6	890	2	T21000	hypothetical prote	1234	63	5.6	517	2	A49367	phosphoenolpyruvat
1162	63.5	5.6	937	2	A56517	nucleoporin Nup98	1235	63	5.6	535	2	S18606	hypothetical prote
1163	63.5	5.6	977	2	S49004	tyrosine kinase Mp	1236	63	5.6	535	2	T38244	hypothetical prote
1164	63.5	5.6	988	2	I50611	protein-tyrosine k	1237	63	5.6	537	2	B97013	and cellulose-bind
1165	63.5	5.6	1009	2	S60248	protein-tyrosine k	1238	63	5.6	539	2	I46470	estrogen dependent
1166	63.5	5.6	1013	1	S04200	NAD ADP-ribosyltra	1239	63	5.6	547	2	S44841	K06H7.1 protein -
1167	63.5	5.6	1043	2	T13172	gag-like protein p	1240	63	5.6	559	1	WMBES1	71K upper matrix p
1168	63.5	5.6	1067	2	T30061	hypothetical prote	1241	63	5.6	564	2	T12550	hypothetical prote
1169	63.5	5.6	1138	2	S64484	phosphatidyletine	1242	63	5.6	595	2	B82203	methyl-accepting c
1170	63.5	5.6	1199	2	T15826	hypothetical prote	1243	63	5.6	609	2	S36481	E1 protein - human
1171	63.5	5.6	1208	2	T27822	hypothetical prote	1244	63	5.6	609	2	T34371	hypothetical prote
1172	63.5	5.6	1218	2	AC3580	1-pyrroline-5-carb	1245	63	5.6	610	1	A49082	calcium-dependent
1173	63.5	5.6	1324	2	S06187	RNA2 polyprotein -	1246	63	5.6	611	2	S76211	hypothetical prote
1174	63.5	5.6	1326	2	B56395	secretory phosphol	1247	63	5.6	623	2	H69435	indolepyruvate fer
1175	63.5	5.6	1332	2	T23024	hypothetical prote	1248	63	5.6	630	2	A34041	5'-nucleotidase pr
1176	63.5	5.6	1382	2	S70310	hypothetical prote	1249	63	5.6	632	2	C98264	serotonin receptor
1177	63.5	5.6	1460	2	T00095	hypothetical prote	1250	63	5.6	635	2	T37239	5'-nucleotidase [i
1178	63.5	5.6	1465	2	A56395	secretory phosphol	1251	63	5.6	636	2	AF3020	FUN36 protein - ye
1179	63.5	5.6	1467	2	T17138	CL1AA protein - ra	1252	63	5.6	638	2	S36723	hypothetical prote
1180	63.5	5.6	1467	2	T18411	latrophilin-1, bra	1253	63	5.6	640	2	S75114	hypothetical prote
1181	63.5	5.6	1471	2	T17149	CL1BA protein - ra	1254	63	5.6	677	2	T39590	hypothetical prote
1182	63.5	5.6	1472	2	T18413	latrophilin-1, bra	1255	63	5.6	683	2	T37240	serotonin receptor
1183	63.5	5.6	1475	2	S42718	nuclear pore compl	1256	63	5.6	714	2	AF2479	ABC transporter At
1184	63.5	5.6	1510	2	T17145	CL1AB protein - ra	1257	63	5.6	719	2	T47727	hypothetical prote
1185	63.5	5.6	1515	2	T17156	CL1BB protein - ra	1258	63	5.6	722	2	E71403	hypothetical prote
1186	63.5	5.6	1544	2	T29482	hypothetical prote	1259	63	5.6	729	2	T15076	hypothetical prote
1187	63.5	5.6	1634	2	T26517	hypothetical prote	1260	63	5.6	763	2	T22843	hypothetical prote
1188	63.5	5.6	1796	2	S65004	probable membrane	1261	63	5.6	776	2	A55448	An receptor nuclea
1189	63.5	5.6	1854	2	S36859	cipa protein - Clo	1262	63	5.6	779	2	A57177	NIMA-like protein
1190	63.5	5.6	2145	2	JC4747	adenylate cyclase	1263	63	5.6	813	2	A72203	cellobiose-phospho
1191	63.5	5.6	2211	1	KFYBO5	coagulation factor	1264	63	5.6	838	2	G81444	myoblastotin-cont
1192	63.5	5.6	2512	1	XYCHFA	enoyl-[acyl-carrie	1265	63	5.6	843	2	T01438	hypothetical prote
1193	63.5	5.6	2700	2	D88450	protein F21H11.2 [1266	63	5.6	862	2	S51493	major nitrogen reg
1194	63.5	5.6	3027	2	JQ1917	polyprotein - pars	1267	63	5.6	865	2	B96558	probable protein k
1195	63	5.6	125	2	S24703	lg heavy chain V6	1268	63	5.6	918	1	PXB11P	H+-exporting ATPas
1196	63	5.6	126	2	S14131	hypothetical prote	1269	63	5.6	982	2	T43676	hunchback-related
1197	63	5.6	135	2	T49996	AtAGP4 - Arabidops	1270	63	5.6	986	2	T33135	hypothetical prote

1271	63	5.6	1002	2	T19226	hypothetical prote	1344	62.5	5.6	521	2	C82922	methionyl-tRNA syn
1272	63	5.6	1028	2	E85089	probable transposo	1345	62.5	5.6	545	2	T10662	aromatic amino-aci
1273	63	5.6	1028	2	C88364	protein C13B4.1 [i	1346	62.5	5.6	557	2	JC5487	cellulase (EC 3.2.
1274	63	5.6	1036	2	B63368	hypothetical prote	1347	62.5	5.6	585	1	B70747	probable serine/th
1275	63	5.6	1065	2	S19482	hypothetical prote	1348	62.5	5.6	586	2	D84710	hypothetical prote
1276	63	5.6	1106	2	T18739	hypothetical prote	1349	62.5	5.6	596	2	S61146	probable membrane
1277	63	5.6	1133	2	T30302	p-type ATPase - Te	1350	62.5	5.6	601	2	T34396	hypothetical prote
1278	63	5.6	1215	2	T43916	chitinase A limpor	1351	62.5	5.6	609	2	F87237	phosphoenolpyruvat
1279	63	5.6	1219	2	H84464	probable helicase	1352	62.5	5.6	617	2	A90644	probable membrane
1280	63	5.6	1279	2	T13613	hypothetical prote	1353	62.5	5.6	617	2	A85495	probable membrane
1281	63	5.6	1320	1	S66279	proline dehydrogen	1354	62.5	5.6	621	1	YRNC	monophenol monooxy
1282	63	5.6	1320	2	AE0633	proline dehydrogen	1355	62.5	5.6	626	2	S53871	Pmel 17 protein -
1283	63	5.6	1636	2	S60403	probable membrane	1356	62.5	5.6	647	2	S26386	transcription fact
1284	63	5.6	1817	2	T34249	hypothetical prote	1357	62.5	5.6	653	2	E86787	hypothetical prote
1285	63	5.6	1820	2	S71853	genome polyprotein	1358	62.5	5.6	671	1	VCWCE	env polyprotein -
1286	63	5.6	1902	2	C97702	cell surface antiq	1359	62.5	5.6	697	2	E96752	hypothetical prote
1287	63	5.6	1972	2	S68176	TOM protein - huma	1360	62.5	5.6	706	2	T49700	related to Ap-1-li
1288	63	5.6	2628	2	T28651	hemagglutinin A -	1361	62.5	5.6	722	2	T37970	probable G2-specif
1289	63	5.6	2697	2	T25444	hypothetical prote	1362	62.5	5.6	725	2	JC1300	endo-beta-1,4-gluc
1290	63	5.6	3066	1	JQ1662	genome polyprotein	1363	62.5	5.6	728	2	F72693	probable phosphos
1291	63	5.6	3163	1	JQ1895	genome polyprotein	1364	62.5	5.6	761	2	A96810	probable Mutator-1
1292	63	5.6	6420	2	T30283	polyketide synthas	1365	62.5	5.6	761	2	A81985	probable secretin NWA
1293	62.5	5.6	123	2	B75546	hypothetical prote	1366	62.5	5.6	823	2	G90848	probable exonuclea
1294	62.5	5.6	130	2	T12478	hypothetical prote	1367	62.5	5.6	823	2	F90914	hypothetical prote
1295	62.5	5.6	139	2	G98226	hypothetical prote	1368	62.5	5.6	823	2	E85706	probable exonuclea
1296	62.5	5.6	139	2	A13059	hypothetical prote	1369	62.5	5.6	853	2	H70939	probable nirB prot
1297	62.5	5.6	142	2	G84194	hypothetical prote	1370	62.5	5.6	873	2	B41054	fasciclin II Pi-li
1298	62.5	5.6	147	2	T34803	hypothetical prote	1371	62.5	5.6	874	2	AC2287	hypothetical prote
1299	62.5	5.6	157	2	S36784	mucin - rat (fragm	1372	62.5	5.6	887	2	G88484	protein F23F12.8 [
1300	62.5	5.6	177	2	G75285	hypothetical prote	1373	62.5	5.6	893	2	A47550	bride of sevenless
1301	62.5	5.6	198	2	S43994	hypothetical prote	1374	62.5	5.6	899	2	C84765	hypothetical prote
1302	62.5	5.6	210	2	S53300	self-incompatibili	1375	62.5	5.6	903	2	T00074	hypothetical prote
1303	62.5	5.6	219	2	F65018	hypothetical prote	1376	62.5	5.6	907	2	T04820	aconitate hydratase
1304	62.5	5.6	220	2	AC2961	thiamin-phosphate	1377	62.5	5.6	929	2	JC6124	diacylglycerol kin
1305	62.5	5.6	234	2	T35448	hypothetical prote	1378	62.5	5.6	955	4	C40045	probable transcrip
1306	62.5	5.6	238	2	C98322	probable thiamin b	1379	62.5	5.6	968	2	S46992	protein p130 - rat
1307	62.5	5.6	245	2	S43565	R01H10.4 protein (1380	62.5	5.6	988	1	S35362	protein kinase C (
1308	62.5	5.6	252	2	T04739	hypothetical prote	1381	62.5	5.6	1018	2	T40253	hypothetical prote
1309	62.5	5.6	257	2	C84890	hypothetical prote	1382	62.5	5.6	1033	2	I48775	Smcx protein (esca
1310	62.5	5.6	277	2	H97266	mind family ATPase	1383	62.5	5.6	1117	2	T19727	hypothetical prote
1311	62.5	5.6	287	2	S45662	histone H1 - tomat	1384	62.5	5.6	1197	2	D86317	protein F15H18.21
1312	62.5	5.6	289	2	T52354	hypothetical prote	1385	62.5	5.6	1203	2	H87687	helicase, Uvrp/Rep
1313	62.5	5.6	294	2	F84810	hypothetical prote	1386	62.5	5.6	1302	2	T23236	hypothetical prote
1314	62.5	5.6	304	2	H86332	T20H2-26 protein -	1387	62.5	5.6	1309	1	BVBVD9	hypothetical prote
1315	62.5	5.6	306	2	T48715	hypothetical prote	1388	62.5	5.6	1337	2	T30291	RAD9 protein - yea
1316	62.5	5.6	314	2	B75588	Frah-related prote	1389	62.5	5.6	1387	2	JC5502	dextranase - Strept
1317	62.5	5.6	329	2	T43012	conserved hypothet	1390	62.5	5.6	1560	2	I54361	G-protein signalin
1318	62.5	5.6	343	2	F95915	probable sugar ABC	1391	62.5	5.6	1577	2	T30858	SMCX protein - hum
1319	62.5	5.6	348	2	C85578	galactose-1-phosph	1392	62.5	5.6	1729	2	T18396	glucosyltransferas
1320	62.5	5.6	348	2	B90727	galactose-1-phosph	1393	62.5	5.6	1784	2	A49420	erythrocyte membra
1321	62.5	5.6	356	2	A32945	GTP-binding protei	1394	62.5	5.6	1802	2	S69703	tuberosus sclerosi
1322	62.5	5.6	359	2	T31821	hypothetical prote	1395	62.5	5.6	1872	2	T00339	HKR1 protein precu
1323	62.5	5.6	364	2	T16837	hypothetical prote	1396	62.5	5.6	2054	2	T46612	hypothetical prote
1324	62.5	5.6	372	2	T23680	hypothetical prote	1397	62.5	5.6	2090	2	S26058	multi PDZ domain p
1325	62.5	5.6	385	2	JC7783	hypothetical prote	1398	62.5	5.6	2114	2	E96505	probable transform
1326	62.5	5.6	389	2	A38302	RAD 23B protein -	1399	62.5	5.6	2366	2	S10317	hypothetical prote
1327	62.5	5.6	391	2	JC6193	pepsin (EC 3.4.23.	1400	62.5	5.6	2367	2	S70172	toxin B - Clostrid
1328	62.5	5.6	393	2	T33103	tumor suppressor p	1401	62.5	5.6	3002	2	A47221	toxin B - Clostrid
1329	62.5	5.6	396	2	S54999	lin-1 protein - Ca	1402	62.5	5.6	3033	1	JQ1303	fibrillin 1 precur
1330	62.5	5.6	396	2	PC4236	ubiquinol-cytochro	1403	62.5	5.6	3343	2	S44887	genome polyprotein
1331	62.5	5.6	398	1	W2WL42	trans-cinnamate 4-	1404	62.5	5.6	5107	2	T29144	ZK112.7 protein -
1332	62.5	5.6	412	2	T50944	E2 protein - human	1405	62	5.6	125	2	E90350	partial CDS - Caen
1333	62.5	5.6	426	2	T50944	P-selectin glycop	1406	62	5.5	165	1	KTHUB	hypothetical prote
1334	62.5	5.6	428	1	Q4EACD	hypothetical prote	1407	62	5.5	170	2	E84257	chorigonadotropin
1335	62.5	5.6	433	2	T49675	damx protein (arob	1408	62	5.5	174	2	AH1979	flagellin A2 precu
1336	62.5	5.6	458	1	MHRB	origin recognition	1409	62	5.5	181	2	T31481	hypothetical prote
1337	62.5	5.6	462	1	A29491	Ig mu chain C regi	1410	62	5.5	189	2	G70512	hypothetical prote
1338	62.5	5.6	479	1	MHRBM	retinoic acid rece	1411	62	5.5	192	2	T51463	probable lppK prot
1339	62.5	5.6	493	2	S73752	Ig mu chain C regi	1412	62	5.5	194	1	B28944	hypothetical prote
1340	62.5	5.6	503	2	T37119	hypothetical prote	1413	62	5.5	197	2	F72356	flagellin A2 precu
1341	62.5	5.6	513	2	S11439	probable membrane-	1414	62	5.5	197	2	B49247	hypothetical prote
1342	62.5	5.6	513	2	S50915	cellulose 1,4-beta	1415	62	5.5	222	2	T16381	merozoite surface
1343	62.5	5.6	518	2	T33196	SIN3 protein-bindi	1416	62	5.5	250	2	D71710	hypothetical prote

S13530
CD44E protein, epithelial - human
C:Species: Homo sapiens (man)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: S13530
R:Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B.
EMBO J. 10, 343-348, 1991
A:Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with different extracellular domains
A:Reference number: S13530; MUID:91122041; PMID:1991450
A:Accession: S13530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-493 <STA>
A:Cross-references: EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PID:g29801
C:Keywords: transmembrane protein

Query Match 17.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.5e-10;
Matches 66; Conservative 39; Mismatches 100; Indels 75; Gaps 8;

QY 9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTAEACRLLGLSLAGKQOVETALKASFET 68
DB 17 LSLAQIDLNITCFAGVFHVEKNGRYSISRTEAALCKAFNSTLPTMAQMEKALSIGFET 76
QY 69 CSYGVGDFVVISRISPNKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 124
DB 77 CRYGFI-EGHVVIPRIHPNSICAAANTGVYILTNTS-QYDYTCFNASAPPEEDCTSVTD 134
QY 125 -----PELIITKDPINFNTQTATQTE-----FI 147
DB 135 LNAFDGPTITIVNRDGRYVQKEYNPNPDIYPSNPTDDVSSGSSERSSTSGGYI 194
QY 148 -----VSDST-----YSVASPYSTIPAPTTTPAPASTSPRKKLIC 185
DB 195 FYTESVHPIDEDSPWIDSTDRIPRTNWDSSHSTLTQTPANTGLVEDLDRGLPSM 254
QY 186 VTEVMEVETMTETETEPFVENK-----AAFKNEAAG 216
DB 255 TTQQ-SNSQSFSTSHGLEEDKHPTTSLTSSNRNDVTG 293

RESULT 7
A34424
CD44 membrane glycoprotein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 01-Dec-2000
C:Accession: A34424; A34907
R:Nottenburg, C.; Rees, G.; St. John, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989
A:Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate CD44
A:Reference number: A34424; MUID:90046029; PMID:2682651
A:Accession: A34424
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-365 <NOT>
A:Cross-references: GB:M27130; NID:g192530; PIDN:AAA37407.1; PID:g309161
R:Wolfe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.
J. Biol. Chem. 265, 341-347, 1990
A:Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antigen
A:Reference number: A34907; MUID:90094420; PMID:2403559
A:Accession: A34907
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 8-195, 'G' 197-365 <WOL>
A:Cross-references: GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:g200335
C:Superfamily: human cell adhesion protein CD44
C:Keywords: cell adhesion; Glycoprotein; membrane protein

Query Match 17.6%; Score 198.5; DB 2; Length 365;
Best Local Similarity 31.8%; Pred. No. 8.1e-10;
Matches 48; Conservative 24; Mismatches 72; Indels 7; Gaps 3;

QY 12 EELSIQVSCRIMGITLVSKKANQQLNFTAEACRLLGLSLAGKQOVETALKASFETCSY 71

Db 24 QQIDLNVTCRYAGVFHVEKNGRYSISRTEAALCOAFNSTLPTMDQMKLALSKGFETCRY 83
QY 72 GWVGDFVVISRISPNKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCIPIIITTK 131
Db 84 GFI-EGHVVIPRIHPNAICAAANTGVYILTNTSHYDTCFNASAPPEEDC-----TSV 137
QY 132 DFIFNTQTATQTEFIVSDST-YSVASPYST 161
Db 138 TDLPSNFDGPTITIVNRDGRYKKGVEYRT 168

RESULT 8
JH0518
Lymphocyte homing receptor CD44, splice form CD44R1 - human
N:Alternate names: cell adhesion molecule core protein CD44E, keratinocyte; cell surface receptor; lymphocyte homing receptor CD44, splice form CD44R1; lymphocyte homing receptor CD44
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
A:Accession: JH0518; JH0519; PH0859; A39209; A42402; C42402; A53029; S16147
R:Dougherty, G.J.; Lansdorf, P.M.; Cooper, D.L.; Humphries, R.K.
J. Exp. Med. 174, 1-5, 1991
A:Title: Molecular cloning of CD44R1 and CD44R2, two novel isoforms of the human CD44 lymphocyte homing receptor
A:Reference number: JH0518; MUID:91277598; PMID:2056274
A:Accession: JH0518
A:Molecule type: mRNA
A:Residues: 1-426 <DOU>
A:Cross-references: UNIPROT:Q9UCB0
A:Experimental source: lymphocytes, cell line KGIA
A:Accession: JH0519
A:Molecule type: mRNA
A:Residues: 1-223,288-426 <DO2>
A:Experimental source: lymphocyte, cell line KGIA
R:Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Data, Biochem. Biophys. Res. Commun. 182, 569-578, 1992
A:Title: The complex CD44 transcriptional unit: alternative splicing of three internal exons
A:Reference number: PH0859; MUID:92134271; PMID:1734871
A:Accession: PH0859
A:Molecule type: DNA
A:Residues: 223-357 <COO>
R:Brown, T.A.; Bouchard, T.; St. John, T.; Wayner, E.; Carter, W.G.
J. Cell Biol. 113, 207-221, 1991
A:Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfate proteoglycan
A:Reference number: A39209; MUID:91177958; PMID:2007624
A:Accession: A39209
A:Molecule type: mRNA
A:Residues: 184-376 <BRO>
A:Cross-references: GB:X55938; NID:g29802; PIDN:CAA39404.1; PID:g930047
R:Jackson, D.G.; Buckley, J.; Bell, J.I.
J. Biol. Chem. 267, 4732-4739, 1992
A:Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by independent gene duplication
A:Reference number: A42402; MUID:92165834; PMID:1537855
A:Accession: A42402
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 217-223,288-359 <JAC>
A:Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIP:83965)
A:Note: variant B
A:Accession: C42402
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 217-320 <JAC2>
A:Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIP:83969)
R:Shepley, M.P.; Racaniello, V.R.
J. Virol. 68, 1301-1308, 1994
A:Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocyte homing receptor CD44
A:Reference number: A53029; MUID:94149816; PMID:7508992
A:Accession: A53029
A:Status: preliminary
A:Molecule type: protein
A:Residues: 67-76, 'X', 78-89 <SHE>
C:Genetics:

A:Reference number: I57483; MUID:93356912; PMID:8352881

A:Accession: I77371

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-395 <RES>

A:Cross-references: GB:S66400; NID:G435697; PIDN:AAB27919.1; PID:G435700

C:GeneID: CD44

A:Cross-references: GDB:I20739; OMIM:107269

A:Map position: llptcr-llp13

A:Introns: 257/1

C:Superfamily: human cell adhesion protein CD44

Query Match 17.4%; Score 196; DB 2; Length 395;
Best Local Similarity 30.9%; Pred. No. 1.5e-09;
Matches 54; Conservative 23; Mismatches 84; Indels 14; Gaps 5;

QY 9 LRAEELSIQVSCRMIGITLVSKKANQNLNFTKEACRLLGLSLAGKQDVETALKASPET 68

Db 17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

QY 69 CSYGVWGDGFVVISRISPNPKCGKGVGLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 128

Db 77 CRYGFI-EGHVIPRIHPNSICANNVTGVILTSNTS-QYDYCFNASAPPEDC----- 129

QY 129 TTKDPINFNTQTATQTFEIVSDST-YSVASPYSTIPA-----PTTTPAPASTS 176

Db 130 TSVTDLNAPADGPTITIVNRDGTQRYVQKGEYRTNPEDIYPSNPTDDVSSGSS 184

RESULT 12

S45305

C:Species: Canis lupus familiaris (dog)

C:Date: 20-Oct-1994 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S45305

R:Milde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L.

Biochim. Biophys. Acta 1218, 112-114, 1994

A:Title: Molecular cloning of the canine CD44 antigen cDNA.

A:Reference number: S45305; MUID:94250687; PMID:7514890

A:Accession: S45305

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-351 <MIL>

A:Cross-references: UNIPROT:Q28284; EMBL:Z27115; NID:G473226; PIDN:CAA81630.1; PID:G4732

C:Superfamily: human cell adhesion protein CD44

Query Match 17.2%; Score 194; DB 2; Length 351;

Best Local Similarity 30.3%; Pred. No. 1.9e-09;

Matches 53; Conservative 25; Mismatches 83; Indels 14; Gaps 5;

QY 9 LRAEELSIQVSCRMIGITLVSKKANQNLNFTKEACRLLGLSLAGKQDVETALKASPET 68

Db 10 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMERALSIGFET 69

QY 69 CSYGVWGDGFVVISRISPNPKCGKGVGLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 128

Db 70 CRYGFI-EGHVIPRIQPNVIACAANTHTGYI-LISNTSQDYDYCFNASAPPEDC----- 122

QY 129 TTKDPINFNTQTATQTFEIVSDST-YSVASPYSTIPA-----PTTTPAPASTS 176

Db 123 TSVTDLNAPADGPTITIVNRDGTQRYVQKGEYRTNPEDIYPSNPTDDVSSGSS 177

RESULT 13

A53286

N:Alternate names: CD44 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A53286; S22123

R:Boesworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.

Mol. Immunol. 28, 1131-1135, 1991

A:Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.

A:Reference number: A53286; MUID:92017904; PMID:1922105

A:Accession: A53286

A:Molecule type: mRNA

A:Residues: 1-366 <ROS>

A:Cross-references: UNIPROT:Q29423; EMBL:X62881; NID:G186; PIDN:CAA44675.1; PID:G187

A>Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBIP:63419)

C:Superfamily: human cell adhesion protein CD44

C:Keywords: cell adhesion; glycoprotein; transmembrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>

F:274-294/Domain: transmembrane #status predicted <TMW>

F:25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 17.2%; Score 194; DB 2; Length 366;

Best Local Similarity 29.9%; Pred. No. 2e-09;

Matches 56; Conservative 27; Mismatches 86; Indels 18; Gaps 6;

QY 4 LVQSLRAEELSIQVSCRMIGITLVSKKANQNLNFTKEACRLLGLSLAGKQDVETALK 63

Db 14 LVQSL--AQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEARN 71

QY 64 ASFTCSYGVWGDGFVVISRISPNPKCGKGVGLIWKVPVSRQFAAYCYNSSDTWTNSC 123

Db 72 IGFETCRYGFI-EGHVIPRIHPNSICANNVTGVILTSNTS-QYDYTCFNASAPPEDC 129

QY 124 IPEILTKDPIENTQTATQTFEIVSDST-YSVASPYSTIP-----APTTPPAPAS 174

Db 130 -----TSVTDLPNAPFGPTITIVNRDGTQRYVQKGEYRTNPEDINPSVSPSPDDEMS 184

QY 175 TSIPRRK 181

Db 185 SCSPSPR 191

RESULT 14

S24240

Lymphocyte surface antigen CD44 precursor - horse

C:Species: Equus caballus (domestic horse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: I46245; S24240

R:Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis, W.; But

Immunogenetics 37, 474-477, 1993

A:Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.

A:Reference number: I46245; MUID:93170897; PMID:8436424

A:Accession: I46245

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-359 <TA2>

A:Cross-references: UNIPROT:Q05078; EMBL:X66862; NID:G1059; PIDN:CAA47331.1; PID:G1060

C:Superfamily: human cell adhesion protein CD44

C:Keywords: surface antigen; transmembrane protein

Query Match 16.3%; Score 183.5; DB 2; Length 359;

Best Local Similarity 29.4%; Pred. No. 1.6e-08;

Matches 50; Conservative 24; Mismatches 87; Indels 9; Gaps 5;

QY 9 LRAEELSIQVSCRMIGITLVSKKANQNLNFTKEACRLLGLSLAGKQDVETALKASPET 68

Db 17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMKALNIGFET 76

QY 69 CSYGVWGDGFVVISRISPNPKCGKGVGLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 128

Db 77 CRIGFI-EGHVIPPIHPNSICANNVTGVILTSNTS-QYDYTCFNASAPPEDC----- 129

QY 129 TTKDPINFNTQTATQTFEIVSDST-YSVASPYSTIPAPTTTPPAPASTSI 177

Db 130 TSVTDLNAPFGPTITIVNRDGTQRYVQKGEYRTNP-EDINPSTADDDV 178

RESULT 15

A47171

chondroitin sulfate proteoglycan PG-M core protein - chicken

Search completed: October 5, 2005, 17:27:24
Job time : 29.5889 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 5, 2005, 17:27:34 ; Search time 92.8519 Seconds
(without alignments)
974.620 Million cell updates/sec

Perfect score: 1125
Sequence: 1 FRLVQSLRAELSIQVSC.....ETEPFVENKAFFKNEAGFG 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
3	1125	100.0	322	9	US-09-905-291A-201
93	1125	100.0	322	14	US-10-223-085-32
94	1125	100.0	322	14	US-10-223-084-32
95	1125	100.0	322	14	US-10-223-088-32
96	1125	100.0	322	14	US-10-223-090-32
98	1125	100.0	322	14	US-10-223-087-32
101	1125	100.0	322	14	US-10-223-083-32
102	1125	100.0	322	14	US-10-079-111-1
103	1125	100.0	322	14	US-10-223-089-32
108	1125	100.0	322	14	US-10-299-976-201
136	1125	100.0	322	14	US-10-063-742-6
211	1125	100.0	322	14	US-10-299-937-201

Sequence 32, Appl	1125	100.0	322	14	US-10-223-081-32
Sequence 32, Appl	1125	100.0	322	14	US-10-223-082-32
Sequence 201, Appl	1125	100.0	322	15	US-10-298-993-201
Sequence 32, Appl	1125	100.0	322	15	US-10-305-654-32
Sequence 201, Appl	1125	100.0	322	15	US-10-448-923-201
Sequence 201, Appl	1125	100.0	322	15	US-10-449-656-201
Sequence 201, Appl	1125	100.0	322	15	US-10-448-713-201
Sequence 201, Appl	1125	100.0	322	15	US-10-425-447-201
Sequence 32, Appl	1125	100.0	322	15	US-10-081-056-32
Sequence 201, Appl	1125	100.0	322	16	US-10-215-371-201
Sequence 201, Appl	1125	100.0	322	16	US-10-771-187-201
Sequence 6, Appl	1125	100.0	322	17	US-10-972-317-6
Sequence 201, Appl	1125	100.0	322	17	US-10-963-467-201
Sequence 201, Appl	1125	100.0	322	17	US-10-978-255-201
Sequence 201, Appl	1125	100.0	322	18	US-10-797-366-201
Sequence 64, Appl	1125	100.0	322	18	US-10-820-474A-64
Sequence 5685, Ap	1125	100.0	322	18	US-10-756-149-5685
Sequence 2349, Ap	1125	100.0	344	15	US-10-276-774-2349
Sequence 2, Appl	1119	99.5	322	14	US-10-291-634-2
Sequence 2665, Ap	1106	98.3	322	15	US-10-264-237-2665
Sequence 3909, Ap	979.5	87.1	297	15	US-10-138-588-2
Sequence 2, Appl	669	59.5	255	10	US-09-866-050A-700
Sequence 700, App	213.5	19.0	339	14	US-10-291-634-3
Sequence 3, Appl	213.5	19.0	364	18	US-10-024-607-8
Sequence 341, App	208.5	18.5	668	16	US-10-741-601-341
Sequence 1285, Ap	208.5	18.5	668	16	US-10-473-127-1285
Sequence 1047, Ap	208.5	18.5	668	17	US-10-741-600-1047
Sequence 253, App	203	18.0	742	16	US-10-482-029-253
Sequence 176, App	203	18.0	742	16	US-10-648-593-176
Sequence 1282, Ap	203	18.0	742	16	US-10-473-127-1282
Sequence 1319, Ap	203	18.0	742	16	US-10-473-127-1319
Sequence 1054, Ap	203	18.0	742	17	US-10-741-600-1054
Sequence 545, App	203	18.0	742	18	US-10-287-436A-545
Sequence 1236, Ap	202	18.0	742	18	US-10-287-436A-1236
Sequence 1284, Ap	202	18.0	675	16	US-10-473-127-1284
Sequence 344, App	202	18.0	691	16	US-10-741-601-344
Sequence 1287, Ap	202	18.0	691	17	US-10-473-127-1287
Sequence 1053, Ap	202	18.0	691	17	US-10-741-600-1053
Sequence 16, Appl	202	18.0	742	15	US-09-983-000A-16
Sequence 206, App	202	18.0	742	15	US-10-116-275-206
Sequence 1, Appl	202	18.0	742	16	US-10-663-244-1
Sequence 338, App	202	18.0	742	16	US-10-741-601-338
Sequence 339, App	202	18.0	742	16	US-10-741-601-339
Sequence 1286, Ap	202	18.0	742	16	US-10-473-127-1286
Sequence 1311, Ap	202	18.0	742	16	US-10-473-127-1311
Sequence 40, Appl	202	18.0	742	17	US-10-690-880-40
Sequence 1046, Ap	202	18.0	742	17	US-10-741-600-1046
Sequence 1049, Ap	202	18.0	742	17	US-10-741-600-1049
Sequence 16, Appl	200.5	17.8	607	17	US-10-486-226-2
Sequence 2, Appl	200.5	17.8	700	16	US-10-473-127-1306
Sequence 1306, Ap	199.5	17.7	493	11	US-09-836-544-34
Sequence 34, Appl	199.5	17.7	493	16	US-10-473-127-1279
Sequence 1279, Ap	199.5	17.7	493	16	US-10-473-127-1279
Sequence 1293, Ap	199.5	17.7	493	16	US-10-473-127-1293
Sequence 1237, Ap	199.5	17.7	493	16	US-10-473-127-1297
Sequence 1299, Ap	199.5	17.7	493	16	US-10-473-127-1299
Sequence 1301, Ap	199.5	17.7	493	16	US-10-473-127-1301
Sequence 1303, Ap	199.5	17.7	493	16	US-10-473-127-1303
Sequence 1305, Ap	199.5	17.7	493	16	US-10-473-127-1305
Sequence 73, Appl	198.5	17.6	365	9	US-09-870-759-73
Sequence 73, Appl	198.5	17.6	365	10	US-09-751-708A-73
Sequence 69, Appl	198.5	17.6	365	16	US-10-428-817A-69
Sequence 50, Appl	198.5	17.6	365	17	US-10-937-758A-50
Sequence 2, Appl	198.5	17.6	493	16	US-10-663-244-2
Sequence 1278, Ap	198.5	17.6	493	16	US-10-473-127-1278
Sequence 1289, Ap	198.5	17.6	493	16	US-10-473-127-1289
Sequence 1283, Ap	198	17.6	425	16	US-10-473-127-1283
Sequence 32, Appl	197	17.5	361	11	US-09-836-544-32
Sequence 1275, Ap	197	17.5	361	16	US-10-473-127-1275
Sequence 1276, Ap	197	17.5	361	16	US-10-473-127-1276
Sequence 1292, Ap	197	17.5	361	16	US-10-473-127-1292
Sequence 1296, Ap	197	17.5	361	16	US-10-473-127-1296

302	197	17.5	361	16	US-10-473-127-1298	Sequence 1298, Ap	375	128.5	11.4	95	16	US-10-473-127-1291	Sequence 1291, Ap
303	197	17.5	361	16	US-10-473-127-1300	Sequence 1300, Ap	376	127.5	11.3	649	10	US-09-759-1308-333	Sequence 333, App
304	197	17.5	361	16	US-10-473-127-1302	Sequence 1302, Ap	377	127.5	11.3	649	14	US-10-189-123-63	Sequence 63, Appl
305	197	17.5	361	16	US-10-473-127-1304	Sequence 1304, Ap	378	127.5	11.3	649	14	US-10-188-495-63	Sequence 63, Appl
306	197	17.5	361	16	US-10-473-127-1309	Sequence 1309, Ap	379	127.5	11.3	649	16	US-10-741-790-333	Sequence 333, App
307	197	17.5	361	16	US-10-473-127-1310	Sequence 1310, Ap	380	127.5	11.3	671	10	US-09-759-1308-331	Sequence 331, App
308	197	17.5	361	17	US-10-489-029-255	Sequence 255, App	381	127.5	11.3	671	10	US-09-983-000A-14	Sequence 14, Appl
309	197	17.5	361	17	US-10-852-335A-131	Sequence 131, App	382	127.5	11.3	671	14	US-10-189-123-61	Sequence 61, Appl
310	197	17.5	431	16	US-10-473-127-1307	Sequence 1307, Ap	383	127.5	11.3	671	14	US-10-188-495-61	Sequence 61, Appl
311	197	17.5	436	16	US-10-473-127-1308	Sequence 1308, Ap	384	127.5	11.3	671	16	US-10-741-790-331	Sequence 331, App
312	197	17.5	719	16	US-10-473-127-1270	Sequence 1270, Ap	385	127.5	11.3	671	17	US-10-652-981-14	Sequence 14, Appl
313	197	17.5	719	16	US-10-473-127-1316	Sequence 1316, Ap	386	127.5	11.3	671	17	US-10-936-626-90	Sequence 90, Appl
314	196.5	17.5	535	16	US-10-741-601-336	Sequence 336, App	387	127.5	11.3	671	17	US-10-938-061-90	Sequence 90, Appl
315	196.5	17.5	535	17	US-10-741-600-1044	Sequence 1044, Ap	388	127.5	11.3	671	17	US-10-852-335A-97	Sequence 97, Appl
316	196.5	17.5	699	16	US-10-473-127-1274	Sequence 1274, Ap	389	127.5	11.3	883	14	US-10-195-970-6	Sequence 6, Appl
317	196.5	17.5	699	16	US-10-473-127-1280	Sequence 1280, Ap	390	127.5	11.3	883	15	US-10-453-420-6	Sequence 6, Appl
318	196.5	17.5	699	16	US-10-473-127-1313	Sequence 1313, Ap	399	127.5	11.3	911	14	US-10-237-535-52	Sequence 52, Appl
319	196.5	17.5	699	17	US-10-696-639-71	Sequence 71, Appl	408	127.5	11.3	911	14	US-10-239-196-52	Sequence 52, Appl
320	196.5	17.5	700	14	US-10-012-969C-2	Sequence 2, Appli	499	127.5	11.3	911	15	US-10-453-420-8	Sequence 8, Appli
321	196	17.4	293	16	US-10-473-127-1277	Sequence 1277, Ap	500	127.5	11.3	911	15	US-10-295-027-260	Sequence 260, App
322	196	17.4	294	16	US-10-473-127-1290	Sequence 1290, Ap	501	127.5	11.3	911	15	US-10-312-352-24	Sequence 24, Appl
323	196	17.4	294	16	US-10-473-127-1312	Sequence 1312, Ap	502	127.5	11.3	911	17	US-10-936-626-89	Sequence 89, Appl
324	196	17.4	361	16	US-10-663-244-3	Sequence 3, Appli	503	127.5	11.3	911	17	US-10-938-061-89	Sequence 89, Appl
325	196	17.4	361	16	US-10-741-601-340	Sequence 340, App	504	127	11.3	277	15	US-10-295-027-294	Sequence 294, App
326	196	17.4	361	16	US-10-473-127-1288	Sequence 1288, Ap	505	127	11.3	277	15	US-10-755-889-118	Sequence 118, App
327	196	17.4	361	17	US-10-741-600-1048	Sequence 1048, Ap	506	124	11.0	482	15	US-10-104-047-3794	Sequence 3794, Ap
328	196	17.4	395	16	US-10-741-601-345	Sequence 345, App	507	124	11.0	2570	15	US-10-028-484A-42	Sequence 42, Appl
329	196	17.4	395	16	US-10-473-127-1281	Sequence 1281, Ap	508	124	11.0	2570	15	US-10-107-782-42	Sequence 42, Appl
330	196	17.4	425	17	US-10-741-600-1052	Sequence 1052, Ap	509	123	10.9	1082	15	US-10-264-237-2725	Sequence 2725, Ap
331	196	17.4	425	16	US-10-741-601-337	Sequence 337, App	510	123	10.9	2212	15	US-10-028-484A-43	Sequence 43, Appl
332	196	17.4	425	17	US-10-741-600-1045	Sequence 1045, Ap	511	123	10.9	2212	15	US-10-107-782-43	Sequence 43, Appl
333	196	17.4	493	16	US-10-741-601-343	Sequence 343, App	514	121.5	10.8	360	9	US-09-905-291A-213	Sequence 213, Appl
334	196	17.4	493	17	US-10-741-600-1051	Sequence 1051, App	1045	121.5	10.8	360	14	US-10-174-587-28	Sequence 28, Appl
335	194.5	17.3	742	18	US-10-450-763-47430	Sequence 47430, A	1080	121.5	10.8	360	14	US-10-299-976-213	Sequence 213, App
336	194	17.2	361	16	US-10-473-127-1273	Sequence 1273, Ap	1082	121.5	10.8	360	14	US-10-299-937-213	Sequence 213, App
337	191.5	17.0	676	16	US-10-473-127-1268	Sequence 1268, Ap	1092	121.5	10.8	360	15	US-10-298-993-213	Sequence 213, App
338	191.5	17.0	676	16	US-10-473-127-1318	Sequence 1318, Ap	1097	121.5	10.8	360	15	US-10-448-923-213	Sequence 213, App
339	191	17.0	271	16	US-10-473-127-1272	Sequence 1272, Ap	1098	121.5	10.8	360	15	US-10-449-556-213	Sequence 213, App
340	191	17.0	271	16	US-10-473-127-1314	Sequence 1314, Ap	1099	121.5	10.8	360	15	US-10-448-713-213	Sequence 213, App
341	191	17.0	338	16	US-10-473-127-1271	Sequence 1271, Ap	1101	121.5	10.8	360	15	US-10-425-447-213	Sequence 213, App
342	191	17.0	338	16	US-10-473-127-1315	Sequence 1315, Ap	1109	121.5	10.8	360	16	US-10-215-371-213	Sequence 213, App
343	191	17.0	470	16	US-10-473-127-1269	Sequence 1269, Ap	1110	121.5	10.8	360	16	US-10-771-187-213	Sequence 213, App
344	191	17.0	470	16	US-10-473-127-1317	Sequence 1317, Ap	1111	121.5	10.8	360	17	US-10-963-467-213	Sequence 213, App
345	187	16.6	112	17	US-10-487-620-2	Sequence 2, Appli	1112	121.5	10.8	360	17	US-10-978-255-213	Sequence 213, App
346	186.5	16.6	113	17	US-10-487-620-6	Sequence 6, Appli	1113	121.5	10.8	360	18	US-10-797-366-213	Sequence 213, App
347	185	16.4	112	17	US-10-487-620-8	Sequence 8, Appli	1117	121	10.8	528	10	US-09-759-1308-341	Sequence 341, App
348	183	16.3	112	17	US-10-487-620-10	Sequence 10, Appl	1118	121	10.8	528	14	US-10-189-123-71	Sequence 71, Appl
349	182	16.2	112	17	US-10-487-620-4	Sequence 4, Appli	1119	121	10.8	528	14	US-10-188-495-71	Sequence 71, Appl
350	181	16.1	112	17	US-10-487-620-12	Sequence 12, Appl	1120	121	10.8	528	16	US-10-741-790-341	Sequence 341, App
351	175.5	15.6	920	18	US-10-450-763-47426	Sequence 47426, A	1121	121	10.8	528	17	US-10-314-942-20	Sequence 20, Appl
352	170	15.1	34	9	US-09-864-761-47905	Sequence 47905, A	1122	119	10.6	457	10	US-09-774-839-108	Sequence 108, App
353	161	14.3	90	9	US-09-799-118-3	Sequence 3, Appli	1123	119	10.6	457	10	US-09-969-730-110	Sequence 110, App
354	153.5	13.6	90	10	US-09-927-463-8	Sequence 8, Appli	1124	119	10.6	457	15	US-10-621-363-110	Sequence 110, App
355	153.5	13.6	90	16	US-10-837-671-8	Sequence 8, Appli	1125	118.5	10.5	1642	17	US-10-741-600-1176	Sequence 1176, Ap
356	150	13.3	510	15	US-10-104-047-2580	Sequence 2580, Ap	1126	118.5	10.5	1642	17	US-10-741-600-1178	Sequence 1178, Ap
357	148.5	13.2	80	17	US-10-487-620-23	Sequence 23, Appl	1127	118.5	10.5	3396	16	US-10-788-792-170	Sequence 170, App
358	145	12.9	277	9	US-09-799-118-2	Sequence 2, Appli	1128	118.5	10.5	3396	17	US-10-741-600-1172	Sequence 1172, App
359	145	12.9	277	14	US-10-247-671-185	Sequence 185, App	1129	118.5	10.5	3396	17	US-10-741-600-1173	Sequence 1173, Ap
360	145	12.9	277	15	US-10-295-027-292	Sequence 292, App	1130	118.5	10.5	3396	18	US-10-631-467-773	Sequence 773, App
361	145	12.9	277	15	US-10-295-027-1237	Sequence 1237, App	1131	116	10.3	2397	18	US-10-631-467-1518	Sequence 1518, Ap
362	145	12.9	277	16	US-10-723-860-4326	Sequence 4326, Ap	1132	113.5	10.1	97	9	US-09-799-118-5	Sequence 5, Appli
363	145	12.9	2626	15	US-10-634-574-4	Sequence 4, Appli	1133	112.5	10.0	287	9	US-09-764-853-576	Sequence 576, App
364	143.5	12.8	95	15	US-10-424-599-248857	Sequence 248857, A	1134	112.5	10.0	340	15	US-10-112-944-397	Sequence 397, App
365	131.5	11.7	883	14	US-10-195-970-3	Sequence 3, Appli	1135	112	10.0	897	15	US-10-028-484A-41	Sequence 41, Appl
366	131.5	11.7	883	15	US-10-453-420-3	Sequence 3, Appli	1136	112	10.0	897	15	US-10-028-484A-211	Sequence 211, App
367	130.5	11.6	883	10	US-09-759-1308-342	Sequence 342, App	1137	112	10.0	897	15	US-10-107-782-41	Sequence 41, Appl
368	130.5	11.6	883	14	US-10-189-123-72	Sequence 72, Appl	1138	112	10.0	897	15	US-10-107-782-211	Sequence 211, App
369	130.5	11.6	883	14	US-10-188-495-72	Sequence 72, Appl	1139	112	10.0	1192	15	US-10-028-484A-40	Sequence 40, Appl
370	130.5	11.6	883	16	US-10-741-790-342	Sequence 342, App	1140	112	10.0	1192	15	US-10-107-782-40	Sequence 40, Appl
371	130.5	11.6	2316	16	US-10-287-436A-566	Sequence 566, App	1141	112	10.0	1394	9	US-09-842-930A-25	Sequence 25, Appl
372	129	11.5	1431	9	US-09-842-930A-2	Sequence 2, Appli	1142	112	10.0	1394	17	US-10-990-844-25	Sequence 25, Appl
373	129	11.5	1431	14	US-10-133-172-2	Sequence 2, Appli	1143	112	10.0	1416	14	US-10-133-172-4	Sequence 4, Appli
374	129	11.5	1431	17	US-10-990-844-2	Sequence 2, Appli	1144	112	10.0	1653	14	US-10-133-172-20	Sequence 20, Appl

1145	111	9.9	104	15	US-10-028-248A-46	Sequence 46, Appl	1218	98	8.7	2112	20	US-11-097-143-8001	Sequence 8001, Ap
1146	111	9.9	104	15	US-10-107-782-46	Sequence 46, Appl	1219	94.5	8.4	183	20	US-11-097-143-24753	Sequence 24753, A
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1148	111	9.9	655	17	US-10-741-600-1174	Sequence 1174, Ap	1221	93.5	8.3	258	9	US-09-764-853-840	Sequence 840, App
1149	111	9.9	2409	14	US-10-177-293-90	Sequence 90, Appl	1222	93.5	8.3	258	14	US-10-091-438-205	Sequence 205, App
1150	111	9.9	2409	17	US-10-741-600-1175	Sequence 1175, Ap	1223	93.5	8.3	261	9	US-09-764-853-669	Sequence 669, App
1151	111	9.9	2409	17	US-10-741-600-1177	Sequence 1177, Ap	1224	93.5	8.3	261	14	US-10-091-438-144	Sequence 144, App
1152	111	9.9	2409	17	US-10-482-029-194	Sequence 194, App	1225	92.5	8.2	40	17	US-10-487-620-26	Sequence 26, Appl
1153	111	9.9	2409	17	US-10-852-335A-184	Sequence 184, App	1226	91.5	8.1	166	9	US-09-764-853-777	Sequence 777, App
1154	111	9.8	2675	15	US-10-028-248A-2	Sequence 2, Appl	1227	91.5	8.1	166	14	US-10-091-438-181	Sequence 181, App
1155	110	9.8	2675	15	US-10-107-782-2	Sequence 2, Appl	1228	91.5	8.1	1126	20	US-11-097-143-35952	Sequence 35952, A
1156	109.5	9.7	1357	18	US-10-698-130-22	Sequence 22, Appl	1229	90.5	8.0	505	15	US-10-442-017-17	Sequence 17, Appl
1157	109	9.7	1069	15	US-10-028-248A-39	Sequence 39, Appl	1230	90.5	8.0	1976	20	US-11-097-143-35049	Sequence 35049, A
1158	109	9.7	1069	15	US-10-107-782-39	Sequence 39, Appl	1231	90	8.0	402	15	US-10-282-122A-64209	Sequence 64209, A
1159	109	9.7	1321	14	US-10-241-220-82	Sequence 82, Appl	1232	90	8.0	1103	15	US-10-369-493-3228	Sequence 3228, Ap
1160	109	9.7	1321	15	US-10-295-027-262	Sequence 262, App	1233	89	7.9	307	20	US-11-097-143-24429	Sequence 24429, A
1161	109	9.7	1321	16	US-10-408-765A-1421	Sequence 1421, Ap	1234	89	7.9	416	15	US-10-371-525-26	Sequence 26, Appl
1162	109	9.7	1321	16	US-10-872-972-82	Sequence 82, Appl	1235	89	7.9	416	15	US-10-371-069-26	Sequence 26, Appl
1163	109	9.7	1321	16	US-10-698-190-18	Sequence 18, Appl	1236	89	7.9	416	15	US-10-371-645-26	Sequence 26, Appl
1164	109	9.7	1321	18	US-10-698-190-18	Sequence 18, Appl	1237	89	7.9	416	15	US-10-371-260-26	Sequence 26, Appl
1165	108	9.6	322	15	US-10-120-907A-32	Sequence 32, Appl	1238	89	7.9	416	16	US-10-684-422-68	Sequence 68, Appl
1166	108	9.6	322	15	US-10-120-907A-33	Sequence 33, Appl	1239	89	7.9	416	18	US-10-287-436A-533	Sequence 533, App
1167	108	9.6	354	15	US-10-120-907A-3	Sequence 3, Appl	1240	89	7.9	416	18	US-10-287-436A-1224	Sequence 1224, Ap
1168	108	9.6	354	15	US-10-120-907A-7	Sequence 7, Appl	1241	89	7.9	1441	16	US-10-437-963-138354	Sequence 138354, Sequence 138279,
1169	108	9.6	354	15	US-10-120-907A-9	Sequence 9, Appl	1242	89	7.9	2588	16	US-10-437-963-138279	Sequence 138279,
1170	108	9.6	354	15	US-10-120-907A-11	Sequence 11, Appl	1243	87.5	7.8	536	14	US-10-218-743-21	Sequence 21, Appl
1171	108	9.6	354	15	US-10-120-907A-13	Sequence 13, Appl	1244	87.5	7.8	536	14	US-10-218-743-21	Sequence 21, Appl
1172	108	9.6	354	15	US-10-120-907A-15	Sequence 15, Appl	1245	87.5	7.8	555	14	US-10-218-743-18	Sequence 18, Appl
1173	108	9.6	354	15	US-10-120-907A-17	Sequence 17, Appl	1246	87.5	7.8	555	14	US-10-218-743-18	Sequence 18, Appl
1174	108	9.6	354	15	US-10-120-907A-19	Sequence 19, Appl	1247	87.5	7.8	1085	14	US-10-159-339-10	Sequence 10, Appl
1175	108	9.6	354	15	US-10-120-907A-21	Sequence 21, Appl	1248	87.5	7.8	1085	15	US-10-041-615-108	Sequence 108, App
1176	108	9.6	354	15	US-10-120-907A-23	Sequence 23, Appl	1249	87.5	7.8	1085	15	US-10-436-715-21	Sequence 21, Appl
1177	108	9.6	354	15	US-10-120-907A-24	Sequence 24, Appl	1250	87.5	7.8	1085	15	US-10-436-715-21	Sequence 21, Appl
1178	108	9.6	354	15	US-10-120-907A-28	Sequence 28, Appl	1251	87	7.7	288	9	US-09-216-393-341	Sequence 341, App
1179	108	9.6	354	15	US-10-120-907A-29	Sequence 29, Appl	1252	87	7.7	288	9	US-09-216-393-341	Sequence 341, App
1180	108	9.6	354	15	US-10-120-907A-30	Sequence 30, Appl	1253	87	7.7	288	14	US-10-321-856-344	Sequence 344, App
1181	108	9.6	354	15	US-10-120-907A-36	Sequence 36, Appl	1254	86.5	7.7	288	14	US-10-321-856-344	Sequence 344, App
1182	108	9.6	354	15	US-10-120-907A-38	Sequence 38, Appl	1255	86.5	7.7	585	17	US-10-425-115-334180	Sequence 334180,
1183	108	9.6	354	15	US-10-120-907A-42	Sequence 42, Appl	1256	85.5	7.6	585	17	US-10-868-381-58	Sequence 58, Appl
1184	108	9.6	354	15	US-10-120-907A-64	Sequence 64, Appl	1257	85.5	7.6	652	16	US-10-467-490-5	Sequence 5, Appl
1185	108	9.6	354	15	US-10-120-907A-66	Sequence 66, Appl	1258	85.5	7.6	841	16	US-10-467-490-2	Sequence 2, Appl
1186	108	9.6	354	18	US-10-754-473-19	Sequence 19, Appl	1259	85.5	7.6	977	16	US-10-467-490-3	Sequence 3, Appl
1187	108	9.6	354	18	US-10-754-473-22	Sequence 22, Appl	1260	85.5	7.6	1367	9	US-09-801-368-108	Sequence 108, App
1188	108	9.6	721	15	US-10-120-907A-5	Sequence 5, Appl	1261	85.5	7.6	1794	10	US-09-965-738-299	Sequence 299, App
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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11	1125	100.0	344	4	US-09-949-016-7765
12	1119	99.5	322	2	US-08-892-880-2
13	669	59.5	318	3	US-09-724-864-60
14	213.5	19.0	339	2	US-08-892-880-3
15	213.5	19.0	303	1	US-07-946-497-2
16	213.5	19.0	503	1	US-08-483-322-2
17	213.5	19.0	503	2	US-08-478-882-2
18	211.5	18.8	363	1	US-07-946-497-7
19	211.5	18.8	363	1	US-08-483-322-7
20	211.5	18.8	363	2	US-08-478-882-7
21	203.5	18.1	362	6	5504194-2
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27	175	15.6	295	4	US-09-949-016-9143
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29	161	14.3	90	3	US-09-206-695-3
30	161	14.3	90	4	US-09-799-118-3
31	145	12.9	259	4	US-09-949-016-10954
32	145	12.9	277	1	US-08-024-868-2
33	145	12.9	277	2	US-08-242-097-2
34	145	12.9	277	3	US-09-206-695-2
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124	82	7.3	553	3	US-08-951-086-2	Sequence 2, Appl	206	75	6.7	736	3	US-09-457-040B-36	Sequence 26, Appl
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131	81	7.2	894	3	US-08-971-692-15	Sequence 15, Appl	212	74.5	6.6	333	4	US-09-107-532A-6475	Sequence 6475, Ap
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150	79	7.0	455	4	US-09-949-016-10761	Sequence 10761, A	231	73.5	6.5	128	4	US-09-588-995A-12	Sequence 12, Appl
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152	79	7.0	629	4	US-08-265-428-6	Sequence 6, Appl	233	73.5	6.5	130	3	US-08-928-361B-13	Sequence 13, Appl
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156	78.5	7.0	130	4	US-09-588-995A-14	Sequence 14, Appl	237	73.5	6.5	138	3	US-08-928-361B-15	Sequence 15, Appl
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164	77.5	6.9	346	2	US-08-687-702-36	Sequence 36, Appl	245	73.5	6.5	570	4	US-09-874-933-104	Sequence 104, App
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166	77.5	6.9	514	3	US-08-738-168B-15	Sequence 15, Appl	247	73.5	6.5	595	3	US-09-006-353A-9	Sequence 9, Appl
167	77.5	6.9	562	2	US-08-687-702-1	Sequence 1, Appl	248	73.5	6.5	595	4	US-09-573-986-9	Sequence 9, Appl
168	77.5	6.9	673	4	US-09-949-016-7388	Sequence 7388, Ap	249	73.5	6.5	595	4	US-09-949-016-6048	Sequence 6048, Ap
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178	76.5	6.8	348	4	US-09-632-570-16	Sequence 16, Appl	259	73.5	6.5	1101	4	US-09-561-709B-5	Sequence 5, Appl
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183	76	6.8	380	3	US-09-134-001C-4558	Sequence 4558, Ap	264	73	6.5	488	2	US-08-599-455B-5	Sequence 5, Appl
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185	75.5	6.7	348	1	US-08-035-392-2	Sequence 2, Appl	266	73	6.5	488	3	US-09-137-132-5	Sequence 5, Appl
186	75.5	6.7	348	1	US-08-511A-2	Sequence 2, Appl	267	73	6.5	488	3	US-08-864-564A-5	Sequence 5, Appl
187	75.5	6.7	430	1	US-08-035-392A-4	Sequence 4, Appl	268	73	6.5	488	4	US-09-094-410-5	Sequence 5, Appl
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284	73	6.5	708	4	US-09-455-962-2	Sequence 2, Appli	357	72	6.4	1693	4	US-09-724-475-1	Sequence 1, Appli
285	73	6.5	712	5	PCT-US95-06530-2	Sequence 2, Appli	358	72	6.4	1693	5	PCT-US93-08849A-1	Sequence 1, Appli
286	73	6.5	712	4	US-09-877-730-22	Sequence 22, Appl	359	72	6.4	1693	5	PCT-US93-08849-1	Sequence 1, Appli
287	73	6.5	733	4	US-09-877-730-28	Sequence 28, Appl	360	72	6.4	1744	4	US-09-438-185A-542	Sequence 542, App
288	73	6.5	852	4	US-09-206-551-19	Sequence 19, Appl	361	72	6.4	1876	4	US-09-418-710-71	Sequence 70, Appl
289	73	6.5	859	4	US-09-313-942-7	Sequence 7, Appli	362	72	6.4	1876	4	US-09-839-479-70	Sequence 13, Appl
290	73	6.5	918	2	US-08-825-558-6	Sequence 6, Appli	363	72	6.4	1878	4	US-09-418-710-13	Sequence 13, Appl
291	73	6.5	918	3	US-09-312-611-6	Sequence 3, Appli	364	72	6.4	1878	4	US-09-839-479-13	Sequence 13, Appl
292	73	6.5	918	4	US-09-853-1808-3	Sequence 3, Appli	365	71.5	6.4	135	4	US-09-252-991A-17514	Sequence 17514, A
293	73	6.5	931	4	US-09-313-942-9	Sequence 9, Appli	366	71.5	6.4	232	4	US-09-333-809-217	Sequence 217, App
294	73	6.5	931	4	US-09-877-730-12	Sequence 12, Appl	367	71.5	6.4	232	4	US-09-746-311B-366	Sequence 366, App
295	73	6.5	1069	4	US-09-877-730-2	Sequence 2, Appli	368	71.5	6.4	240	4	US-09-107-532A-4430	Sequence 4430, Ap
296	73	6.5	1072	4	US-09-877-730-18	Sequence 18, Appl	369	71.5	6.4	321	4	US-09-107-433-4282	Sequence 4282, Ap
297	73	6.5	1150	4	US-09-877-730-8	Sequence 8, Appli	370	71.5	6.4	386	4	US-09-248-796A-18312	Sequence 18312, A
298	73	6.5	1158	4	US-09-313-942-26	Sequence 26, Appl	371	71.5	6.4	442	2	US-08-687-553-6	Sequence 6, Appli
299	73	6.5	1168	4	US-09-313-942-24	Sequence 24, Appl	372	71.5	6.4	442	4	US-09-401-415-6	Sequence 6, Appli
300	73	6.5	1312	3	US-09-345-882-29	Sequence 29, Appl	373	71.5	6.4	529	4	US-09-248-796A-20186	Sequence 20186, A
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302	72.5	6.4	150	3	US-08-928-361B-18	Sequence 18, Appl	375	71.5	6.4	595	1	US-08-225-989-2	Sequence 2, Appli
303	72.5	6.4	150	4	US-09-588-995A-18	Sequence 18, Appl	376	71.5	6.4	595	1	US-08-570-923-2	Sequence 2, Appli
304	72.5	6.4	185	4	US-09-248-796A-18311	Sequence 18311, A	377	71.5	6.4	595	1	US-08-580-014-2	Sequence 2, Appli
305	72.5	6.4	233	4	US-09-496-320-5	Sequence 5, Appli	378	71.5	6.4	595	3	US-09-079-785-2	Sequence 2, Appli
306	72.5	6.4	328	4	US-09-489-039A-12803	Sequence 12803, A	379	71.5	6.4	595	4	US-09-921-667-6	Sequence 6, Appli
307	72.5	6.4	463	1	US-08-162-402B-9	Sequence 9, Appli	380	71.5	6.4	641	4	US-09-613-303-51	Sequence 51, Appl
308	72.5	6.4	841	4	US-09-270-076A-11	Sequence 11, Appl	381	71.5	6.4	641	4	US-10-267-311-51	Sequence 51, Appl
309	72.5	6.4	841	4	US-09-949-016-9669	Sequence 9669, Ap	382	71.5	6.4	641	4	US-10-267-311-51	Sequence 51, Appl
310	72.5	6.4	878	4	US-09-556-706B-2	Sequence 2, Appli	383	71.5	6.4	903	3	US-09-193-562D-46	Sequence 46, Appl
311	72.5	6.4	878	4	US-09-724-418A-2	Sequence 2, Appli	384	71.5	6.4	903	4	US-09-623-624-18	Sequence 18, Appl
312	72.5	6.4	907	3	US-08-783-774-2	Sequence 2, Appli	385	71.5	6.4	903	4	US-10-055-412B-46	Sequence 46, Appl
313	72.5	6.4	907	4	US-09-328-599A-1	Sequence 1, Appli	386	71.5	6.4	903	4	US-10-270-595-18	Sequence 18, Appl
314	72.5	6.4	907	5	PCT-US95-04611A-19	Sequence 19, Appl	387	71.5	6.4	1013	3	US-08-860-886-2	Sequence 2, Appli
315	72	6.4	279	4	US-09-248-796A-16859	Sequence 16859, A	388	71.5	6.4	124	4	US-09-607-510-2	Sequence 2, Appli
316	72	6.4	300	4	US-09-254-465A-10	Sequence 10, Appl	389	71.5	6.4	1751	3	US-09-136-574A-44	Sequence 44, Appl
317	72	6.4	300	4	US-09-397-243D-12	Sequence 12, Appl	390	71	6.3	169	4	US-09-252-991A-32019	Sequence 32019, A
318	72	6.4	300	4	US-09-953-499-10	Sequence 10, Appl	391	71	6.3	189	4	US-09-270-767-39457	Sequence 39457, A
319	72	6.4	489	4	US-09-545-814-29	Sequence 29, Appl	392	71	6.3	216	4	US-09-270-767-54674	Sequence 54674, A
320	72	6.4	557	4	US-09-248-796A-26892	Sequence 26892, A	393	71	6.3	216	4	US-09-248-796A-25076	Sequence 25076, A
321	72	6.4	559	4	US-09-545-814-14	Sequence 14, Appl	394	71	6.3	230	4	US-09-328-352-7443	Sequence 7443, Ap
322	72	6.4	583	4	US-09-545-814-2	Sequence 2, Appli	395	71	6.3	230	4	US-09-248-796A-22910	Sequence 22910, A
323	72	6.4	583	4	US-09-545-814-5	Sequence 5, Appli	396	71	6.3	251	4	US-09-248-796A-20695	Sequence 20695, A
324	72	6.4	609	4	US-09-198-452A-579	Sequence 579, App	397	71	6.3	610	1	US-07-821-717B-6	Sequence 6, Appli
325	72	6.4	635	4	US-09-545-814-32	Sequence 32, Appl	398	71	6.3	610	1	US-08-119-262B-6	Sequence 6, Appli
326	72	6.4	785	3	US-08-374-077C-3	Sequence 3, Appli	399	71	6.3	610	1	US-08-135-929A-11	Sequence 11, Appl
327	72	6.4	785	3	US-08-895-590-3	Sequence 3, Appli	400	71	6.3	610	1	US-08-234-265A-11	Sequence 11, Appl
328	72	6.4	785	4	US-09-539-879A-3	Sequence 3, Appli	401	71	6.3	1014	3	US-09-078-347A-3	Sequence 3, Appli
329	72	6.4	941	4	US-07-757-022B-14	Sequence 14, Appl	402	71	6.3	1014	4	US-09-596-248D-25	Sequence 25, Appl
330	72	6.4	1022	4	US-07-757-022B-84	Sequence 84, Appl	403	71	6.3	1063	4	US-09-596-248D-47	Sequence 47, Appl
331	72	6.4	1038	4	US-07-757-022B-74	Sequence 74, Appl	404	70.5	6.3	153	4	US-09-252-991A-17880	Sequence 17880, A
332	72	6.4	1049	4	US-07-757-022B-58	Sequence 58, Appl	405	70.5	6.3	153	4	US-09-107-532A-4115	Sequence 4115, Ap
333	72	6.4	1129	4	US-09-023-905A-2	Sequence 2, Appli	406	70.5	6.3	198	4	US-09-489-039A-9988	Sequence 9988, Ap
334	72	6.4	1240	4	US-07-757-022B-104	Sequence 104, App	407	70.5	6.3	213	4	US-09-538-092-1255	Sequence 1255, Ap
335	72	6.4	1203	3	US-09-351-200-2	Sequence 2, Appli	408	70.5	6.3	232	4	US-09-333-809-214	Sequence 214, App
336	72	6.4	1270	4	US-07-757-022B-44	Sequence 44, Appl	409	70.5	6.3	232	4	US-09-333-809-215	Sequence 215, App
337	72	6.4	1311	4	US-07-757-022B-42	Sequence 42, Appl	410	70.5	6.3	232	4	US-09-333-809-216	Sequence 216, App
338	72	6.4	1313	4	US-07-757-022B-142	Sequence 142, App	411	70.5	6.3	232	4	US-09-746-311B-363	Sequence 363, App
339	72	6.4	1314	4	US-07-757-022B-50	Sequence 50, Appl	412	70.5	6.3	232	4	US-09-746-311B-364	Sequence 364, App
340	72	6.4	1320	4	US-07-757-022B-46	Sequence 46, Appl	413	70.5	6.3	232	4	US-09-746-311B-365	Sequence 365, App
341	72	6.4	1320	4	US-10-164-595-58	Sequence 58, Appl	414	70.5	6.3	292	1	US-08-286-888B-6	Sequence 6, Appli
342	72	6.4	1320	4	US-09-270-767-44343	Sequence 44343, A	415	70.5	6.3	319	4	US-09-270-767-44343	Sequence 44343, A
343	72	6.4	1354	4	US-07-757-022B-48	Sequence 48, Appl	416	70.5	6.3	330	4	US-09-248-796A-14853	Sequence 14853, A
344	72	6.4	1361	4	US-07-757-022B-40	Sequence 40, Appl	417	70.5	6.3	401	4	US-09-949-016-7956	Sequence 7956, Ap
345	72	6.4	1363	4	US-07-757-022B-52	Sequence 52, Appl	418	70.5	6.3	441	4	US-09-248-796A-20171	Sequence 20171, A
346	72	6.4	1404	4	US-07-757-022B-62	Sequence 62, Appl	419	70.5	6.3	591	4	US-09-270-767-32687	Sequence 32687, A
347	72	6.4	1404	4	US-07-757-022B-62	Sequence 62, Appl	420	70.5	6.3	591	4	US-09-270-767-47904	Sequence 47904, A

421	70.5	6.3	639	4	US-09-252-991A-24474	Sequence 24474, A	494	67.5	6.0	140	4	US-09-270-757-42846	Sequence 42846, A
422	70	6.2	222	4	US-09-252-991A-27628	Sequence 27628, A	495	67.5	6.0	159	4	US-09-252-991A-20138	Sequence 20138, A
423	70	6.2	340	4	US-09-492-709A-2622	Sequence 2622, App	496	67.5	6.0	218	1	US-08-463-115-92	Sequence 92, Appl
424	70	6.2	722	4	US-09-252-991A-26452	Sequence 26452, A	497	67.5	6.0	218	1	US-08-463-115-92	Sequence 92, Appl
425	69.5	6.2	51	4	US-09-902-540-15148	Sequence 15148, A	498	67.5	6.0	284	4	US-09-270-767-46344	Sequence 46344, A
426	69.5	6.2	139	4	US-09-248-796A-14268	Sequence 14268, A	499	67.5	6.0	291	4	US-09-248-796A-14273	Sequence 14273, A
427	69.5	6.2	300	4	US-09-248-796A-16245	Sequence 16245, A	500	67.5	6.0	312	4	US-10-101-464A-930	Sequence 930, App
428	69.5	6.2	360	4	US-09-489-039A-9383	Sequence 9383, Ap	501	67.5	6.0	338	4	US-09-538-092-144	Sequence 144, App
429	69.5	6.2	398	4	US-09-248-796A-14978	Sequence 14978, A	502	67.5	6.0	362	1	US-08-437-027-21	Sequence 21, Appl
430	69.5	6.2	401	4	US-09-270-767-44680	Sequence 44680, A	503	67.5	6.0	363	1	US-08-437-027-20	Sequence 20, Appl
431	69.5	6.2	462	6	5171671-2	Patent No. 5171671	504	67.5	6.0	383	4	US-09-107-532A-5105	Sequence 5105, Ap
432	69.5	6.2	462	6	5171671-2	Patent No. 5171671	505	67.5	6.0	394	4	US-09-949-016-9565	Sequence 9565, Ap
433	69.5	6.2	554	4	US-09-599-360B-78	Sequence 78, Appl	506	67.5	6.0	427	4	US-09-328-352-5205	Sequence 5205, Ap
434	69.5	6.2	559	4	US-09-543-681A-7241	Sequence 7241, Ap	507	67.5	6.0	428	4	US-09-489-039A-10901	Sequence 10901, A
435	69.5	6.2	643	4	US-09-248-796A-18427	Sequence 18427, A	508	67.5	6.0	498	4	US-09-718-096-26	Sequence 26, Appl
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437	69	6.1	88	4	US-09-252-991A-23868	Sequence 23868, A	510	67.5	6.0	591	4	US-09-949-016-10915	Sequence 10915, A
438	69	6.1	111	4	US-09-248-796A-14291	Sequence 14291, A	511	67.5	6.0	630	2	US-08-797-366-3	Sequence 3, Appli
439	69	6.1	153	4	US-09-489-039A-12486	Sequence 12486, A	512	67.5	6.0	630	2	US-08-956-268-3	Sequence 3, Appli
440	69	6.1	184	4	US-09-252-991A-25661	Sequence 25661, A	513	67.5	6.0	630	4	US-09-493-522-16	Sequence 16, Appl
441	69	6.1	189	4	US-09-489-039A-11063	Sequence 11063, A	514	67.5	6.0	630	4	US-09-269-939A-10	Sequence 10, Appl
442	69	6.1	211	4	US-09-248-796A-26891	Sequence 26891, A	515	67.5	6.0	649	4	US-09-499-522-14	Sequence 14, Appl
443	69	6.1	226	4	US-09-721-908-3	Sequence 3, Appli	516	67.5	6.0	649	4	US-09-269-939A-8	Sequence 8, Appli
444	69	6.1	237	4	US-09-721-908-4	Sequence 4, Appli	517	67.5	6.0	656	2	US-08-343-443B-2	Sequence 2, Appli
445	69	6.1	237	4	US-09-248-796A-22928	Sequence 22928, A	518	67.5	6.0	656	2	US-09-214-564A-4	Sequence 4, Appli
446	69	6.1	288	4	US-09-902-540-14377	Sequence 14377, A	519	67.5	6.0	656	4	US-09-538-092-1250	Sequence 1250, Ap
447	69	6.1	397	3	US-08-991-428-4	Sequence 4, Appli	520	67.5	6.0	744	4	US-09-021-560-2	Sequence 2, Appli
448	69	6.1	397	3	US-09-143-470-4	Sequence 4, Appli	521	67.5	6.0	744	4	US-09-202-178A-3	Sequence 3, Appli
449	69	6.1	397	4	US-08-649-006A-4	Sequence 4, Appli	522	67	6.0	185	4	US-09-902-540-13687	Sequence 13687, A
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453	69	6.1	509	4	US-09-292-225-35	Sequence 35, Appl	526	67	6.0	292	4	US-09-270-767-46802	Sequence 46802, A
454	69	6.1	509	4	US-09-292-225-38	Sequence 38, Appl	527	67	6.0	305	4	US-09-248-796A-23097	Sequence 23097, A
455	69	6.1	801	4	US-09-248-796A-18375	Sequence 18375, A	528	67	6.0	385	4	US-09-314-847A-4	Sequence 4, Appli
456	69	6.1	845	3	US-08-804-439A-94	Sequence 94, Appl	529	67	6.0	387	3	US-09-570-778A-2	Sequence 2, Appli
457	69	6.1	947	3	US-08-720-229-94	Sequence 94, Appl	530	67	6.0	387	4	US-09-570-778A-7	Sequence 7, Appli
458	69	6.1	1650	4	US-09-252-991A-21798	Sequence 21798, A	531	67	6.0	387	4	US-09-570-778A-8	Sequence 8, Appli
459	69	6.1	1338	4	US-09-949-016-6609	Sequence 6609, Ap	532	67	6.0	387	4	US-09-570-778A-9	Sequence 9, Appli
460	69	6.1	2035	1	US-08-046-585-5	Sequence 5, Appli	533	67	6.0	387	4	US-09-991-138-2	Sequence 2, Appli
461	69	6.1	2035	5	PCT-US93-11721-5	Sequence 5, Appli	534	67	6.0	387	4	US-09-991-138-7	Sequence 7, Appli
462	69	6.1	2035	5	PCT-US93-11721-5	Sequence 5, Appli	535	67	6.0	387	4	US-09-991-138-8	Sequence 8, Appli
463	69	6.1	2045	4	US-09-949-016-10491	Sequence 10491, A	536	67	6.0	387	4	US-09-991-138-9	Sequence 9, Appli
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465	68.5	6.1	291	4	US-09-270-767-43280	Sequence 43280, A	538	67	6.0	387	4	US-09-902-540-9960	Sequence 9960, Ap
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469	68.5	6.1	498	4	US-09-718-096-4	Sequence 4, Appli	542	67	6.0	416	4	US-09-601-478-4	Sequence 4, Appli
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472	68.5	6.1	697	4	US-09-270-767-41650	Sequence 41650, A	545	67	6.0	543	4	US-09-949-016-8822	Sequence 8822, Ap
473	68.5	6.1	756	3	US-09-085-199B-9	Sequence 9, Appli	546	67	6.0	650	3	US-08-362-525-2	Sequence 2, Appli
474	68.5	6.1	827	4	US-09-248-796A-17307	Sequence 17307, A	547	67	6.0	650	4	US-09-134-000C-5177	Sequence 5177, Ap
475	68	6.0	147	4	US-09-252-991A-21137	Sequence 21137, A	548	67	6.0	699	4	US-09-949-016-6158	Sequence 6158, Ap
476	68	6.0	155	4	US-10-101-464A-573	Sequence 573, App	549	67	6.0	702	4	US-09-949-016-11476	Sequence 11476, A
477	68	6.0	204	4	US-09-252-991A-29026	Sequence 29026, A	550	67	6.0	702	4	US-09-949-016-11477	Sequence 11477, A
478	68	6.0	270	4	US-09-134-000C-3553	Sequence 3553, Ap	551	67	6.0	784	4	US-09-538-092-1254	Sequence 1254, Ap
479	68	6.0	372	4	US-09-489-039A-13193	Sequence 13193, A	552	67	6.0	786	4	US-09-949-016-10170	Sequence 10170, A
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481	68	6.0	387	4	US-09-991-138-11	Sequence 11, Appl	554	67	6.0	915	3	US-09-138-716-2	Sequence 2, Appli
482	68	6.0	843	4	US-09-252-991A-32668	Sequence 32668, A	555	67	6.0	915	4	US-08-988-242-2	Sequence 2, Appli
483	68	6.0	873	1	US-08-571-758-6	Sequence 6, Appli	556	67	6.0	1401	3	US-08-781-891-206	Sequence 206, App
484	68	6.0	873	1	US-08-909-984A-6	Sequence 6, Appli	557	67	6.0	1401	3	US-09-618-166-206	Sequence 206, App
485	68	6.0	873	1	US-08-909-983-6	Sequence 6, Appli	558	67	6.0	1900	4	US-09-538-092-564	Sequence 564, App
486	68	6.0	1401	3	US-09-127-670-6	Sequence 6, Appli	559	67	6.0	2476	2	US-08-276-967-2	Sequence 2, Appli
487	68	6.0	1675	4	US-09-540-236-1994	Sequence 1994, Ap	560	67	6.0	4377	4	US-09-949-016-6978	Sequence 6978, Ap
488	68	6.0	2441	1	US-08-194-468-2	Sequence 2, Appli	561	66.5	5.9	91	3	US-08-700-651-14	Sequence 14, Appl
489	68	6.0	2441	3	US-08-961-733-2	Sequence 2, Appli	562	66.5	5.9	91	3	US-08-928-361B-19	Sequence 19, Appl
490	68	6.0	2441	3	US-09-514-247A-8	Sequence 8, Appli	563	66.5	5.9	154	4	US-09-588-995A-19	Sequence 19, Appl
491	68	6.0	2441	3	US-09-686-316-2	Sequence 2, Appli	564	66.5	5.9	191	3	US-09-252-991A-32034	Sequence 32034, A
492	68	6.0	2442	3	US-09-514-247A-10	Sequence 10, Appl	565	66.5	5.9	239	4	US-08-745-404-4	Sequence 4, Appli
493	68	6.0	2442	4	US-09-538-092-1370	Sequence 1370, Ap	566	66.5	5.9	239	4	US-09-248-796A-21096	Sequence 21096, A

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581	66.5	5.9	387	4	US-09-489-847-372	Sequence 372, App	662	65.5	5.8	145	4	US-09-710-279-1504	Sequence 1504, App
582	66.5	5.9	406	4	US-09-248-796A-20860	Sequence 20860, A	663	65.5	5.8	145	4	US-09-252-991A-22917	Sequence 22917, A
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584	66.5	5.9	499	3	US-09-049-672A-1	Sequence 1, Appl	665	65.5	5.8	158	4	US-09-902-540-11916	Sequence 11916, A
585	66.5	5.9	516	2	US-08-762-106-8	Sequence 8, Appl	666	65.5	5.8	198	4	US-09-252-991A-28720	Sequence 28720, A
586	66.5	5.9	516	3	US-08-745-404-2	Sequence 2, Appl	666	65.5	5.8	202	4	US-09-252-991A-32054	Sequence 32054, A
587	66.5	5.9	527	2	US-09-320-774-8	Sequence 8, Appl	667	65.5	5.8	214	4	US-08-722-570-2	Sequence 2, Appl
588	66.5	5.9	527	3	US-08-762-106-9	Sequence 9, Appl	668	65.5	5.8	214	4	US-08-932-411A-2	Sequence 2, Appl
589	66.5	5.9	527	3	US-09-320-774-9	Sequence 9, Appl	669	65.5	5.8	230	4	US-09-248-796A-18704	Sequence 18704, A
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592	66.5	5.9	562	6	5258502-2	Patent No. 5258502	672	65.5	5.8	354	4	US-09-248-796A-15271	Sequence 15271, A
593	66.5	5.9	582	4	US-09-489-039A-12055	Sequence 12055, A	673	65.5	5.8	355	4	US-09-902-540-13397	Sequence 13397, A
594	66.5	5.9	681	3	US-08-760-615-4	Sequence 4, Appl	674	65.5	5.8	362	3	US-08-899-437-3	Sequence 3, Appl
595	66.5	5.9	681	4	US-09-336-910A-2	Sequence 2, Appl	675	65.5	5.8	362	3	US-09-126-121-3	Sequence 3, Appl
596	66.5	5.9	815	4	US-09-914-259-18	Sequence 18, Appl	676	65.5	5.8	416	3	US-08-978-289-12	Sequence 12, Appl
597	66.5	5.9	872	3	US-08-337-797A-2	Sequence 2, Appl	677	65.5	5.8	448	4	US-09-520-781-32	Sequence 32, Appl
598	66.5	5.9	872	3	US-09-258-523-2	Sequence 2, Appl	678	65.5	5.8	476	4	US-09-248-796A-18994	Sequence 18994, A
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601	66.5	5.9	993	1	US-08-571-785-1	Sequence 1, Appl	681	65.5	5.8	540	2	US-08-368-834-20	Sequence 20, Appl
602	66.5	5.9	993	3	US-09-192-435-1	Sequence 1, Appl	682	65.5	5.8	541	2	US-08-467-822-34	Sequence 34, Appl
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604	66.5	5.9	1338	4	US-09-071-035-258	Sequence 217, App	684	65.5	5.8	541	3	US-08-432-697-34	Sequence 34, Appl
605	66.5	5.9	1338	4	US-09-071-035-258	Sequence 258, App	685	65.5	5.8	541	3	US-08-466-248-34	Sequence 34, Appl
606	66.5	5.9	1638	4	US-09-071-035-262	Sequence 262, App	686	65.5	5.8	555	4	US-09-107-532A-6422	Sequence 6422, App
607	66.5	5.9	1747	4	US-09-134-000C-5999	Sequence 266, App	687	65.5	5.8	635	4	US-09-248-796A-19562	Sequence 19562, A
608	66	5.9	187	4	US-09-248-796A-21855	Sequence 5999, App	688	65.5	5.8	676	3	US-09-003-574-34	Sequence 34, Appl
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610	66	5.9	208	4	US-09-252-991A-23162	Sequence 23162, A	690	65.5	5.8	713	3	US-09-864-541A-34	Sequence 34, Appl
611	66	5.9	208	4	US-09-248-796A-21781	Sequence 21781, A	691	65.5	5.8	713	3	US-08-899-437-2	Sequence 2, Appl
612	66	5.9	231	4	US-09-717-364A-13	Sequence 13, Appl	692	65.5	5.8	746	4	US-09-589-892B-2	Sequence 2, Appl
613	66	5.9	342	4	US-09-252-991A-1903	Sequence 1903, A	693	65.5	5.8	821	1	US-07-935-311A-4	Sequence 4, Appl
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615	66	5.9	440	4	US-09-270-767-37864	Sequence 37864, A	696	65.5	5.8	821	4	US-09-886-319A-33	Sequence 33, Appl
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620	66	5.9	540	4	US-09-468-041-3	Sequence 3, Appl	701	65.5	5.8	872	3	US-09-196-466-3	Sequence 3, Appl
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623	66	5.9	580	4	US-09-248-796A-26639	Sequence 26639, A	704	65.5	5.8	1306	4	US-09-538-092-330	Sequence 330, App
624	66	5.9	584	4	US-09-693-746-22	Sequence 22, Appl	705	65.5	5.8	1442	2	US-08-015-986A-3	Sequence 3, Appl
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644	66	5.9	758	3	US-09-348-886-1	Sequence 1, Appl	716	65	5.8	166	4	US-09-252-991A-25442	Sequence 25442, A
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652	66	5.9	1619	4	US-09-328-352-7347	Sequence 4, Appl	724	65	5.8	552	4	US-09-773-877B-14	Sequence 14, Appl
653	66	5.9	2169	4	US-09-949-016-6930	Sequence 7347, App	725	65	5.8	567	4	US-09-773-877B-20	Sequence 20, Appl
654	66	5.9	313	4	US-09-349-016-10933	Sequence 6930, App	726	65	5.8	630	4	US-09-485-529-8	Sequence 8, Appl
655	65.5	5.8	101	4	US-09-270-767-44082	Sequence 10933, A	727	65	5.8	692	3	US-09-003-574-31	Sequence 31, Appl
656	65.5	5.8	103	4	US-09-107-532A-4889	Sequence 44082, A	728	65	5.8	692	3	US-09-864-541A-31	Sequence 31, Appl
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						Sequence 38128, A	730	65	5.8	883	4	US-09-489-039A-12755	Sequence 12755, A

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732	65	5.8	921	1	US-08-646-715-2	Sequence 2, Appli	805	64	5.7	562	4	US-09-538-092-779	Sequence 779, App
733	65	5.8	921	4	US-09-430-723-2	Sequence 2, Appli	806	64	5.7	574	4	US-09-248-796A-16162	Sequence 16162, A
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737	65	5.8	1992	4	US-08-621-944A-3	Sequence 3, Appli	810	64	5.7	636	4	US-09-949-016-11656	Sequence 11656, A
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739	64.5	5.7	94	4	US-09-621-976-5361	Sequence 5361, App	812	64	5.7	639	4	US-09-248-796A-20583	Sequence 20583, A
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741	64.5	5.7	133	4	US-09-252-991A-24089	Sequence 24089, A	814	64	5.7	693	4	US-09-248-796A-26890	Sequence 26890, A
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743	64.5	5.7	279	3	US-08-397-411-13	Sequence 13, Appli	816	64	5.7	737	1	US-08-188-582-16	Sequence 16, Appli
744	64.5	5.7	349	4	US-09-270-767-44336	Sequence 44336, A	817	64	5.7	737	1	US-08-646-715-16	Sequence 16, Appli
745	64.5	5.7	391	4	US-09-200-090-4	Sequence 4, Appli	818	64	5.7	740	4	US-09-949-016-10931	Sequence 10931, A
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747	64.5	5.7	407	4	US-09-972-784-3	Sequence 3, Appli	820	64	5.7	750	4	US-09-508-824-12	Sequence 12, Appli
748	64.5	5.7	420	4	US-09-538-092-703	Sequence 703, App	821	64	5.7	854	4	US-09-590-304-7	Sequence 7, Appli
749	64.5	5.7	425	4	US-09-748-537-14	Sequence 14, Appli	822	64	5.7	897	4	US-09-590-304-2	Sequence 2, Appli
750	64.5	5.7	491	4	US-09-107-532A-6115	Sequence 6115, App	823	64	5.7	923	4	US-09-825-147-2	Sequence 2, Appli
751	64.5	5.7	553	4	US-09-949-016-10648	Sequence 10648, A	824	64	5.7	932	4	US-09-813-148-2	Sequence 2, Appli
752	64.5	5.7	566	4	US-09-513-783A-142	Sequence 142, App	825	64	5.7	999	4	US-09-747-371-2	Sequence 2, Appli
753	64.5	5.7	566	4	US-09-430-656-142	Sequence 142, App	826	64	5.7	1330	4	US-09-543-681A-8057	Sequence 8057, Ap
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756	64.5	5.7	638	1	US-08-463-262A-11	Sequence 11, Appli	829	64	5.7	1574	4	US-08-446-363-2	Sequence 2, Appli
757	64.5	5.7	638	1	US-08-463-989-11	Sequence 11, Appli	830	64	5.7	1574	4	US-09-302-626B-179	Sequence 179, App
758	64.5	5.7	638	3	US-09-003-574-11	Sequence 11, Appli	831	64	5.7	1978	4	US-09-302-626B-60	Sequence 60, Appli
759	64.5	5.7	638	3	US-09-003-570-11	Sequence 11, Appli	832	64	5.7	2781	4	US-09-698-295-10	Sequence 10, Appli
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761	64.5	5.7	648	4	US-09-715-858-4	Sequence 4, Appli	834	63.5	5.6	83	4	US-09-252-991A-21499	Sequence 21499, A
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764	64.5	5.7	712	4	US-09-949-016-10600	Sequence 10600, A	837	63.5	5.6	210	4	US-09-270-767-48168	Sequence 48168, A
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767	64.5	5.7	812	4	US-09-513-783A-4	Sequence 4, Appli	840	63.5	5.6	264	1	US-08-465-388-93	Sequence 93, Appli
768	64.5	5.7	812	4	US-09-513-783A-6	Sequence 6, Appli	841	63.5	5.6	319	3	US-08-832-399-2	Sequence 2, Appli
769	64.5	5.7	812	4	US-09-430-656-4	Sequence 4, Appli	842	63.5	5.6	319	3	US-09-372-498-2	Sequence 2, Appli
770	64.5	5.7	812	4	US-09-430-656-6	Sequence 6, Appli	843	63.5	5.6	347	4	US-09-252-991A-19498	Sequence 19498, A
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773	64.5	5.7	994	4	US-09-248-796A-15273	Sequence 15273, A	846	63.5	5.6	399	1	US-08-414-926A-5	Sequence 5, Appli
774	64.5	5.7	1039	4	US-09-902-540-13739	Sequence 13739, A	847	63.5	5.6	399	3	US-08-926-922-5	Sequence 5, Appli
775	64.5	5.7	1056	4	US-09-513-783A-32	Sequence 32, Appli	848	63.5	5.6	399	3	US-09-253-682-5	Sequence 5, Appli
776	64.5	5.7	1056	4	US-09-430-656-32	Sequence 32, Appli	849	63.5	5.6	399	3	US-09-527-657-5	Sequence 5, Appli
777	64.5	5.7	1125	4	US-09-513-783A-152	Sequence 152, App	850	63.5	5.6	410	3	US-09-892-100-5	Sequence 2, Appli
778	64.5	5.7	1125	4	US-09-430-656-152	Sequence 152, App	851	63.5	5.6	410	3	US-08-858-876A-2	Sequence 2, Appli
779	64.5	5.7	1140	4	US-09-538-092-647	Sequence 647, App	852	63.5	5.6	410	3	US-09-472-880-2	Sequence 2, Appli
780	64.5	5.7	1310	4	US-09-170-496D-290	Sequence 290, App	853	63.5	5.6	428	4	US-09-826-509-537	Sequence 537, App
781	64.5	5.7	1310	4	US-09-364-425B-55	Sequence 55, Appli	854	63.5	5.6	428	4	US-09-134-000C-6457	Sequence 6457, App
782	64.5	5.7	1481	4	US-09-231-899-70	Sequence 70, Appli	855	63.5	5.6	447	1	US-08-450-360-4	Sequence 4, Appli
783	64.5	5.7	1610	4	US-09-513-783A-22	Sequence 22, Appli	856	63.5	5.6	459	4	US-09-691-220-4	Sequence 4, Appli
784	64.5	5.7	1610	4	US-09-430-656-22	Sequence 22, Appli	857	63.5	5.6	465	3	US-08-845-258-30	Sequence 30, Appli
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786	64	5.7	134	4	US-09-270-767-56066	Sequence 56066, A	859	63.5	5.6	465	3	US-08-723-142A-30	Sequence 30, Appli
787	64	5.7	152	4	US-09-252-991A-19284	Sequence 19284, A	860	63.5	5.6	465	4	US-09-528-784A-30	Sequence 30, Appli
788	64	5.7	176	4	US-09-252-991A-21933	Sequence 21933, A	861	63.5	5.6	465	4	US-09-569-099A-30	Sequence 30, Appli
789	64	5.7	198	4	US-09-252-991A-18773	Sequence 18773, A	862	63.5	5.6	468	3	US-08-802-805D-21	Sequence 21, Appli
790	64	5.7	198	4	US-09-248-796A-19318	Sequence 19318, A	863	63.5	5.6	468	4	US-08-837-199A-4	Sequence 4, Appli
791	64	5.7	219	1	US-08-463-115-91	Sequence 91, Appli	864	63.5	5.6	468	4	US-08-860-370-2	Sequence 2, Appli
792	64	5.7	219	1	US-08-465-388-91	Sequence 91, Appli	865	63.5	5.6	468	4	US-09-187-906-2	Sequence 2, Appli
793	64	5.7	206	4	US-09-302-540-9859	Sequence 9859, App	866	63.5	5.6	468	4	US-08-861-990-1	Sequence 1, Appli
794	64	5.7	341	4	US-09-252-991A-26208	Sequence 26208, A	867	63.5	5.6	468	4	US-09-388-316C-21	Sequence 21, Appli
795	64	5.7	354	4	US-09-949-016-10392	Sequence 10392, A	868	63.5	5.6	486	1	US-08-450-360-2	Sequence 2, Appli
796	64	5.7	380	4	US-09-248-796A-19662	Sequence 19662, A	869	63.5	5.6	486	4	US-09-134-000C-4392	Sequence 4392, Ap
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800	64	5.7	501	4	US-09-248-796A-14118	Sequence 14118, A	873	63.5	5.6	658	4	US-09-248-796A-17674	Sequence 17674, A
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878	63.5	5.6	699	4	US-10-237-551-143	Sequence 143, App	951	63	5.6	1065	4	US-09-538-092-84	Sequence 84, Appl
879	63.5	5.6	699	4	US-10-237-551-143	Sequence 254, App	952	63	5.6	1557	4	US-09-410-551B-27	Sequence 27, Appl
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882	63.5	5.6	973	1	US-08-162-809-10	Sequence 10, Appl	955	63	5.6	1574	4	US-09-940-316B-25	Sequence 25, Appl
883	63.5	5.6	973	1	US-08-162-809-14	Sequence 14, Appl	956	63	5.6	1578	4	US-09-410-551B-31	Sequence 31, Appl
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887	63.5	5.6	1036	4	US-09-902-540-14218	Sequence 14218, A	960	63	5.6	1605	4	US-09-410-551B-33	Sequence 33, Appl
888	63.5	5.6	1132	4	US-09-528-784A-87	Sequence 87, Appl	961	63	5.6	1605	4	US-09-410-551B-33	Sequence 33, Appl
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893	63.5	5.6	1382	4	US-09-538-092-590	Sequence 590, App	966	62.5	5.6	159	4	US-09-270-767-59460	Sequence 59460, A
894	63.5	5.6	1466	4	US-09-262-537-20	Sequence 20, Appl	967	62.5	5.6	170	4	US-09-252-991A-28560	Sequence 28560, A
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903	63	5.6	128	3	US-08-990-571-41	Sequence 41, Appl	976	62.5	5.6	331	3	US-09-467-638-5	Sequence 5, Appli
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907	63	5.6	133	4	US-09-252-991A-23872	Sequence 23872, A	980	62.5	5.6	362	4	US-09-248-796A-21767	Sequence 21767, A
908	63	5.6	141	4	US-09-252-991A-25829	Sequence 25829, A	981	62.5	5.6	366	4	US-09-328-352-6517	Sequence 6517, Ap
909	63	5.6	157	4	US-09-270-767-59757	Sequence 59757, A	982	62.5	5.6	367	3	US-09-378-088A-54	Sequence 54, Appl
910	63	5.6	161	4	US-09-252-991A-27097	Sequence 27097, A	983	62.5	5.6	367	4	US-09-643-596B-84	Sequence 84, Appl
911	63	5.6	178	4	US-09-252-991A-20280	Sequence 20280, A	984	62.5	5.6	371	3	US-09-378-088A-64	Sequence 64, Appl
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915	63	5.6	204	4	US-09-248-796A-16962	Sequence 16962, A	988	62.5	5.6	385	3	US-08-844-188-11	Sequence 11, Appl
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918	63	5.6	248	4	US-09-533-023-22	Sequence 22, Appl	991	62.5	5.6	385	3	US-09-378-088A-116	Sequence 116, App
919	63	5.6	291	6	5194600-2	Sequence 22, Appl	992	62.5	5.6	385	4	US-09-548-334A-11	Sequence 11, Appl
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921	63	5.6	302	4	US-09-252-991A-21231	Sequence 21231, A	994	62.5	5.6	385	4	US-09-547-621-11	Sequence 11, Appl
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931	63	5.6	436	4	US-09-252-991A-17926	Sequence 17926, A	1004	62.5	5.6	402	3	US-09-063-237-1	Sequence 1, Appli
932	63	5.6	442	4	US-09-248-796A-26457	Sequence 26457, A	1005	62.5	5.6	402	3	US-08-713-556F-2	Sequence 2, Appli
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937	63	5.6	462	2	US-08-865-597A-2	Sequence 2, Appli	1010	62.5	5.6	412	2	US-08-477-254B-4	Sequence 4, Appli
938	63	5.6	463	4	US-09-248-796A-14184	Sequence 14184, A	1011	62.5	5.6	412	2	US-08-428-734B-4	Sequence 4, Appli
939	63	5.6	516	4	US-09-902-540-11496	Sequence 11496, A	1012	62.5	5.6	412	3	US-08-713-556F-4	Sequence 4, Appli
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947	63	5.6	817	4	US-09-248-796A-20276	Sequence 20276, A	1020	62.5	5.6	462	2	US-08-095-728B-4	Sequence 4, Appli
948	63	5.6	881	4	US-09-248-796A-18627	Sequence 18627, A	1021	62.5	5.6	462	5	PCT-US92-02320A-4	Sequence 4, Appli
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1036	62.5	5.6	797	5	PCt-US92-02320A-2	Sequence 2, Appli	1109	62	5.5	165	4	US-09-675-776-2	Sequence 2, Appli
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1041	62.5	5.6	877	2	US-08-916-917-2	Sequence 2, Appli	1114	62	5.5	166	4	US-09-252-991A-17450	Sequence 17450, A
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1043	62.5	5.6	877	2	US-08-972-623-2	Sequence 2, Appli	1116	62	5.5	167	2	US-08-997-362-112	Sequence 112, App
1044	62.5	5.6	877	2	US-08-972-630-2	Sequence 2, Appli	1117	62	5.5	167	3	US-09-095-855-112	Sequence 112, App
1045	62.5	5.6	877	2	US-08-672-211-2	Sequence 2, Appli	1118	62	5.5	167	3	US-09-324-542-112	Sequence 112, App
1046	62.5	5.6	877	3	US-09-225-170-2	Sequence 2, Appli	1119	62	5.5	167	4	US-09-205-436-112	Sequence 112, App
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1058	62.5	5.6	1813	4	US-09-949-016-8284	Sequence 8284, Ap	1131	62	5.5	235	4	US-09-102-530-2	Sequence 2, Appli
1059	62.5	5.6	1813	4	US-09-949-016-8285	Sequence 8285, Ap	1132	62	5.5	235	4	US-09-949-016-6661	Sequence 6661, Ap
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1197	62	5.5	1852	4	US-10-023-649A-2	Sequence 2, Appli	1270	61.5	5.5	716	3	US-08-971-188-11	Sequence 11, Appl
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1332	61	5.4	523	3	US-09-302-620B-95	Sequence 95, Appli	1405	60.5	5.4	274	4	US-09-270-767-40695	Sequence 40695, A
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1335	61	5.4	533	1	US-08-413-118-15	Sequence 15, Appli	1408	60.5	5.4	277	4	US-09-270-767-43705	Sequence 43705, A
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1338	61	5.4	587	4	US-09-857-669-6	Sequence 6, Appli	1411	60.5	5.4	289	4	US-09-071-035-480	Sequence 480, App
1339	61	5.4	608	4	US-09-489-039A-13204	Sequence 13204, A	1412	60.5	5.4	296	4	US-09-667-135-36	Sequence 36, Appli
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1341	61	5.4	635	4	US-09-417-197-125	Sequence 125, App	1414	60.5	5.4	305	1	US-08-090-013-2	Sequence 2, Appli
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1343	61	5.4	682	4	US-09-270-767-45389	Sequence 45389, A	1416	60.5	5.4	305	1	US-08-232-249-2	Sequence 2, Appli
1344	61	5.4	726	4	US-09-583-110-2782	Sequence 2782, Ap	1417	60.5	5.4	305	2	US-08-921-426-8	Sequence 8, Appli
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1346	61	5.4	732	4	US-09-134-000C-6359	Sequence 6359, Ap	1419	60.5	5.4	305	2	US-08-140-008A-4	Sequence 4, Appli
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1350	61	5.4	784	3	US-09-371-913A-7	Sequence 7, Appli	1423	60.5	5.4	305	3	US-09-189-060B-56	Sequence 56, Appli
1351	61	5.4	784	4	US-09-967-805-7	Sequence 7, Appli	1424	60.5	5.4	305	3	US-09-230-665-2	Sequence 2, Appli
1352	61	5.4	860	1	US-08-092-817-4	Sequence 4, Appli	1425	60.5	5.4	305	4	US-09-402-664A-12	Sequence 12, Appli
1353	61	5.4	860	1	US-08-485-128-4	Sequence 4, Appli	1426	60.5	5.4	305	4	US-09-189-028-2	Sequence 2, Appli
1354	61	5.4	860	4	US-09-804-778A-8	Sequence 8, Appli	1427	60.5	5.4	305	5	PCT-US95-07743-8	Sequence 8, Appli
1355	61	5.4	860	4	US-09-824-637-4	Sequence 4, Appli	1428	60.5	5.4	342	3	US-09-193-562D-13	Sequence 13, Appli
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1368	61	5.4	1410	3	US-09-037-188-4	Sequence 4, Appli	1441	60.5	5.4	446	3	US-09-004-393B-4	Sequence 4, Appli
1369	61	5.4	1410	3	US-09-285-310-4	Sequence 4, Appli	1442	60.5	5.4	450	4	US-09-071-035-256	Sequence 256, App
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1383	60.5	5.4	162	4	US-09-252-991A-24953	Sequence 24953, A	1456	60.5	5.4	586	2	US-09-005-069-70	Sequence 70, Appli
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1386	60.5	5.4	173	4	US-09-825-561A-86	Sequence 86, Appli	1459	60.5	5.4	586	4	US-09-981-799A-30	Sequence 30, Appli
1387	60.5	5.4	174	4	US-09-248-796A-25211	Sequence 25211, A	1460	60.5	5.4	608	4	US-09-270-767-43297	Sequence 43297, A


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; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match          100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114; Mismatches 0; Indels 0; Gaps 0;
Matches 218; Conservative 0;

QY 1 TRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 60
Db 17 TRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 76
QY 61 ALKASFTCSYGVWDGFWVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db 77 ALKASFTCSYGVWDGFWVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
QY 121 NSCIPEIITTKDPIENTOTATOTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI 180
Db 137 NSCIPEIITTKDPIENTOTATOTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI 196
QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAGFG 218
Db 197 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAGFG 234
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RESULT 3

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; Sequence 201, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
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; CURRENT APPLICATION NUMBER: US/09/905.125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match          100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114; Mismatches 0; Indels 0; Gaps 0;
Matches 218; Conservative 0;

QY 1 TRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 60
Db 17 TRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 76
QY 61 ALKASFTCSYGVWDGFWVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db 77 ALKASFTCSYGVWDGFWVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
QY 121 NSCIPEIITTKDPIENTOTATOTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI 180
Db 137 NSCIPEIITTKDPIENTOTATOTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI 196
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RESULT 4

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; Sequence 201, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match      100.08; Score 1125; DB 4; Length 322;
Best Local Similarity 100.08; Pred. No. 7,7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1  TRLLVQGSRAEELSIOVSCRIMGTLTVSKKANQOLNFEATEACRLGLSLAGKDQVET 60
Db      17  TRLLVQGSRAEELSIOVSCRIMGTLTVSKKANQOLNFEATEACRLGLSLAGKDQVET 76

Qy      61  ALKASFETCSYGVWGDFPWWISRISSPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
Db      77  ALKASFETCSYGVWGDFPWWISRISSPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy      121  NSCIPEIITTKDPINFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTTPPAPASTSI 180
Db      137  NSCIPEIITTKDPINFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTTPPAPASTSI 196

Qy      181  KKLICVTEVFNETSTMSTETETPEFVENKAAFKNKAAAGFG 218
Db      197  KKLICVTEVFNETSTMSTETETPEFVENKAAFKNKAAAGFG 234

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RESULT 6

Sequence 201, Application US/09903603A
Patent No. 6767995
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A

RESULT 7

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; Sequence 201, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
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; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLGLSLAGKDQVET 60
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Db 137 NSCIPEIITTKDPIENTQTATQTTFEIVSDSTYSVASPYSTIPAPTTTPAPASTSIPRR 196
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RESULT 8

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; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match      100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 60
Db 17 TRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 76

QY 61 ALKASFETCSYGVWGDGFVVISRIENPKCGKNGVGLWKVPVSRQFAAYCYNSSDWT 120
Db 77 ALKASFETCSYGVWGDGFVVISRIENPKCGKNGVGLWKVPVSRQFAAYCYNSSDWT 136

QY 121 NSCIPEIITTKDPIFNQTQTATTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 180
Db 137 NSCIPEIITTKDPIFNQTQTATTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 196

QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFG 218
Db 197 KKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFG 234
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RESULT 9

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; Sequence 201, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
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; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match      100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 60
Db 17 TRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 76

QY 61 ALKASFETCSYGVWGDGFVVISRIENPKCGKNGVGLWKVPVSRQFAAYCYNSSDWT 120
Db 77 ALKASFETCSYGVWGDGFVVISRIENPKCGKNGVGLWKVPVSRQFAAYCYNSSDWT 136

QY 121 NSCIPEIITTKDPIFNQTQTATTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 180
Db 137 NSCIPEIITTKDPIFNQTQTATTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 196

QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFG 218
Db 197 KKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFG 234
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RESULT 10

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; Sequence 201, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
```


APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,618
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 201
LENGTH: 322
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic protein
Query Match 100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7,7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TRLLVQGSRLAEELSIQVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQVET 60
Db 17 TRLLVQGSRLAEELSIQVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQVET 76

QY 61 ALKASFETCSYGVGDGFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db 77 ALKASFETCSYGVGDGFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
QY 121 NSCIPEIITTKDPIFNQTQTATOTTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 180
Db 137 NSCIPEIITTKDPIFNQTQTATOTTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 196
QY 181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFG 218
Db 197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFG 234
RESULT 11.
US-09-949-016-7765
Sequence 7765: Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7765
LENGTH: 344
TYPE: PRT
ORGANISM: Human
US-09-949-016-7765
Query Match 100.0%; Score 1125; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 8.5e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TRLLVQGSRLAEELSIQVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQVET 60
Db 39 TRLLVQGSRLAEELSIQVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQVET 98
QY 61 ALKASFETCSYGVGDGFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db 99 ALKASFETCSYGVGDGFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 158
QY 121 NSCIPEIITTKDPIFNQTQTATOTTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 180
Db 159 NSCIPEIITTKDPIFNQTQTATOTTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 218
QY 181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFG 218
Db 219 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFG 256

RESULT 12
US-08-892-880-2
Sequence 2, Application US/08892880
Patent No. 5942417
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

```

; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 322 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-892-880-2

Query Match 99.5%; Score 1119; DB 2; Length 322;
Best Local Similarity 99.5%; Pred. No. 3.5e-113;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRLLVQSLRAEELSIOVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKDOVET 60
DB 17 TRLLVQSLRAEELSIOVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKDOVET 76
QY 61 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
DB 77 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
QY 121 NSCIPETITKDPINFTQTATQTFEIVSDSTYSVASPYSTIPATPTTTPAPASTSIPRR 180
DB 137 NSCIPETITKDPINFTQTATQTFEIVSDSTYSVASPYSTIPATPTTTPAPASTSIPRR 196
QY 181 KKLICVTEVFMTETSTMSTETEPFVENKAAFKNEAGFG 218
DB 197 KKLICVTEVFMTETSTMSTETEPFVENKAAFKNEAGFG 234

RESULT 13
US-09-724-864-60
; Sequence 60, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-60

; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 322 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-892-880-2

Query Match 99.5%; Score 669; DB 3; Length 318;
Best Local Similarity 61.0%; Pred. No. 2.7e-64;
Matches 133; Conservative 28; Mismatches 53; Indels 4; Gaps 3;

QY 1 TRLLVQSLRAEELSIOVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKDOVET 60
DB 17 TRHPVQGADLVQDLISLIS-TCRIMGVALVGRKNPOMNFTNEACRMLGLTILASRDQVES 75
QY 61 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
DB 76 AOKSGFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 135
QY 121 NSCIPETITKDPINFTQTATQTFEIVSDSTYSVASPYSTIPATPTTTPAPASTSIPRR 180
DB 136 NSCIPETITKDPINFTQTATQTFEIVSDSTYSVASPYSTIPATPTTTPAPASTSIPRR 192
QY 181 KKLICVTEVFMTETSTMSTETEPFVENKAAFKNEAGFG 218
DB 193 TKKICITEVYETPMATETEAFAVSGAFAFKNEAGFG 230

RESULT 14
US-08-892-880-3
; Sequence 3, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-892-880-3

Query Match 19.0%; Score 213.5; DB 2; Length 339;
Best Local Similarity 32.1%; Pred. No. 9.6e-15;
Matches 51; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 4 LVQGSRLAEELSIOVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKDOVETALK 63
DB 17 TRLLVQSLRAEELSIOVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKDOVET 76
QY 181 KKLICVTEVFMTETSTMSTETEPFVENKAAFKNEAGFG 218
DB 197 KKLICVTEVFMTETSTMSTETEPFVENKAAFKNEAGFG 234
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Db 15 LLQLSLAQOQIDLNTCRVAGVHVHVEKNGRYSISRTEAADLCEAFNTTLPTHAQMELALR 74
QY 64 ASFETCSYGVWGDGFVVISRI8PNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDWTWNSC 123
Db 75 KGFETCRYGFI-EGHVVI8PRIHPNAICAAANTGVYILLASNTSHYDYTCFNASAPLEEDC 133
QY 124 IPEIITTKDPIENTQTATOTTEFIVSDST-YVASPYST 161
Db 134 -----TSVTDLPNSFDGVPVTITIVNRDGRYKKGGEYRT 167

RESULT 15
US-07-946-497-2
; Sequence 2, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-946-497-2

Query Match 19.0%; Score 213.5; DB 1; Length 503;
Best Local Similarity 32.1%; Pred. No. 1.7e-14;
Matches 51; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 4 LVQGSRLAEELSIOVSCRIMGITLVSKKANQOQINFTEAKEACRLILGLSLAGKQVETALK 63
Db 15 LLQLSLAQOQIDLNTCRVAGVHVHVEKNGRYSISRTEAADLCEAFNTTLPTHAQMELALR 74
QY 64 ASFETCSYGVWGDGFVVISRI8PNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDWTWNSC 123
Db 75 KGFETCRYGFI-EGHVVI8PRIHPNAICAAANTGVYILLASNTSHYDYTCFNASAPLEEDC 133
QY 124 IPEIITTKDPIENTQTATOTTEFIVSDST-YVASPYST 161
Db 134 -----TSVTDLPNSFDGVPVTITIVNRDGRYKKGGEYRT 167
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Search completed: October 5, 2005, 17:26:16
Job time : 34.5296 secs

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GenCore version 5.1.6
 OM protein - protein search, using sw model
 Run on: October 5, 2005, 17:07:32 ; Search time 93.6593 Seconds
 (without alignments)
 900.218 Million cell updates/sec

Title: US-10-063-510-6_COPY_17_234
 Perfect score: 1125
 Sequence: 1 TRLLVQSLRAELSLQVSC.....ETEPFVENKAAPKNEAGFG 218
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 2105692
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%

Database :
 Listing first 1500 summaries
 Maximum Match 100%
 1: A_Geneseq_16Dec04:*
 2: Geneseqp1980s:*
 3: Geneseqp1990s:*
 4: Geneseqp2000s:*
 5: Geneseqp2001s:*
 6: Geneseqp2002s:*
 7: Geneseqp2003as:*
 8: Geneseqp2003bs:*
 9: Geneseqp2004s:*
 10: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAB34702	standard; protein; 250 AA.				
DE	Human secreted protein encoded by DNA clone vb28 1.					
PN	WO200055175-A1.					
PD	21-SEP-2000.					
PA	(ALPH-) ALPHAGENE INC.					
Query Match	100.0%;	Score 1125;	DB 3;	Length 250;		
Best Local Similarity	100.0%;	Pred. No. 4.5e-102;				
RESULT 2						
ID	AAV13379	standard; protein; 322 AA.				
DE	Amino acid sequence of protein PRO263.					
PN	WO9914328-A2.					
PD	25-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1125;	DB 2;	Length 322;		
Best Local Similarity	100.0%;	Pred. No. 6.3e-102;				
RESULT 3						
ID	AAV87287	standard; protein; 322 AA.				
DE	Human signal peptide containing protein HSPP-64 SEQ ID NO:64.					
PN	WO20000610-A2.					
PD	06-JAN-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match	100.0%;	Score 1125;	DB 3;	Length 322;		
Best Local Similarity	100.0%;	Pred. No. 6.3e-102;				
RESULT 4						
ID	ADC78521	standard; protein; 322 AA.				
DE	Human PRO263 protein.					
PN	WO200015796-A2.					
PD	23-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1125;	DB 3;	Length 322;		
Best Local Similarity	100.0%;	Pred. No. 6.3e-102;				
RESULT 5						
ID	AAB80247	standard; protein; 322 AA.				
DE	Human PRO263 protein.					
PN	WO200104311-A1.					
PD	18-JAN-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1125;	DB 4;	Length 322;		
Best Local Similarity	100.0%;	Pred. No. 6.3e-102;				
RESULT 6						
ID	AAB87528	standard; protein; 322 AA.				

DE Human PRO263.
 PN WO200116318-A2.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1125; DB 4; Length 322;
 Best Local Similarity 100.0%; Pred. No. 6.3e-102;
 RESULT 7
 ID AAB88391 standard; protein; 322 AA.
 DE Human membrane or secretory protein clone PSEC0135.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELL-) HELIX RES INST.
 Query Match 100.0%; Score 1125; DB 4; Length 322;
 Best Local Similarity 100.0%; Pred. No. 6.3e-102;
 RESULT 8
 ID ABG95853 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein PRO263.
 PN US200219130-A1.
 PD 29-AUG-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1125; DB 5; Length 322;
 Best Local Similarity 100.0%; Pred. No. 6.3e-102;
 RESULT 9
 ID ABB84832 standard; protein; 322 AA.
 DE Human PRO263 protein sequence SEQ ID NO:32.
 PN WO200200690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1125; DB 5; Length 322;
 Best Local Similarity 100.0%; Pred. No. 6.3e-102;
 RESULT 10
 ID ABB95438 standard; protein; 322 AA.
 DE Human angiogenesis related protein PRO263 SEQ ID NO: 32.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANT/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 1125; DB 5; Length 322;
 Best Local Similarity 100.0%; Pred. No. 6.3e-102;
 RESULT 11
 ID ABU71625 standard; protein; 322 AA.
 DE Human PRO polypeptide #36.
 PN US2002146709-A1.
 PD 10-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1125; DB 6; Length 322;
 Best Local Similarity 100.0%; Pred. No. 6.3e-102;
 RESULT 12
 ID ABU71480 standard; protein; 322 AA.
 DE Human PRO polypeptide #36.
 PN US2002192859-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1125; DB 6; Length 322;
 Best Local Similarity 100.0%; Pred. No. 6.3e-102;
 RESULT 13
 ID ABU71926 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein PRO263.
 PN US2003003530-A1.

PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 14
ID ABO01809 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 15
ID ABU09078 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 16
ID ABO33937 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 17
ID ABU71954 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 18
ID ABU54382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 19
ID ABO47397 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 20
ID ABU71508 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 21
ID ABU7289 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 22
ID ABU90962 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 23
ID ABO27283 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 24
ID ABU64534 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 25
ID ABU67380 standard; protein; 322 AA.
DE Human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 26
ID ABU92478 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 27
ID ABO14900 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 28
ID ABU81148 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 29
ID ABO53263 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 30
ID ABU98265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 31
ID ABU9270 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 32
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 33
ID ABO69657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 34
ID ABO96441 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 35
ID ABO72111 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 36
ID ABO14839 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 37
ID ADB29406 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 38
ID ADB17063 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 39
ID ABO44241 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 40
ID ADA18262 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 41
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 42
ID ADA19868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 43
ID ADB17251 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 44
ID ABO34851 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 45
ID ADA16237 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 46
ID ADA20040 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 47
ID ABO34169 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 48
ID ADA42382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 49
ID ABO17529 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 50
ID ADA00337 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 51
ID ADA16661 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US200303969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 52
ID ADA13090 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 53
ID ADA11958 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 54
ID ADA17305 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 55
ID ADA42808 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 56
ID ABO17590 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 57
ID ADB85579 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 58
ID ADB77727 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 59

ID ADB74863 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 60
ID ADB68258 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 61
ID ADB68065 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 62
ID ADB90882 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 63
ID ADC28509 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 64
ID ADC39709 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 65
ID ADC40223 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 66
ID ADC19047 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 67
ID ADC34347 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 68
ID ADC29402 standard; protein; 322 AA.

DE Human secreted/transmembrane protein, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 69
ID ADC28933 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 70
ID ADC40818 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 71
ID ADC19475 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 72
ID ADC06962 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 73
ID ADC17141 standard; protein; 322 AA.
DE Mammalian PRO polypeptide (SeqID 6).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 74
ID ADC33923 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 75
ID ADC12993 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 76
ID ADC14839 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 77
ID ADC52334 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.

PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 78
ID ADC12445 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 79
ID ADD10321 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 80
ID ADD05000 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 81
ID ADD11281 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 82
ID ADD04006 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 83
ID ADD03582 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 84
ID ADD37074 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 85
ID ADD36010 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 86
ID ADE34834 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077583-A1.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 87
ID ADG01011 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003078387-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 88
ID ADG08564 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 89
ID ADF95185 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 90
ID ADH24038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 91
ID ADH34064 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 92
ID ADH29897 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 93
ID ADH23868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 94
ID ADG85272 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 95
ID ADH24548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 96
ID ADH37404 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 97
ID ADH01993 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 98
ID ADH37574 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 99
ID ADG85612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 100
ID ADH24208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 101
ID ADH38502 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 102
ID ADG83623 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 103
ID ADH29431 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 104
ID ADH27547 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 105
ID ADH37744 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 106
ID ADH37921 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 107
ID ADH57341 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 108
ID ADH59317 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 109
ID ADH53483 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 110
ID ADH53653 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 111
ID ADH51989 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 112
ID ADH49844 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 113
ID ADI25354 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 114
ID ADH90147 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 115
ID ADI25524 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 116
ID ADH97698 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 117
ID ADI38096 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 118
ID ADI03546 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 119
ID ADI11903 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 120
ID ADH89977 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 121
ID ADH98378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 122
ID ADI11053 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 123
ID ADI25354 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1125; DB 7; Length 322;
RESULT 124
ID ADH90147 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

DE Human PRO polypeptide #3.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 142
ID ADI05370 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 143
ID ADH79442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 144
ID ADI19399 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 145
ID ADI05200 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 146
ID ADH79612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 147
ID ADI01438 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 148
ID ADI01608 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 149
ID ADI01778 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 150
ID ADH7982 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 151
ID ADI04600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 152
ID ADI02736 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 153
ID ADH78055 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 154
ID ADI25694 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 155
ID ADI25864 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 156
ID ADK65376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 157
ID ADH98718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 158
ID ADH79959 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 159
ID ADJ26364 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054349-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 160
ID ADL93690 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 161
ID ADC52144 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 162
ID ADE79279 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 163
ID ADE79703 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 164
ID ADE73379 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 165
ID ADE41282 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 166
ID ADE71444 standard; protein; 322 AA.
DE Human PDEBC Incyte 3044710CD1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 167
ID ADE73914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 168
ID ADE99468 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211576-A1.

PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 169
ID ADE98587 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 170
ID ADE99014 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 171
ID ADG40484 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 172
ID ADF73878 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 173
ID ADF73454 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 174
ID ADH06576 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 175
ID ADH06406 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 176
ID ADG68827 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;

Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 177
ID ADH2717 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 178
ID ADH25058 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 179
ID ADH33690 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 180
ID ADG92297 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 181
ID ADH02333 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 182
ID ADH07940 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 183
ID ADG69337 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 184
ID ADH39158 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 185
ID ADG92724 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 186
ID ADG3898 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 187
ID ADG85442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 188
ID ADH06236 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 189
ID ADH30066 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 190
ID ADH24378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 191
ID ADG69507 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 192
ID ADH07770 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 193
ID ADG85782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 194
ID ADH39328 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 195

ID ADH33520 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 196
ID ADH33860 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 197
ID ADH01070 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 198
ID ADG59677 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 199
ID ADH02163 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 200
ID ADG59167 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 201
ID ADG85952 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 202
ID ADH24888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 203
ID ADH39505 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 204
ID ADH02503 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180940-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 205
ID ADG68997 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 206
ID ADH07600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 207
ID ADG86122 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 208
ID ADH24718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 209
ID ADH25766 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 210
ID ADH38332 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 211
ID ADH20513 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 212
ID ADH57171 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 213
ID ADH43465 standard; protein; 322 AA.
DE Human PRO polypeptide #16.

PN US2003224984-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 214
ID ADH07368 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 215
ID ADH52159 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 216
ID ADH59913 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 217
ID ADH49525 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 218
ID ADH06941 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 219
ID ADH90487 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 220
ID ADI11223 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 221
ID ADI18683 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 222
ID ADH98888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 223
ID ADI65403 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 224
ID ADI02118 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 225
ID ADH90657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 226
ID ADI37666 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 227
ID ADH97462 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 228
ID ADI65830 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 229
ID ADH60573 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.

PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 230
ID ADJ99630 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 231
ID ADL08823 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 232
ID ADJ99532 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 233
ID ADJ98702 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 234
ID ADH78861 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 235
ID ADJ99095 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 236
ID ADJ99265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 237
ID ADJ98883 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 238
ID ADH79031 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181702-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 239
ID ADK00891 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 240
ID ADK14412 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 241
ID ADM25164 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 242
ID ADM29914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 243
ID ADK82810 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 244
ID ADM80861 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 245
ID ADO06236 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 246
ID ADR11088 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 247
ID ADR19997 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004147017-A1.
PD 29-JUL-2004.

PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 248
ID ADT03673 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004185531-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 249
ID ADS74636 standard; protein; 322 AA.
DE Human secreted/transmembrane protein #40.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 250
ID ABB11979 standard; peptide; 344 AA.
DE Human PRO263 homologue, SEQ ID NO:2349.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1125; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 6.9e-102;
RESULT 251
ID ADR41495 standard; protein; 344 AA.
DE Human CD-like molecule HEMFC27, SEQ ID NO:294.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1125; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 6.9e-102;
RESULT 252
ID AAW56249 standard; protein; 322 AA.
DE Amino acid sequence of a CD44-like protein.
PN WO9806839-A1.
PD 19-FEB-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.5%; Score 1119; DB 2; Length 322;
Best Local Similarity 99.5%; Pred. No. 2.5e-101;
RESULT 253
ID ABB90289 standard; protein; 322 AA.
DE Human polypeptide SEQ ID NO 2665.
PN WO200130304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.5%; Score 1119; DB 5; Length 322;
Best Local Similarity 99.5%; Pred. No. 2.5e-101;
RESULT 254
ID ADN05866 standard; protein; 322 AA.
DE Antipsoriatic protein sequence #1096.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 98.3%; Score 1106; DB 8; Length 322;
Best Local Similarity 98.6%; Pred. No. 4.7e-100;
RESULT 255
ID ADQ21089 standard; protein; 322 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3909.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 98.3%; Score 1106; DB 8; Length 322;
Best Local Similarity 98.6%; Pred. No. 4.7e-100;
RESULT 256
ID ABU69126 standard; protein; 297 AA.
DE Human NOVX polypeptide #1.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 87.1%; Score 979.5; DB 6; Length 297;
Best Local Similarity 88.5%; Pred. No. 1.2e-87;
RESULT 257
ID ADO08255 standard; protein; 297 AA.
DE Human NOVX polypeptide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLER I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.

PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHINKETS R A.
PA (SPYER/) SPYTER K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 87.1%; Score 979.5; DB 8; Length 297;
Best Local Similarity 88.5%; Pred. No. 1.2e-87;
RESULT 258
ID ABB72376 standard; protein; 255 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 700.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 59.5%; Score 669; DB 5; Length 255;
Best Local Similarity 61.0%; Pred. No. 3.4e-57;
RESULT 259
ID AAE05364 standard; protein; 318 AA.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 59.5%; Score 669; DB 4; Length 318;
Best Local Similarity 61.0%; Pred. No. 4.6e-57;
RESULT 260
ID AAY12323 standard; protein; 116 AA.
DE Human 5' EST secreted protein SEQ ID NO:354.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 45.3%; Score 510; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.3e-42;
RESULT 261
ID ABB81033 standard; protein; 364 AA.
DE Rat glycoprotein CD44 polypeptide.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM-) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 19.0%; Score 213.5; DB 5; Length 364;
Best Local Similarity 32.1%; Pred. No. 3.6e-12;
RESULT 262
ID AAR14768 standard; protein; 503 AA.
DE Metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL-) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Query Match 19.0%; Score 213.5; DB 2; Length 503;
Best Local Similarity 32.1%; Pred. No. 5.6e-12;
RESULT 263
ID ADE57911 standard; protein; 503 AA.
DE Rat Protein P26051, SEQ ID NO 3777.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 19.0%; Score 213.5; DB 7; Length 503;
Best Local Similarity 32.1%; Pred. No. 5.6e-12;
RESULT 264
ID ABU04619 standard; protein; 668 AA.
DE Human expressed protein tag (EPT) #1285.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.5%; Score 208.5; DB 6; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.5e-11;
RESULT 265
ID ADQ39384 standard; protein; 668 AA.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 18.5%; Score 208.5; DB 8; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.5e-11;
RESULT 266
ID AAR07355 standard; protein; 362 AA.
DE B7 adhesion receptor.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.
Query Match 18.1%; Score 203.5; DB 2; Length 362;
Best Local Similarity 27.3%; Pred. No. 3.5e-11;
RESULT 267
ID ABU04653 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1319.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 268
ID ABU04616 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1282.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 269
ID ADP65295 standard; protein; 742 AA.
DE Human CD44 antigen (homing function and Indian blood group system), CD44.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 18.0%; Score 203; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 270
ID ADL61252 standard; protein; 742 AA.
DE Human protein tyrosine kinase biomarker CD44 antigen protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 18.0%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 271
ID ADQ39391 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 18.0%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 272
ID ADR67253 standard; protein; 742 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR-) HERR A.
PA (HINZ-) HINZMANN B.
PA (DAHL-) DAHL E.
PA (STAU-) STAUB E.
PA (PILA-) PILARSKY C.
PA (SPEC-) SPECHT T.
Query Match 18.0%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 273
ID ABU04618 standard; protein; 675 AA.
DE Human expressed protein tag (EPT) #1284.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.

Query Match 18.0%; Score 202; DB 6; Length 675;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 274
ID ABU04621 standard; protein; 691 AA.
DE Human expressed protein tag (EPT) #1287.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 202; DB 6; Length 691;
Best Local Similarity 26.0%; Pred. No. 1.2e-10;
RESULT 275
ID ADQ39390 standard; protein; 691 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 18.0%; Score 202; DB 8; Length 691;
Best Local Similarity 26.0%; Pred. No. 1.2e-10;
RESULT 276
ID ADQ39386 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1286.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 277
ID ABU04645 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1311.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 278
ID ADN95511 standard; protein; 742 AA.
DE Human BEC/LEC-related protein sequence SeqID434.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN-) LICENTIA LTD.
Query Match 18.0%; Score 202; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 279
ID ADL93506 standard; protein; 742 AA.
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 18.0%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 280
ID ADQ55181 standard; protein; 742 AA.
DE Protein #83 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 18.0%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 281
ID ADQ39383 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 18.0%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 282
ID ADQ39386 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.

Query Match 18.0%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 283
ID ABP72424 standard; protein; 608 AA.
DE Human CD44 variant CD44VRA associated with rheumatoid arthritis.
PN WO2003014160-A2.
PD 20-FEB-2003.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.8%; Score 200.5; DB 6; Length 608;
Best Local Similarity 25.2%; Pred. No. 1.4e-10;
RESULT 284
ID ADD90596 standard; protein; 699 AA.
DE Human CD44v glycoprotein SEQ ID NO:6.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.8%; Score 200.5; DB 7; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.7e-10;
RESULT 285
ID AAY97579 standard; protein; 700 AA.
DE Human CD44 splice variant (RA-CD44) protein sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Query Match 17.8%; Score 200.5; DB 4; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.7e-10;
RESULT 286
ID ABU04640 standard; protein; 700 AA.
DE Human expressed protein tag (EPT) #1306.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.8%; Score 200.5; DB 6; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.7e-10;
RESULT 287
ID ADD90594 standard; protein; 700 AA.
DE Human CD44v glycoprotein SEQ ID NO:4.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.8%; Score 200.5; DB 7; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.7e-10;
RESULT 288
ID AAR20817 standard; protein; 493 AA.
DE Epithelial CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GHO) GEN HOSPITAL CORP.
Query Match 17.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.3e-10;
RESULT 289
ID AAR91445 standard; protein; 493 AA.
DE Human epithelial CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GHO) GEN HOSPITAL CORP.
Query Match 17.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.3e-10;
RESULT 290
ID AAW80454 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GHO) GEN HOSPITAL CORP.
Query Match 17.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.3e-10;
RESULT 291
ID AAW89151 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5849898-A.
PD 15-DEC-1998.

PA (GEHO) GEN HOSPITAL CORP. Query Match 17.7%; Score 199.5; DB 2; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 292 ID AAY96140 standard; protein; 493 AA. DE Human epithelial CD44. PN US6111093-A. PD 29-AUG-2000. PA (GEHO) GEN HOSPITAL CORP. Query Match 17.7%; Score 199.5; DB 3; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 293 ID AAU02449 standard; protein; 493 AA. DE Human epithelial antigen CD44 polypeptide. PN US6218525-B1. PD 17-APR-2001. PA (GEHO) GEN HOSPITAL CORP. Query Match 17.7%; Score 199.5; DB 4; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 294 ID ABU04637 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1303. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 295 ID ABU04627 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1293. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 296 ID ABU04639 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1305. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 297 ID ABU04631 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1297. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 298 ID ABU04633 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1299. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 299 ID ABU04635 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1301. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 300 ID ABU04613 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1279. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC.	Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 301 ID ADO49375 standard; protein; 493 AA. DE Human CD44 #2. PN US2004072283-A1. PD 15-APR-2004. PA (SEED/) SEED B. PA (ALIE/) ALLEN J. PA (ARUF/) ARUFFO A. PA (CAME/) CAMERINI D. PA (LAUF/) LAUFFER L. PA (OQUE/) OQUENDO C. PA (SINK/) SIMMONS D. PA (STAM/) STAMENKOVIC I. PA (STEN/) STENGELIN S. PA (AMIO/) AMIOT M. Query Match 17.7%; Score 199.5; DB 8; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 302 ID ABU79109 standard; protein; 365 AA. DE CD44 protein. PN US2002177551-A1. PD 28-NOV-2002. PA (TERM/) TERMAN D S. Query Match 17.6%; Score 198.5; DB 6; Length 365; Best Local Similarity 31.8%; Pred. No. 1.1e-10; RESULT 303 ID ADF43353 standard; protein; 365 AA. DE CD44 receptor polypeptide seq id 73. PN US2003157113-A1. PD 21-AUG-2003. PA (TERM/) TERMAN D S. Query Match 17.6%; Score 198.5; DB 7; Length 365; Best Local Similarity 31.8%; Pred. No. 1.1e-10; RESULT 304 ID AAU99123 standard; protein; 493 AA. DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein. PN WO200244342-A2. PD 06-JUN-2002. PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC. Query Match 17.6%; Score 198.5; DB 5; Length 493; Best Local Similarity 23.6%; Pred. No. 1.6e-10; RESULT 305 ID ABU04623 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1289. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.6%; Score 198.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.6e-10; RESULT 306 ID ABU04612 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1278. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.6%; Score 198.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.6e-10; RESULT 307 ID ADL91507 standard; protein; 493 AA. DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2. PN WO2004024750-A2. PD 25-MAR-2004. PA (DYAX-) DYAX CORP. Query Match 17.6%; Score 198.5; DB 8; Length 493; Best Local Similarity 23.6%; Pred. No. 1.6e-10; RESULT 308 ID ABU04617 standard; protein; 425 AA. DE Human expressed protein tag (EPT) #1283. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC.
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Query Match 17.6%; Score 198; DB 6; Length 425;
Best Local Similarity 24.4%; Pred. No. 1.5e-10;
RESULT 309
ID AAR20816 standard; protein; 361 AA.
DE Haematopoietic CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 310
ID AAR91444 standard; protein; 361 AA.
DE Human haematopoietic CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 311
ID AAW80453 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 312
ID AAW86200 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 313
ID AAY9851 standard; protein; 361 AA.
DE Human CD44 cell surface adhesion receptor.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 17.5%; Score 197; DB 3; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 314
ID AAY96139 standard; protein; 361 AA.
DE Human haematopoietic CD44.5.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 3; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 315
ID AAU02448 standard; protein; 361 AA.
DE Human haematopoietic antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 4; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 316
ID ABU04632 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1298.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 317
ID ABU04643 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1309.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 318
ID ABU04610 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 319
ID ABU04638 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1304.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 320
ID ABU04634 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1300.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 321
ID ABU04626 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1294.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 322
ID ABU04630 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1296.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 323
ID ABU04609 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 324
ID ABU04644 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1310.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 325
ID ABU04636 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1302.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 326
ID ADO49373 standard; protein; 361 AA.
DE Human CD44 #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALIE/) ALLEN J.
PA (ARUF/) ARUFFO A.

PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAN/) STANKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 17.5%; Score 197; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 327
ID AAY97650 standard; protein; 431 AA.
DE CD4HextraFASm/cyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 17.5%; Score 197; DB 4; Length 431;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 328
ID ABU04641 standard; protein; 431 AA.
DE Human expressed protein tag (EPT) #1307.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 431;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 329
ID AAY97651 standard; protein; 436 AA.
DE CD4Hextra/cmfAScyco protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 17.5%; Score 197; DB 4; Length 436;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 330
ID ABU04642 standard; protein; 436 AA.
DE Human expressed protein tag (EPT) #1308.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 436;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 331
ID ABU04604 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1270.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 3.8e-10;
RESULT 332
ID ABU04650 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1316.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 3.8e-10;
RESULT 333
ID ABM83594 standard; protein; 535 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 17.5%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.9e-10;
RESULT 334
ID ADQ39381 standard; protein; 535 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.5%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.9e-10;

RESULT 335
ID ABU56470 standard; protein; 699 AA.
DE Lung cancer-associated polypeptide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 17.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.1e-10;
RESULT 336
ID ABU04647 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1313.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.1e-10;
RESULT 337
ID ABU04614 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1280.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.1e-10;
RESULT 338
ID ABU04608 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1274.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.1e-10;
RESULT 339
ID ADI60182 standard; protein; 261 AA.
DE Secreted polypeptide #66.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 17.5%; Score 196.5; DB 6; Length 261;
Best Local Similarity 30.9%; Pred. No. 1.2e-10;
RESULT 340
ID ABU04611 standard; protein; 293 AA.
DE Human expressed protein tag (EPT) #1277.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 293;
Best Local Similarity 30.9%; Pred. No. 1.4e-10;
RESULT 341
ID ABU04624 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1290.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1.4e-10;
RESULT 342
ID ABU04646 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1312.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1.4e-10;
RESULT 343
ID ADH1898 standard; protein; 330 AA.
DE Human cell adhesion and extracellular matrix CAECW-25 protein - SEQ 25.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 17.4%; Score 196; DB 8; Length 330;
Best Local Similarity 30.9%; Pred. No. 1.7e-10;
RESULT 344

ID ABU04622 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1288.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 345
ID AAE30338 standard; protein; 361 AA.
DE Human CD44 antigen.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 17.4%; Score 196; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 346
ID ADD90592 standard; protein; 361 AA.
DE Human CD44std glycoprotein SEQ ID NO:2.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.4%; Score 196; DB 7; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 347
ID ADL93508 standard; protein; 361 AA.
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 17.4%; Score 196; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 348
ID ADQ39385 standard; protein; 361 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.4%; Score 196; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 349
ID ABU04615 standard; protein; 395 AA.
DE Human expressed protein tag (EPT) #1281.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 395;
Best Local Similarity 30.9%; Pred. No. 2.1e-10;
RESULT 350
ID ADQ39389 standard; protein; 395 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.4%; Score 196; DB 8; Length 395;
Best Local Similarity 30.9%; Pred. No. 2.1e-10;
RESULT 351
ID ADQ39382 standard; protein; 425 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.4%; Score 196; DB 8; Length 425;
Best Local Similarity 30.9%; Pred. No. 2.4e-10;
RESULT 352
ID ADQ39388 standard; protein; 493 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.4%; Score 196; DB 8; Length 493;
Best Local Similarity 30.9%; Pred. No. 2.9e-10;
RESULT 353

ID AAY12853 standard; protein; 58 AA.
DE Human 5' EST secreted protein SEQ ID NO:443.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 17.3%; Score 195; DB 2; Length 58;
Best Local Similarity 97.6%; Pred. No. 2.1e-11;
RESULT 354
ID ABG17071 standard; protein; 742 AA.
DE Novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 17.3%; Score 194.5; DB 4; Length 742;
Best Local Similarity 25.4%; Pred. No. 7e-10;
RESULT 355
ID AAM48306 standard; protein; 194 AA.
DE Protein R2 SEQ ID 29.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 17.2%; Score 194; DB 5; Length 194;
Best Local Similarity 30.8%; Pred. No. 1.3e-10;
RESULT 356
ID AAM48307 standard; protein; 200 AA.
DE Protein R3 SEQ ID 30.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 17.2%; Score 194; DB 5; Length 200;
Best Local Similarity 30.8%; Pred. No. 1.4e-10;
RESULT 357
ID AAM48308 standard; protein; 273 AA.
DE Protein R4 SEQ ID 31.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 17.2%; Score 194; DB 5; Length 273;
Best Local Similarity 30.8%; Pred. No. 2.1e-10;
RESULT 358
ID ABU04607 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1273.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.2%; Score 194; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 3e-10;
RESULT 359
ID ABU04602 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1268.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 1.2e-09;
RESULT 360
ID ABU04652 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1318.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 1.2e-09;
RESULT 361
ID ABU04648 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1314.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 4e-10;
RESULT 362
ID ABU04606 standard; protein; 271 AA.

DE Human expressed protein tag (EPT) #1272.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 4e-10;
RESULT 363
ID ABU04649 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1315.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 338;
Best Local Similarity 31.5%; Pred. No. 5.4e-10;
RESULT 364
ID ABU04605 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1271.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 338;
Best Local Similarity 31.5%; Pred. No. 5.4e-10;
RESULT 365
ID ABU04651 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1317.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 8.4e-10;
RESULT 366
ID ABU04603 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1269.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 8.4e-10;
RESULT 367
ID AAM48305 standard; protein; 170 AA.
DE Protein R1 SEQ ID 28.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 16.7%; Score 188; DB 5; Length 170;
Best Local Similarity 35.7%; Pred. No. 4.3e-10;
RESULT 368
ID ABP73148 standard; protein; 112 AA.
DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.6%; Score 187; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 3.1e-10;
RESULT 369
ID ABP73150 standard; protein; 113 AA.
DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.6%; Score 186.5; DB 6; Length 113;
Best Local Similarity 36.3%; Pred. No. 3.5e-10;
RESULT 370
ID ABP73151 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
Query Match 15.1%; Score 170; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e-09;
RESULT 371
ID ABP73152 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.3%; Score 183; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 7.6e-10;
RESULT 372
ID ABP73149 standard; protein; 112 AA.
DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.2%; Score 182; DB 6; Length 112;
Best Local Similarity 34.2%; Pred. No. 9.5e-10;
RESULT 373
ID ABP73153 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.1%; Score 181; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 1.2e-09;
RESULT 374
ID AAY12170 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO: 483.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 15.9%; Score 179; DB 2; Length 69;
Best Local Similarity 95.0%; Pred. No. 9.9e-10;
RESULT 375
ID ABG17067 standard; protein; 920 AA.
DE Novel human diagnostic protein #17058.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.6%; Score 175.5; DB 4; Length 920;
Best Local Similarity 25.9%; Pred. No. 6.9e-08;
RESULT 376
ID AD160410 standard; protein; 920 AA.
DE Secreted polypeptide encoded by gene splice variant #46.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 15.6%; Score 175.5; DB 7; Length 920;
Best Local Similarity 25.9%; Pred. No. 6.9e-08;
RESULT 377
ID AAM28056 standard; protein; 34 AA.
DE Peptide #2093 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 15.1%; Score 170; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e-09;
RESULT 378
ID ABG37308 standard; peptide; 34 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 15.1%; Score 170; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e-09;

RESULT 379
ID ADB64426 standard; protein; 510 AA.
DE Human protein encoded by clone FEBRA20038970.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.3%; Score 150; DB 7; Length 510;
Best Local Similarity 23.6%; Pred. No. 1e-05;
RESULT 380
ID ABP73154 standard; protein; 80 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 13.2%; Score 148.5; DB 6; Length 80;
Best Local Similarity 37.0%; Pred. No. 1.2e-06;
RESULT 381
ID ADP07712 standard; protein; 162 AA.
DE Human secreted protein, seq id 195.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 12.9%; Score 145; DB 8; Length 162;
Best Local Similarity 33.0%; Pred. No. 6.8e-06;
RESULT 382
ID ADM80807 standard; protein; 237 AA.
DE Human CADECM-36 protein SEQ ID NO:36.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.9%; Score 145; DB 8; Length 237;
Best Local Similarity 33.0%; Pred. No. 1.1e-05;
RESULT 383
ID AAR36044 standard; protein; 277 AA.
DE Tumour necrosis factor-induced glycoprotein TSG-6.
PN WO9212175-A1.
PD 23-JUL-1992.
PA (UINY-) UNIV NEW YORK STATE.
Query Match 12.9%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 384
ID AAW13654 standard; protein; 277 AA.
DE Tumour necrosis factor-stimulated gene-6 protein.
PN WO9704075-A1.
PD 06-FEB-1997.
PA (UINY-) UNIV NEW YORK STATE.
Query Match 12.9%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 385
ID AAW84087 standard; protein; 277 AA.
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.
PN US5846763-A.
PD 08-DEC-1998.
PA (UINY-) UNIV NEW YORK STATE.
Query Match 12.9%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 386
ID AAE02361 standard; protein; 277 AA.
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.
PN US6210905-B1.
PD 03-APR-2001.
PA (UINY-) UNIV NEW YORK STATE.
Query Match 12.9%; Score 145; DB 4; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 387
ID ABG70870 standard; protein; 277 AA.
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.
PN US2002090708-A1.
PD 11-JUL-2002.
PA (UINY-) UNIV NEW YORK STATE.

Query Match 12.9%; Score 145; DB 5; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 388
ID ABR58556 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:213.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.9%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 389
ID ABUS6653 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #246.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.9%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 390
ID ADE25781 standard; protein; 277 AA.
DE Human protein differentially expressed in foam cells #58.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.9%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 391
ID ADN39919 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.9%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 392
ID ADN38974 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.9%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 393
ID ADQ21506 standard; protein; 277 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4326.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.9%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 394
ID ADR51534 standard; protein; 277 AA.
DE Human lipopolysaccharide-sensitive polypeptide #14.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 12.9%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 395
ID ADK67822 standard; protein; 2626 AA.
DE Human BRCC300 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match 12.9%; Score 145; DB 8; Length 2626;
Best Local Similarity 33.0%; Pred. No. 0.00028;
RESULT 396
ID ADS95081 standard; protein; 275 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID83.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.

Query Match 12.8%; Score 144; DB 8; Length 275;
Best Local Similarity 33.0%; Pred. No. 1.7e-05;
RESULT 397
ID ABM84174 standard; protein; 2285 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4423.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.8%; Score 132.5; DB 8; Length 2285;
Best Local Similarity 27.4%; Pred. No. 0.0039;
RESULT 398
ID ABM84173 standard; protein; 2384 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4422.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.8%; Score 132.5; DB 8; Length 2384;
Best Local Similarity 27.4%; Pred. No. 0.0042;
RESULT 399
ID ABP72603 standard; protein; 883 AA.
DE Rat mutant brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match 11.7%; Score 131.5; DB 6; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0014;
RESULT 400
ID ADK67779 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match 11.7%; Score 131.5; DB 8; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0014;
RESULT 401
ID AAB61242 standard; protein; 883 AA.
DE Murine brevidin protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.6%; Score 130.5; DB 4; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 402
ID ABO32678 standard; protein; 883 AA.
DE Secreted polypeptide-related protein #119.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 11.6%; Score 130.5; DB 6; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 403
ID ADB90787 standard; protein; 883 AA.
DE Mouse brevicain protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.6%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 404
ID ADF71522 standard; protein; 883 AA.
DE Murine brevidin protein.

PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.6%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 405
ID ADQ10338 standard; protein; 883 AA.
DE Human polypeptide #172.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.6%; Score 130.5; DB 8; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 406
ID AAM47675 standard; protein; 1431 AA.
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 11.5%; Score 129; DB 5; Length 1431;
Best Local Similarity 32.3%; Pred. No. 0.0047;
RESULT 407
ID ABG72498 standard; protein; 1431 AA.
DE Rat 175kDa Hyaluronan receptor for endocytosis (HARE).
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 11.5%; Score 129; DB 6; Length 1431;
Best Local Similarity 32.3%; Pred. No. 0.0047;
RESULT 408
ID AAB08023 standard; protein; 95 AA.
DE The domain of hyaluronic acid which interacts with CD44.
PN WO200047163-A2.
PD 17-AUG-2000.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 11.4%; Score 128.5; DB 3; Length 95;
Best Local Similarity 28.7%; Pred. No. 0.00014;
RESULT 409
ID ABU04625 standard; protein; 95 AA.
DE Human expressed protein tag (EPT) #1291.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.4%; Score 128.5; DB 6; Length 95;
Best Local Similarity 28.7%; Pred. No. 0.00014;
RESULT 410
ID AAB61236 standard; protein; 649 AA.
DE Mature human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 4; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 411
ID ABO32673 standard; protein; 649 AA.
DE Secreted polypeptide-related protein #74.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 11.3%; Score 127.5; DB 6; Length 649;

Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 412
ID ADB90778 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 7; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 413
ID ADF71513 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 7; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 414
ID AAD61234 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 8; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 415
ID AAB61234 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 4; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 416
ID ABO32671 standard; protein; 671 AA.
DE Secreted polypeptide-related protein #73.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 11.3%; Score 127.5; DB 6; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 417
ID ADB90776 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 7; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 418
ID ADF71511 standard; protein; 671 AA.
DE Human TANGO 332.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 7; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 419
ID ADQ10329 standard; protein; 671 AA.
DE Human polypeptide #165.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 11.3%; Score 127.5; DB 8; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 420
ID ABM83434 standard; protein; 761 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.3%; Score 127.5; DB 8; Length 761;
Best Local Similarity 24.7%; Pred. No. 0.0028;
RESULT 421
ID ADH18992 standard; protein; 806 AA.
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 11.3%; Score 127.5; DB 8; Length 806;
Best Local Similarity 24.7%; Pred. No. 0.0033;
RESULT 422
ID ABM83431 standard; protein; 825 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3680.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.3%; Score 127.5; DB 8; Length 825;
Best Local Similarity 24.7%; Pred. No. 0.0031;
RESULT 423
ID ABM83430 standard; protein; 863 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3679.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.3%; Score 127.5; DB 8; Length 863;
Best Local Similarity 24.7%; Pred. No. 0.0033;
RESULT 424
ID ABP72604 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV VALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match 11.3%; Score 127.5; DB 6; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0034;
RESULT 425
ID ADE62581 standard; protein; 883 AA.
DE Rat Protein P55068, SEQ ID NO 8512.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.3%; Score 127.5; DB 7; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0034;
RESULT 426
ID ADK67782 standard; protein; 883 AA.
DE Rat glycosylation-variant BEHAV isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV VALE.
Query Match 11.3%; Score 127.5; DB 8; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0034;
RESULT 427
ID AAY97583 standard; protein; 911 AA.
DE Human secreted protein PRO6018.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 4; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 428
ID ABG34055 standard; protein; 911 AA.
DE Human Pro peptide #26.
PN WO200224888-A2.

PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 5; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 429
ID ADI28032 standard; protein; 911 AA.
DE ECMCAD protein 6755002CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.3%; Score 127.5; DB 5; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 430
ID AAE30340 standard; protein; 911 AA.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 431
ID ADA01320 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 432
ID ADA43749 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 433
ID ADA43517 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 434
ID ADA01192 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 435
ID ADA01076 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 436
ID ADA43633 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 437
ID ADA06895 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068781-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 438
ID ADA08383 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 439
ID ADB99676 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 440
ID ADB86959 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 441
ID ADB66114 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 442
ID ADB99792 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 443
ID ADB99447 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 444
ID ADB65998 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 445
ID ADC23396 standard; protein; 911 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 446
ID ADC26089 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

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Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 447
ID ADE62583 standard; protein; 911 AA.
DE Human Protein NP_068767, SEQ ID NO 8514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 448
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 449
ID ADE11222 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 450
ID ADD88153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 451
ID ADD95448 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 452
ID ADE06378 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 453
ID ADE38153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 454
ID ADD88269 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 455
ID ADD90850 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 456
ID ADF99405 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 457
ID ADG06498 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 458
ID ADG05449 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 459
ID ADG82450 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 460
ID ADN38942 standard; protein; 911 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 461
ID ADE51703 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 462
ID ADE51819 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 463
ID ADE37677 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 464
ID ADE37561 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 465
ID ADD90850 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 465
ID ADE95332 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 466
ID ADE38032 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 467
ID ADE76121 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 468
ID ADE39444 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 469
ID ADE04248 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US200309364-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 470
ID ADE39845 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138856-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 471
ID ADE19710 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 472
ID ADE77288 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 473
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 474
ID ADE76005 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 475
ID ADE37916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 476
ID ADE64526 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 477
ID ADE38861 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US200309363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 478
ID ADE51935 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 479
ID ADD90966 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 480
ID ADE38745 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 481
ID ADE37445 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 482
ID ADE06262 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 483
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
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ID ADD90121 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 484
ID ADE38629 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 485
ID ADE39560 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 486
ID ADD89165 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 487
ID ADD88932 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 488
ID ADE19826 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 489
ID ADE77404 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 490
ID ADE65280 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 491
ID ADE39328 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 492
ID ADE38513 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 493
ID ADG11066 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 494
ID ADG10950 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US200307743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 495
ID ADH31478 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 496
ID ADH38726 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 497
ID ADH29361 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 498
ID ADH23664 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 499
ID ADH26994 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 500
ID ADH38262 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 501
ID ADH26878 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.

PD US2003119134-A1.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 502
ID ADH38146 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 503
ID ADH38842 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 504
ID ADH23780 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 505
ID ADH40156 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 506
ID ADH40040 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 507
ID ADH31362 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 508
ID ADH29240 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 509
ID ADH49455 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 510
ID ADH51919 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119125-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 511
ID ADH49774 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 512
ID ADH52375 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 513
ID ADH52491 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 514
ID ADH58488 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 515
ID ADH51803 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 516
ID ADH58364 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 517
ID ADI13561 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 518
ID ADK00817 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 519
ID ADL08558 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 520
ID ADK67784 standard; protein; 911 AA.
DE Human glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 521
ID ABM80156 standard; protein; 911 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 522
ID ABR58557 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:214.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.3%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 523
ID ABUS6654 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #247.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.3%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 524
ID ADN38976 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.3%; Score 127; DB 7; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 525
ID ADO24439 standard; protein; 277 AA.
DE Human PRO87335 protein SEQ ID NO:78.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 526
ID ADRI4117 standard; protein; 277 AA.
DE Human NF-kappaB pathway-associated protein SeqID118.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 11.3%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 527
ID ADO24485 standard; protein; 277 AA.
DE Human PRO87343 protein SEQ ID NO:124.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 126; DB 8; Length 277;
Best Local Similarity 34.1%; Pred. No. 0.001;
RESULT 528
ID ADB65640 standard; protein; 482 AA.
DE Human protein encoded by clone THYM20143230.
PN EP108459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.0%; Score 124; DB 7; Length 482;
Best Local Similarity 34.5%; Pred. No. 0.0034;
RESULT 529
ID ABR82200 standard; protein; 2570 AA.
DE Human CLEVER-1 protein SEQ ID NO:1.
PN WO2003057130-A2.
PD 17-JUL-2003.
PA (JALK/) JALKANEN S.
PA (IRJA/) IRJALA H.
PA (SALM/) SALMI M.
Query Match 11.0%; Score 124; DB 6; Length 2570;
Best Local Similarity 34.5%; Pred. No. 0.032;
RESULT 530
ID AAY93911 standard; protein; 457 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO20039166-A1.
PD 06-JUL-2000.
PA (HUNA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 10.9%; Score 123; DB 3; Length 457;
Best Local Similarity 33.3%; Pred. No. 0.004;
RESULT 531
ID ABR90349 standard; protein; 1082 AA.
DE Human polypeptide SEQ ID NO 2725.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 10.9%; Score 123; DB 5; Length 1082;
Best Local Similarity 33.3%; Pred. No. 0.012;
RESULT 532
ID AAY93910 standard; protein; 2157 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO20039166-A1.
PD 06-JUL-2000.
PA (HUNA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 10.9%; Score 123; DB 3; Length 2157;
Best Local Similarity 33.3%; Pred. No. 0.031;
RESULT 533
ID ABM80463 standard; protein; 2570 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.9%; Score 123; DB 8; Length 2570;
Best Local Similarity 33.3%; Pred. No. 0.04;
RESULT 534
ID ADM80804 standard; protein; 259 AA.
DE Human CADECM-33 protein SEQ ID NO:33.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.8%; Score 121.5; DB 8; Length 259;
Best Local Similarity 34.9%; Pred. No. 0.0026;
RESULT 535
ID AAY13381 standard; protein; 360 AA.
DE Amino acid sequence of protein PRO271.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 2; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 536
ID ADC78533 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 3; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 537
ID AAB80249 standard; protein; 360 AA.

DE Human PRO271 protein.
PN WO200104311-A1.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 538
ID AAU29037 standard; protein; 360 AA.
DE Human PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 539
ID AAM38965 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 2110.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.8%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 540
ID ABUS8413 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US200302722-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 541
ID ABU71627 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 542
ID ABU87961 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 543
ID ABUS4276 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 544
ID ABR66150 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 545
ID ABR65540 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 546
ID ABUS9480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 547

ID ABUS2719 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 548
ID ABUS9840 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 549
ID ABU71482 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 550
ID ABR68089 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 551
ID ABUS6142 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 552
ID ABUS2573 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 553
ID ABO08650 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 554
ID ABO02702 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 555
ID ABR74856 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 556
ID ABR94618 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 557
ID ABUS5591 standard; protein; 360 AA.
DE Human PRO polypeptide #14.

PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 558
ID ABU98751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 559
ID ABU97966 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 560
ID ABU91672 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 561
ID ABU71928 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 562
ID ABU89365 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 563
ID ABU86206 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 564
ID ABU67419 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 565
ID ABU80447 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 566
ID ABO01811 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 567
ID ABR99365 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 568
ID ABR98755 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 569
ID ABO16278 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 570
ID ABR92178 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 571
ID ABO18819 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 572
ID ABR78240 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 573
ID ABU84976 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 574
ID ABO00115 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 575
ID ABO11447 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 576
ID ABO02092 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 577
ID ABU54384 standard; protein; 360 AA.

DE Human secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 578
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 579
ID ABUS93361 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 580
ID ABO06162 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 581
ID ABR59198 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 582
ID ABO09260 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 583
ID ABO19124 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 584
ID ABO11142 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 585
ID ABR66760 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 586
ID ABO15973 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 587
ID ABO13679 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036143-A1.

PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 588
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 589
ID ABUS5582 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, SEQ ID 28.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 590
ID ABO07430 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 591
ID ABO03617 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 592
ID ABR67065 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 593
ID ABO15668 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 594
ID ABUS5949 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 595
ID ABUS277 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 596
ID ABUS9522 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 597
ID ABU71125 standard; protein; 360 AA.
DE Human PRO271 protein.
PN US2003036143-A1.

PD 20-FEB-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
RESULT 598					
ID AB007735 standard; protein; 360 AA.					
DE Human PRO polypeptide #14.					
PN US2003032130-A1.					
PD 13-FEB-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
RESULT 599					
ID ABR69976 standard; protein; 360 AA.					
DE Human secreted polypeptide PRO271, SEQ ID NO:28.					
PN US2003032138-A1.					
PD 13-FEB-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
PA (GETH) GENENTECH INC.					
RESULT 600					
ID ABR69309 standard; protein; 360 AA.					
DE Human secreted polypeptide PRO271, SEQ ID NO:28.					
PN US2003036132-A1.					
PD 20-FEB-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
RESULT 601					
ID AB001450 standard; protein; 360 AA.					
DE Human PRO polypeptide #14.					
PN US2003008353-A1.					
PD 09-JAN-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
PA (GETH) GENENTECH INC.					
RESULT 602					
ID ABU81252 standard; protein; 360 AA.					
DE Human PRO polypeptide #14.					
PN US2003017542-A1.					
PD 23-JAN-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
RESULT 603					
ID ABR60049 standard; protein; 360 AA.					
DE Human secreted polypeptide PRO271, SEQ ID NO:28.					
PN US2003032137-A1.					
PD 13-FEB-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
RESULT 604					
ID ABR67784 standard; protein; 360 AA.					
DE Human secreted polypeptide PRO271, SEQ ID NO:28.					
PN US2003027269-A1.					
PD 06-FEB-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
RESULT 605					
ID ABR65172 standard; protein; 360 AA.					
DE Human secreted polypeptide PRO271, SEQ ID NO:28.					
PN US2003027268-A1.					
PD 06-FEB-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
RESULT 606					
ID ABR68394 standard; protein; 360 AA.					
DE Human secreted polypeptide PRO271, SEQ ID NO:28.					
PN US2003027274-A1.					
PD 06-FEB-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		
RESULT 607					
ID ABR71806 standard; protein; 360 AA.					
DE Human secreted polypeptide PRO271, SEQ ID NO:28.					
PN US2003032135-A1.					
PD 13-FEB-2003.	Query Match	10.8%;	Score 121.5;	DB 6;	Length 360;
	Best Local Similarity	34.9%;	Pred. No. 0.0041;		

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 608
ID ABU85286 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 609
ID ABU88976 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 610
ID ABU83056 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 611
ID ABU94912 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 612
ID ABU90460 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 613
ID ABU83971 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 614
ID ABU93622 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 615
ID ABR64867 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 616
ID ABR68699 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 617
ID ABO06515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;

Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 628			
ID	ABU81751 standard; protein; 360 AA.		
DE	Novel human secreted and transmembrane protein PRO271.		
PN	US2003032104-A1.		
PD	13-FEB-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 629			
ID	ABU65915 standard; protein; 360 AA.		
DE	Novel human secreted and transmembrane protein PRO271.		
PN	US2003036157-A1.		
PD	20-FEB-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 630			
ID	ABR59744 standard; protein; 360 AA.		
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.		
PN	US2003032120-A1.		
PD	13-FEB-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 631			
ID	ABU93932 standard; protein; 360 AA.		
DE	Novel human secreted and transmembrane protein PRO271.		
PN	US2003036155-A1.		
PD	20-FEB-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 632			
ID	ABU99785 standard; protein; 360 AA.		
DE	Novel human secreted and transmembrane protein PRO271.		
PN	US2003022296-A1.		
PD	30-JAN-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 633			
ID	ABR66455 standard; protein; 360 AA.		
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.		
PN	US2003027281-A1.		
PD	06-FEB-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 634			
ID	ABR90873 standard; protein; 360 AA.		
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.		
PN	US2003040058-A1.		
PD	27-FEB-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 635			
ID	ABU94300 standard; protein; 360 AA.		
DE	Human PRO polypeptide #14.		
PN	US2003017540-A1.		
PD	23-JAN-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 636			
ID	ABU79182 standard; protein; 360 AA.		
DE	Human PRO polypeptide #14.		
PN	US2003032106-A1.		
PD	13-FEB-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 637			
ID	ABU86511 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein (PRO) #14.		
PN	US2003032129-A1.		
PD	13-FEB-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	
RESULT 638			
ID	ABU86511 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein (PRO) #14.		
PN	US2003032129-A1.		
PD	13-FEB-2003.		
Query Match	10.8%;	Score 121.5; DB 6; Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.0041;	

ID ABU86916 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 639
ID ABU94605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 640
ID ABO4532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 641
ID ABR70281 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 642
ID ABU98446 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US20030322301-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 643
ID ABR65845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 644
ID ABR64562 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 645
ID ABU79487 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 646
ID ABU92878 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 647
ID ABU95837 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 648
ID ABU91057 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.

PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 649
ID ABU90150 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 650
ID ABO9565 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 651
ID ABO10837 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 652
ID ABR70891 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040089-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 653
ID ABU87499 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 654
ID ABU91367 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 655
ID ABU94581 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 656
ID ABR69671 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 657
ID ABU80048 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 658
ID ABU9659 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 659
ID ABU93317 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 660
ID ABO09870 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 661
ID ABO08955 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 662
ID ABU10523 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 663
ID ABU95532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 664
ID ABU96741 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 665
ID ABR70586 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 666
ID ABO04937 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 667
ID ABO08345 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 668
ID ABO14841 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003027143-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 669
ID ABO05552 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 670
ID ABR73941 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 671
ID ABR95533 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 672
ID ABR80830 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 673
ID ABR81135 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 674
ID ABM00831 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 675
ID ABR88433 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 676
ID ABM77254 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 677
ID ABO28738 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;

RESULT 678
ID ABO31483 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 679
ID ABO07900 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 680
ID ABO40380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 681
ID ABO35805 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 682
ID ABO43944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 683
ID ADA77780 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 684
ID ABM24739 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 685
ID ADB29418 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 686
ID ABO3007 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 687
ID ABR30263 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 688
ID ABM17177 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 689
ID ABR94923 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 690
ID ABR95228 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 691
ID ABO21466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 692
ID ABR97730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 693
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 694
ID ABM77559 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 695
ID ABM27789 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 696
ID ABM06070 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 697
ID ABM03576 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 698
ID ABM35027 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 699
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 700
ID ABO48046 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 701
ID ABR92788 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 702
ID ABO24549 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 703
ID ABM1560 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 704
ID ABM02661 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 705
ID ABM15957 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;

RESULT 706
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 707
ID ABM29009 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 708
ID ABM06985 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 709
ID ABM21079 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 710
ID ABM09425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 711
ID ABO41295 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 712
ID ABO36110 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 713
ID ABO43639 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 714
ID ABM76339 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 715
ID ABM76035 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 716
ID ABM25654 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 717
ID ABM25959 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 718
ID ABO03312 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 719
ID ABO02397 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 720
ID ABR90568 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 721
ID ABR73636 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 722
ID ABO16888 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 723
ID ABR94313 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 724
ID ABR75820 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 725
ID ADA18274 standard; protein; 360 AA.

DE Human secreted/transmembrane protein, #42.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 726
ID ABO32793 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 727
ID ABR71196 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 728
ID ABR93093 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 729
ID ABR93398 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 730
ID ABR87823 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 731
ID ABO27823 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 732
ID ABO29958 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 733
ID ABO33167 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 734
ID ABM04855 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 735
ID ABO08815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 736
ID ABO36415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 737
ID ABO35500 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 738
ID ABO39465 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 739
ID ABO10340 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 740
ID ABM11865 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 741
ID ABO52011 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 742
ID ABO52316 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 743
ID ABO23634 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032134-A1.

PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 744
ID ABR97120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 745
ID ABR86908 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 746
ID ABM10950 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 747
ID ABM28094 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 748
ID ABO32093 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 749
ID ABM15220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 750
ID ABO06375 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 751
ID ABM04186 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 752
ID ABM22299 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 753
ID ABM07595 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 754
ID ABO40685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 755
ID ABM35332 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 756
ID ABM33095 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 757
ID ABO52621 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 758
ID ABO50181 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 759
ID ABU99175 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 760
ID ABO04227 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 761
ID ABO05857 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 762
ID ABO34853 standard; protein; 360 AA.
DE Human PRO polypeptide #38.

PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 763
ID ABM18397 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 764
ID ADA16249 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 765
ID ABR97425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 766
ID ABR80525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 767
ID ABM01136 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 768
ID ABR88738 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 769
ID ABM13390 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 770
ID ABM20774 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 771
ID ABO41905 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049745-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 772
ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 773
ID ABM10035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 774
ID ABO38550 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 775
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 776
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 777
ID ABM74815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US200309353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 778
ID ADA79572 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 779
ID ABR96205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 780
ID ABM02356 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 781
ID ABR86298 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 782
ID ABR86603 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 783
ID ABM16567 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 784
ID ABM29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 785
ID ABO29043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 786
ID ABM23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 787
ID ABM23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 788
ID ABM21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 789
ID ABO37635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 790
ID ABM28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

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PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 791
ID ABM28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 792
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 793
ID ABM75730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 794
ID ABM34010 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 795
ID ABM4315 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 796
ID ABO20246 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 797
ID ABO21161 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 798
ID ABO22076 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 799
ID ABR96510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 800
ID ABR85688 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 801
ID ABR99670 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 802
ID ABM00221 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 803
ID ABM00526 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 804
ID ABO29653 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 805
ID ABM23519 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 806
ID ABM29314 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 807
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 808
ID ABO45545 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 809
ID ABM20469 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
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PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 810
ID ADA42394 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 811
ID ADA81299 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 812
ID ABO16583 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 813
ID ABO18209 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 814
ID ABO22636 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027285-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 815
ID ABO22941 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 816
ID ABR92483 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 817
ID ABR81440 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 818
ID ABO17531 standard; protein; 360 AA.
DE Human PRO polypeptide #39.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 819
ID ABM77864 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 820
ID ABR89653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 821
ID ABM26569 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 822
ID ABM13695 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 823
ID ABO28433 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 824
ID ABO30263 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 825
ID ABM07290 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 826
ID ABM03881 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 827
ID ABO37025 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 828
ID ABO41600 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 829
ID ABO35195 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 830
ID ABM25044 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 831
ID ABO47436 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 832
ID ABO47741 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 833
ID ABO48351 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 834
ID ABO51401 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 835
ID ABO51706 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 836
ID ABO50486 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 837
ID ABR79610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040059-A1.

PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 838
ID ABM16872 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 839
ID ABO17904 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 840
ID ABO20856 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 841
ID ABR96815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 842
ID ABM12170 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 843
ID ABM16262 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 844
ID ABM24129 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 845
ID ABM14610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 846
ID ABM04491 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 847

ID	ABM06680 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003068730-A1.				
PD	10-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 848					Length 360;
ID	ABM09120 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003073174-A1.				
PD	17-APR-2003.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 849					Length 360;
ID	AB0319160 standard; protein; 360 AA.				
DE	Human secreted/transmembrane protein (PRO) #14.				
PN	US2003068775-A1.				
PD	10-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 850					Length 360;
ID	ABM75425 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003104545-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 851					Length 360;
ID	ABM25349 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003104541-A1.				
PD	05-JUN-2003.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 852					Length 360;
ID	ABM19859 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003104554-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 853					Length 360;
ID	AB046765 standard; protein; 360 AA.				
DE	Human PRO polypeptide #14.				
PN	US2003049762-A1.				
PD	13-MAR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 854					Length 360;
ID	AB047070 standard; protein; 360 AA.				
DE	Human PRO polypeptide #14.				
PN	US2003049765-A1.				
PD	13-MAR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 854					Length 360;
ID	ADA83097 standard; protein; 360 AA.				
DE	Human secreted/transmembrane protein (PRO) #14.				
PN	US2003049752-A1.				
PD	13-MAR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 855					Length 360;
ID	ABR71501 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003032133-A1.				
PD	13-MAR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 856					Length 360;
ID	ABR71501 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003032133-A1.				
PD	13-MAR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	10.8%; Score 121.5; DB 6;				
Best Local Similarity	34.9%; Pred. No. 0.0041;				
RESULT 856					Length 360;

[illegible]

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 876
ID ABM05460 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 877
ID ABM15525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 878
ID ABM08510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 879
ID ABO42210 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 880
ID ABO37940 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 881
ID ABO45850 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 882
ID ABM66653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 883
ID ADB20140 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 884
ID ABM19554 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 885

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 867
ID ABO25599 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 868
ID ABR94008 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 869
ID ABR79915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 870
ID ABM11255 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064489-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 871
ID ABO22862 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 872
ID ABO30568 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 873
ID ABO30873 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 874
ID ABM27179 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 875
ID ABM29924 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;

ID ABO49266 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 886
ID ABO49571 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 887
ID ADA78392 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 888
ID ABR98128 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003058720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 889
ID ABM26874 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 890
ID ABM03271 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 891
ID ABO39770 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003058689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 892
ID ABO49876 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 893
ID ABO50791 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 894
ID ABO05247 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003031224-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 895
ID ABR74551 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 896
ID ABR77030 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 897
ID ADA16673 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 898
ID ABM17787 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 899
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 900
ID ADA13102 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 901
ID ABO21771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 902
ID ABO19941 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 903
ID ABO24244 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 904

ID ABR5993 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 905
ID ABM10645 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 906
ID ABM76644 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 907
ID ABR89348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 908
ID ABM12475 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 909
ID ABM05765 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 910
ID ABO34890 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 911
ID ABM02966 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003058764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 912
ID ABM18944 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 913
ID ABM19249 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 914
ID ABO46460 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 915
ID ABO48961 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 916
ID ADA1970 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 917
ID ABR69004 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 918
ID ABR89043 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 919
ID ABR72416 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 920
ID ABR74246 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 921
ID ABO18514 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 922
ID ADA17317 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;

RESULT 923
ID ABR02020 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049739-A1.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 924
ID ABM01441 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 925
ID ABM02051 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 926
ID ABR87213 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 927
ID ABM12780 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 928
ID ABM30534 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 929
ID ABM24434 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 930
ID ABO29348 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 931
ID ABO31178 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 932
ID ABR78845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054456-A1.
PD 20-NAR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 933
ID ABM14305 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 934
ID ABO38855 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 935
ID ABM34620 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 936
ID ABO51096 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 937
ID ADA42820 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054351-A1.
PD 20-NAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 938
ID ABO03922 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 939
ID ABO10392 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 940
ID ABR77635 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 941
ID ABR78845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054456-A1.
PD 20-NAR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;

Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 942
ID ABO23939 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 943
ID ABR93703 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 944
ID ABM01746 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 945
ID ABM78169 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 946
ID ABR89958 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 947
ID ABM27484 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 948
ID ABM13085 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 949
ID ABO31788 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 950
ID ABM14000 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 951

ID ABM08205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 952
ID ABO40075 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 953
ID ABM74510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 954
ID ABM33705 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 955
ID ABM20164 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 956
ID ABO48656 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 957
ID ABR72721 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 958
ID ABO15363 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 959
ID ABR85078 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 960
ID ABO15058 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US200304919-A1.
PD 06-MAR-2003.

Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 961
ID ABO17193 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 962
ID ABM17482 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 963
ID ABR85383 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 964
ID ABO17592 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 965
ID ABM76949 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 966
ID ABO28128 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 967
ID ABM22909 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 968
ID ABM30229 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 969
ID ABM21689 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 970
ID ABM31754 standard; protein; 360 AA.

ID ARM21384 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 971
ID ABM14915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 972
ID ABO40990 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 973
ID ABO36720 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 974
ID ABO37330 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 975
ID ABM75120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 976
ID ABM33400 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 977
ID ABO46155 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 978
ID ADA82463 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 979
ID ABM31754 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 980
ID ABM31144 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 981
ID ADB77739 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 982
ID ADB74875 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 983
ID ADB85771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 984
ID ABM32059 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 985
ID ABM32364 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 986
ID ABM31449 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 987
ID ABM30839 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 988
ID ADC28521 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059772-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 989
ID ADC39721 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 990
ID ADC40235 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 991
ID ADC19059 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 992
ID ADC34359 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 993
ID ADC29414 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 994
ID ADC28945 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 995
ID ADC40830 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 996
ID ADC19487 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 997
ID ADC33935 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073077-A1.
PD 17-APR-2003.


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PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 998
ID ADC13005 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 999
ID ADC12457 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1000
ID ADD05501 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1001
ID ADD05012 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1002
ID ADD04018 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1003
ID ADD03594 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1004
ID ADE34846 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1005
ID ADG02496 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1006
ID ADG01203 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1007
ID ADF95378 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1008
ID ADG12193 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1009
ID ADH08853 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1010
ID ADH59329 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1011
ID ADI38108 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1012
ID ADJ26376 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1013
ID ADL32634 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1014
ID ADM30168 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1015
ID ADE79291 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
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RESULT 1016
ID ADE79715 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1017
ID ADE73391 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1018
ID ADE74165 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1019
ID ADE73926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1020
ID ADE74777 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1021
ID ADE99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1022
ID ADE98599 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1023
ID ADE99026 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1024
ID ADG40496 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1025
ID ADF73890 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1026
ID ADF95990 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1027
ID ADF73466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1028
ID ADG04261 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1029
ID ADG00421 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1030
ID ADG82677 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1031
ID ADG92309 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1032
ID ADG92736 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1033
ID ADH25958 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.0041;			
RESULT 1034			
ID	ADH32927 standard; protein; 360 AA.		
DE	Human PRO polypeptide #14.		
FN	US2003068768-A1.		
PD	10-APR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match			
Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360;			
Best Local Similarity 34.9%; Pred. No. 0.0041;			
RESULT 1035			
ID	ADH20525 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein, #42.		
FN	US2004005553-A1.		
PD	08-JAN-2004.		
PA	(GETH) GENENTECH INC.		
Query Match			
Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360;			
Best Local Similarity 34.9%; Pred. No. 0.0041;			
RESULT 1036			
ID	ADH07380 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein, #42.		
FN	US2004006211-A1.		
PD	08-JAN-2004.		
PA	(DESN/) DESNOYERS L.		
PA	(GODD/) GODDARD A.		
PA	(GODO/) GODOWSKI P J.		
PA	(GURN/) GURNEY A L.		
PA	(MATH/) MATHER J P.		
PA	(WILL/) WILLIAMS P M.		
PA	(WOOD/) WOOD W I.		
Query Match			
Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360;			
Best Local Similarity 34.9%; Pred. No. 0.0041;			
RESULT 1037			
ID	ADH59925 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein, #42.		
FN	US2003215904-A1.		
PD	20-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match			
Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360;			
Best Local Similarity 34.9%; Pred. No. 0.0041;			
RESULT 1038			
ID	ADH06953 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein, #42.		
FN	US2004005665-A1.		
PD	08-JAN-2004.		
PA	(DESN/) DESNOYERS L.		
PA	(GODD/) GODDARD A.		
PA	(GODO/) GODOWSKI P J.		
PA	(GURN/) GURNEY A L.		
PA	(MATH/) MATHER J P.		
PA	(WILL/) WILLIAMS P M.		
PA	(WOOD/) WOOD W I.		
Query Match			
Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360;			
Best Local Similarity 34.9%; Pred. No. 0.0041;			
RESULT 1039			
ID	ADH18695 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein, #42.		
FN	US2003152999-A1.		
PD	14-AUG-2003.		
PA	(GETH) GENENTECH INC.		
Query Match			
Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360;			
Best Local Similarity 34.9%; Pred. No. 0.0041;			
RESULT 1040			
ID	AD165415 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein, #42.		
FN	US2003148419-A1.		
PD	07-AUG-2003.		
PA	(GETH) GENENTECH INC.		
Query Match			
Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360;			
Best Local Similarity 34.9%; Pred. No. 0.0041;			
RESULT 1041			
ID	AD137678 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein, #42.		
FN	US2003096340-A1		
PD			
PA	(GETH) GENENTECH INC.		
Query Match			
Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360;			
Best Local Similarity 34.9%; Pred. No. 0.0041;			

[illegible]

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Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1050
ID ADJ64437 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1051
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1052
ID ADM36380 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1053
ID ADM40185 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1054
ID ADL91793 standard; protein; 360 AA.
DE Human PRO271 protein SEQ ID NO:14.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1055
ID ADO06248 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1056
ID ADN37793 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1057
ID ADR11100 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1058
ID ADRI8009 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1059
ID ADT03685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1060
ID ADS74648 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #42.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1061
ID AAM59882 standard; protein; 528 AA.
DE Amino acid sequence of the cDNA clone BEF (HSXCK41).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
Query Match 10.8%; Score 121.5; DB 2; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1062
ID AAB61241 standard; protein; 528 AA.
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DE Human BEF protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.8%; Score 121; DB 4; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1063
ID ABO32677 standard; protein; 528 AA.
DE Secreted polypeptide-related protein #75.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (WACK/) WACKAY C R.
PA (GOOD/) GODEARL A D J.
Query Match 10.8%; Score 121; DB 6; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1064
ID ADB90786 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.8%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1065
ID ADF71521 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.8%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1066
ID ADQ10337 standard; protein; 528 AA.
DE Human polypeptide #171.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.8%; Score 121; DB 8; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1067
ID AAR85442 standard; protein; 912 AA.
DE Bovine brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 10.7%; Score 120.5; DB 2; Length 912;
Best Local Similarity 24.6%; Pred. No. 0.018;
RESULT 1068
ID ADB47827 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NICU/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C E.
Query Match 10.6%; Score 119; DB 7; Length 457;
Best Local Similarity 33.3%; Pred. No. 0.0098;
RESULT 1069
ID ADJ55382 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 119; DB 8; Length 457;
Best Local Similarity 33.3%; Pred. No. 0.0098;
RESULT 1070
ID ADQ39513 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 10.5%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.06;
RESULT 1071
ID ADQ39515 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 10.5%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.079;
RESULT 1072
ID ADN04531 standard; protein; 2000 AA.
DE Antipsoriatic protein sequence #458.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 10.5%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.079;
RESULT 1073
ID ADP23738 standard; protein; 2000 AA.
DE PRO polypeptide SEQ ID NO:916.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 10.5%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.079;
RESULT 1074
ID ADD48597 standard; protein; 3396 AA.
DE Human Protein P13611, SEQ ID NO 14303.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 10.5%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.16;
RESULT 1075
ID ADN95526 standard; protein; 3396 AA.
DE Human BEC/LEC-related protein sequence SeqID449.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN-) LICENTIA LTD.
Query Match 10.5%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.16;
RESULT 1076
ID ADJ75521 standard; protein; 3396 AA.
DE Marker gene related amino acid sequence SEQ ID NO:773.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 10.5%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.16;
RESULT 1077
ID ADQ39509 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.
PN WO2004058052-A2.

PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 10.5%; Score 118.5; DB 8; Length 3396;
RESULT 1078
ID ADQ39510 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 10.5%; Score 118.5; DB 8; Length 3396;
RESULT 1079
ID ADP99164 standard; protein; 3396 AA.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match
Best Local Similarity 10.5%; Score 118.5; DB 8; Length 3396;
RESULT 1080
ID ADJ76266 standard; protein; 2397 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1518.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 10.3%; Score 116; DB 8; Length 2397;
RESULT 1081
ID AAR46627 standard; protein; 1257 AA.
DE Neurocan core protein.
PN WO9403601-A2.
PD 17-FEB-1994.
PA (UNIV) UNIV NEW YORK STATE.
Query Match
Best Local Similarity 10.3%; Score 115.5; DB 2; Length 1257;
RESULT 1082
ID AAR85443 standard; protein; 908 AA.
DE Rat brevician core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match
Best Local Similarity 10.2%; Score 115; DB 2; Length 908;
RESULT 1083
ID ADD48595 standard; protein; 656 AA.
DE Rat Protein AF072892, SEQ ID NO 14301.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 10.1%; Score 114; DB 7; Length 656;
RESULT 1084
ID ADP71273 standard; protein; 191 AA.
DE Human LP2 protein B-B' domain SeqID8.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 8; Length 191;
RESULT 1085
ID ABB10268 standard; protein; 287 AA.
DE Human cDNA SEQ ID NO: 576.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 4; Length 287;
RESULT 1086
ID ABP66855 standard; protein; 287 AA.
DE Human polypeptide SEQ ID NO 576.
PN US2002090672-A1.

PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 5; Length 287;
RESULT 1087
ID ADM87304 standard; protein; 340 AA.
DE Human protein SEQ ID NO:397.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 8; Length 340;
RESULT 1088
ID ABU11635 standard; protein; 343 AA.
DE Human MDDR polypeptide SEQ ID 582.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 6; Length 343;
RESULT 1089
ID ABJ10588 standard; protein; 897 AA.
DE Human novel protein NOVIC SEQ ID NO: 211.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 10.0%; Score 112; DB 5; Length 897;
RESULT 1090
ID ADH71312 standard; protein; 897 AA.
DE Human protein of the invention NOV9a SEQ ID NO:208.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 10.0%; Score 112; DB 8; Length 897;
RESULT 1091
ID ADO09968 standard; protein; 897 AA.
DE Human NOVIC CDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATUPAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match
Best Local Similarity 10.0%; Score 112; DB 8; Length 897;
RESULT 1092
ID AAM47684 standard; protein; 1394 AA.
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.

PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 10.0%; Score 112; DB 5; Length 1394;
Best Local Similarity 29.0%; Pred. No. 0.21;
RESULT 1093
ID ABG72499 standard; protein; 1416 AA.
DE Human 150kDa Hyaluronan receptor for endocytosis (HARE) #1.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 10.0%; Score 112; DB 6; Length 1416;
Best Local Similarity 29.0%; Pred. No. 0.22;
RESULT 1094
ID ADH71356 standard; protein; 1502 AA.
DE Human protein of the invention NOV9w SEQ ID NO:252.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 112; DB 8; Length 1502;
Best Local Similarity 29.0%; Pred. No. 0.23;
RESULT 1095
ID ADH71358 standard; protein; 1510 AA.
DE Human protein of the invention NOV9x SEQ ID NO:254.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 112; DB 8; Length 1510;
Best Local Similarity 29.0%; Pred. No. 0.24;
RESULT 1096
ID ABG72514 standard; protein; 1633 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 10.0%; Score 112; DB 6; Length 1653;
Best Local Similarity 29.0%; Pred. No. 0.27;
RESULT 1097
ID ADM90835 standard; protein; 1895 AA.
DE Human pharmacaceutically useful protein SeqID 228.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 10.0%; Score 112; DB 8; Length 1895;
Best Local Similarity 29.0%; Pred. No. 0.32;
RESULT 1098
ID ADH71360 standard; protein; 2551 AA.
DE Human protein of the invention NOV9y SEQ ID NO:256.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 112; DB 8; Length 2551;
Best Local Similarity 29.0%; Pred. No. 0.47;
RESULT 1099
ID ADP71271 standard; protein; 200 AA.
DE Human aggrecan protein B-B' domain SeqID6.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEBK-) SEIKAGAKU KOGYO CO LTD.
Query Match 9.9%; Score 111; DB 8; Length 200;
Best Local Similarity 37.4%; Pred. No. 0.02;
RESULT 1100
ID AAMS2242 standard; protein; 655 AA.
DE Human versican isoform V3 SEQ ID NO 2.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH-) WIGHT T N.
PA (MERR-) MERRILEES M.
Query Match 9.9%; Score 111; DB 5; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.097;
RESULT 1101
ID ADQ39511 standard; protein; 655 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.9%; Score 111; DB 8; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.097;
RESULT 1102
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 9.9%; Score 111; DB 2; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.55;
RESULT 1103
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence SEQ ID NO:90.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 9.9%; Score 111; DB 6; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.55;
RESULT 1104
ID ADQ39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.9%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.55;
RESULT 1105
ID ADQ39512 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.9%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.55;
RESULT 1106
ID ABJ10586 standard; protein; 2675 AA.
DE Human novel protein NOVIA SEQ ID NO: 2.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.8%; Score 110; DB 5; Length 2675;
Best Local Similarity 28.0%; Pred. No. 0.79;
RESULT 1107
ID ADO09971 standard; protein; 2675 AA.
DE Human NOVIA variant.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM-) SHIMKETS R A.
PA (PATI-) PATTURAJAN M.
PA (VERN-) VERNET C A M.
PA (CASM-) CASMAN S J.
PA (MALY-) MALYANKAR U M.
PA (SHEN-) SHENOV S G.
PA (SPYT-) SPYTEK K A.
PA (GANG-) GANGOLLI E A.
PA (MILL-) MILLER C E.
PA (BOLD-) BOLDOG F L.
PA (LILL-) LI L.
PA (TAUP-) TAUPIER R J.
PA (KEKU-) KEKUDA R.
PA (SMIT-) SMITHSON G.
PA (ZERH-) ZERHUSEN B D.
PA (LIUX-) LIU X.
PA (COLM-) COLMAN S D.

PA (TCHE/) TCHERNEV V T.
 PA (SIJG/) SI J.
 PA (EDIN/) EDINGER S R.
 PA (STON/) STONE D J.
 PA (SCIO/) SCORE P.
 PA (MILL/) MILLET I.
 PA (ROTH/) ROTHENBERG M E.
 Query Match
 Best Local Similarity 9.8%; Score 110; DB 8; Length 2675;
 RESULT 1108
 ID ADO09836 standard; protein; 2675 AA.
 DE Human NOV1a.
 PN US2004018970-A1.
 PD 29-JAN-2004.
 PA (SHIM/) SHIMKETS R A.
 PA (PATT/) PATTURAJAN M.
 PA (VERN/) VERNET C A M.
 PA (CASM/) CASHMAN S J.
 PA (MALX/) MALYANKAR U M.
 PA (SHEN/) SHENOY S G.
 PA (SPYT/) SPYTEK K A.
 PA (GANG/) GANGOLLI E A.
 PA (MILL/) MILLER C E.
 PA (BOLD/) BOLDG F L.
 PA (LILL/) LI L.
 PA (TAUP/) TAUPIER R J.
 PA (KEKU/) KEKUDA R.
 PA (SMIT/) SMITHSON G.
 PA (ZERH/) ZERHUSEN B D.
 PA (LIUX/) LIU X.
 PA (COLM/) COLMAN S D.
 PA (TCHE/) TCHERNEV V T.
 PA (SIJG/) SI J.
 PA (EDIN/) EDINGER S R.
 PA (STON/) STONE D J.
 PA (SCIO/) SCORE P.
 PA (MILL/) MILLET I.
 PA (ROTH/) ROTHENBERG M E.
 Query Match
 Best Local Similarity 9.8%; Score 110; DB 8; Length 2675;
 RESULT 1109
 ID ADO31200 standard; protein; 1257 AA.
 DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.
 PN WO2004041197-A2.
 PD 21-MAY-2004.
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 Query Match
 Best Local Similarity 9.7%; Score 109.5; DB 8; Length 1257;
 RESULT 1110
 ID AAY93913 standard; protein; 353 AA.
 DE A human hyaluronan-binding protein, designated BM-HABP.
 PN WO200039166-A1.
 PD 06-JUL-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (AMNA-) AMERICAN NAT RED CROSS.
 Query Match
 Best Local Similarity 9.7%; Score 109; DB 3; Length 353;
 RESULT 1111
 ID ABP97200 standard; protein; 1321 AA.
 DE Tumour-associated antigenic target protein TAT185 SEQ ID NO:82.
 PN WO2003024392-A2.
 PD 27-MAR-2003.
 PA (GETH-) GENENTECH INC.
 Query Match
 Best Local Similarity 9.7%; Score 109; DB 6; Length 1321;
 RESULT 1112
 ID ADJ69615 standard; protein; 1321 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1421.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match
 Best Local Similarity 9.7%; Score 109; DB 7; Length 1321;
 RESULT 1113
 ID ADN38944 standard; protein; 1321 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 9.7%; Score 109; DB 7; Length 1321;
 RESULT 1114
 ID ADO31196 standard; protein; 1321 AA.
 DE Human neurocan protein for glucosaminoglycan reduction in glial scars.
 PN WO2004041197-A2.
 PD 21-MAY-2004.
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 Query Match
 Best Local Similarity 9.7%; Score 109; DB 8; Length 1321;
 RESULT 1115
 ID ABJ56909 standard; protein; 322 AA.
 DE 151P3D4 v-2 protein clone-1 from placenta.
 PN WO200283860-A2.
 PD 24-OCT-2002.
 PA (AGEN-) AGENSYS INC.
 Query Match
 Best Local Similarity 9.6%; Score 108; DB 6; Length 322;
 RESULT 1116
 ID ABJ56908 standard; protein; 322 AA.
 DE 151P3D4 v-1 protein clone-1 from placenta.
 PN WO200283860-A2.
 PD 24-OCT-2002.
 PA (AGEN-) AGENSYS INC.
 Query Match
 Best Local Similarity 9.6%; Score 108; DB 6; Length 322;
 RESULT 1117
 ID ABJ56918 standard; protein; 353 AA.
 DE 151P3D4 v-1 protein clone-1 from placenta.
 PN WO200283860-A2.
 PD 24-OCT-2002.
 PA (AGEN-) AGENSYS INC.
 Query Match
 Best Local Similarity 9.6%; Score 108; DB 6; Length 353;
 RESULT 1118
 ID AAY57081 standard; protein; 354 AA.
 DE Human proteoglycan link protein precursor amino acid sequence.
 PN WO9956763-A1.
 PD 11-NOV-1999.
 PA (REGC-) UNIV CALIFORNIA.
 Query Match
 Best Local Similarity 9.6%; Score 108; DB 3; Length 354;
 RESULT 1119
 ID AAY57084 standard; protein; 354 AA.
 DE Human proteoglycan link protein precursor #2.
 PN WO9956763-A1.
 PD 11-NOV-1999.
 PA (REGC-) UNIV CALIFORNIA.
 Query Match
 Best Local Similarity 9.6%; Score 108; DB 3; Length 354;
 RESULT 1120
 ID ABJ56902 standard; protein; 354 AA.
 DE 151P3D4 v-1 354aa protein clone-1 from placenta.
 PN WO200283860-A2.
 PD 24-OCT-2002.
 PA (AGEN-) AGENSYS INC.
 Query Match
 Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
 RESULT 1121
 ID ABJ56906 standard; protein; 354 AA.
 DE 151P3D4 v-1 protein clone-1 from placenta.
 PN WO200283860-A2.
 PD 24-OCT-2002.
 PA (AGEN-) AGENSYS INC.
 Query Match
 Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
 RESULT 1122
 ID ADJ69615 standard; protein; 1321 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1421.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match
 Best Local Similarity 9.7%; Score 109; DB 7; Length 1321;


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RESULT 1122
ID ABJ56914 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1123
ID ABJ56898 standard; protein; 354 AA.
DE 151P3D4 v-8 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1124
ID ABJ56895 standard; protein; 354 AA.
DE 151P3D4 v-5 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1125
ID ABJ56897 standard; protein; 354 AA.
DE 151P3D4 v-7 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1126
ID ABJ56901 standard; protein; 354 AA.
DE 151P3D4 v-11 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1127
ID ABJ56894 standard; protein; 354 AA.
DE 151P3D4 v-4 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1128
ID ABJ56905 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1129
ID ABJ56899 standard; protein; 354 AA.
DE 151P3D4 v-9 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1130
ID ABJ56912 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1131
ID ABJ56890 standard; protein; 721 AA.
DE 151P3D4 v-3 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1132
ID ABJ56891 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1133
ID ABJ56896 standard; protein; 354 AA.
DE 151P3D4 v-6 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1134
ID ABJ56900 standard; protein; 354 AA.
DE 151P3D4 v-10 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1135
ID ABJ56889 standard; protein; 354 AA.
DE Transcript variant I21P1F1 v-1.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1136
ID ABJ56904 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
RESULT 1137
ID ADP07795 standard; protein; 354 AA.
DE Human secreted protein, seq id 278.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 8; Length 354;
RESULT 1138
ID AAR77034 standard; protein; 355 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV YALE.
Query Match
Best Local Similarity 9.6%; Score 108; DB 2; Length 355;
RESULT 1139
ID ADH71348 standard; protein; 552 AA.
DE Human protein of the invention NOV9s SEQ ID NO:244.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.6%; Score 108; DB 8; Length 552;
RESULT 1140
ID ABJ56890 standard; protein; 721 AA.
```

DE Transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.6%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.22;
RESULT 1141
ID ABJ56892 standard; protein; 721 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.6%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.22;
RESULT 1142
ID ABJ56903 standard; protein; 721 AA.
DE 151P3D4 v-1 721aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.6%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.22;
RESULT 1143
ID ABG72500 standard; protein; 93 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) LINK domain.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 9.5%; Score 107; DB 6; Length 93;
Best Local Similarity 29.2%; Pred. No. 0.018;
RESULT 1144
ID AAB83358 standard; protein; 315 AA.
DE NOV2 protein sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 4; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.091;
RESULT 1145
ID ADH71316 standard; protein; 315 AA.
DE Human protein of the invention NOV9c SEQ ID NO:212.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.091;
RESULT 1146
ID AAY57083 standard; protein; 339 AA.
DE Rat proteoglycan link protein precursor.
PN WO956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.5%; Score 107; DB 3; Length 339;
Best Local Similarity 28.6%; Pred. No. 0.1;
RESULT 1147
ID ABJ56915 standard; protein; 354 AA.
DE Rat cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 107; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.11;
RESULT 1148
ID AAY57082 standard; protein; 355 AA.
DE Chicken proteoglycan link protein precursor.
PN WO956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.5%; Score 107; DB 3; Length 355;
Best Local Similarity 34.9%; Pred. No. 0.11;
RESULT 1149
ID ABJ56907 standard; protein; 355 AA.

DE Mouse cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 107; DB 6; Length 355;
Best Local Similarity 28.6%; Pred. No. 0.11;
RESULT 1150
ID ADH71336 standard; protein; 533 AA.
DE Human protein of the invention NOV9m SEQ ID NO:232.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.18;
RESULT 1151
ID ADH71334 standard; protein; 533 AA.
DE Human protein of the invention NOV9l SEQ ID NO:230.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.18;
RESULT 1152
ID ADH71340 standard; protein; 552 AA.
DE Human protein of the invention NOV9o SEQ ID NO:236.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1153
ID ADH71346 standard; protein; 552 AA.
DE Human protein of the invention NOV9r SEQ ID NO:242.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1154
ID ADH71354 standard; protein; 552 AA.
DE Human protein of the invention NOV9v SEQ ID NO:250.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1155
ID ADH71344 standard; protein; 552 AA.
DE Human protein of the invention NOV9q SEQ ID NO:240.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1156
ID ADH71342 standard; protein; 552 AA.
DE Human protein of the invention NOV9p SEQ ID NO:238.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1157
ID ADH71350 standard; protein; 552 AA.
DE Human protein of the invention NOV9t SEQ ID NO:246.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1158
ID ADH71314 standard; protein; 556 AA.
DE Human protein of the invention NOV9b SEQ ID NO:210.

PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 556;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1159
ID ABM83433 standard; protein; 774 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3682.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.5%; Score 107; DB 8; Length 774;
Best Local Similarity 21.5%; Pred. No. 0.3;
RESULT 1160
ID ABM83432 standard; protein; 822 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3681.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.5%; Score 107; DB 8; Length 822;
Best Local Similarity 21.5%; Pred. No. 0.33;
RESULT 1161
ID ADO31202 standard; protein; 1268 AA.
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 9.5%; Score 107; DB 8; Length 1268;
Best Local Similarity 26.2%; Pred. No. 0.58;
RESULT 1162
ID ADH71332 standard; protein; 2417 AA.
DE Human protein of the invention NOV9k SEQ ID NO:228.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 2417;
Best Local Similarity 29.2%; Pred. No. 1.4;
RESULT 1163
ID ABJ10587 standard; protein; 2420 AA.
DE Human novel protein NOV1b SEQ ID NO: 4.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 5; Length 2420;
Best Local Similarity 29.2%; Pred. No. 1.4;
RESULT 1164
ID ADO09838 standard; protein; 2420 AA.
DE Human NOV1b.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTER K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KERU/) KERODA R.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHV/) TCHERNEV V T.
PA (SIJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.

PA (ROTH/) ROTHENBERG M E.
Query Match 9.5%; Score 107; DB 8; Length 2420;
Best Local Similarity 29.2%; Pred. No. 1.4;
RESULT 1165
ID ADH71338 standard; protein; 552 AA.
DE Human protein of the invention NOV9n SEQ ID NO:234.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 106; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.24;
RESULT 1166
ID AAB12304 standard; protein; 341 AA.
DE Human secreted protein encoded by gene 4 clone HFXHC41.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.4%; Score 105.5; DB 3; Length 341;
Best Local Similarity 28.9%; Pred. No. 0.14;
RESULT 1167
ID AAY57080 standard; protein; 354 AA.
DE Human link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.3%; Score 105; DB 3; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.17;
RESULT 1168
ID ABJ56913 standard; protein; 354 AA.
DE Bovine cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.3%; Score 105; DB 6; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.17;
RESULT 1169
ID ABU07339 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2040.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.2%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.06;
RESULT 1170
ID ABU07336 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2037.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.2%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.06;
RESULT 1171
ID ADQ39387 standard; protein; 139 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.2%; Score 104; DB 8; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.06;
RESULT 1172
ID ADP71269 standard; protein; 195 AA.
DE Human LP1 protein B-B' domain SeqID4.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 9.2%; Score 104; DB 8; Length 195;
Best Local Similarity 33.7%; Pred. No. 0.094;
RESULT 1173
ID ADP71267 standard; protein; 200 AA.
DE Human versican protein B-B' domain SeqID2.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.

Query Match 9.2%; Score 104; DB 8; Length 200;
Best Local Similarity 32.5%; Pred. No. 0.098;
RESULT 1174
ID ADH71352 standard; protein; 552 AA.
DE Human protein of the invention NOV9u SEQ ID NO:248.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.2%; Score 104; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.38;
RESULT 1175
ID ADN23553 standard; protein; 380 AA.
DE Bacterial polypeptide #6206.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.0%; Score 101.5; DB 8; Length 380;
Best Local Similarity 25.5%; Pred. No. 0.4;
RESULT 1176
ID AAU76528 standard; protein; 402 AA.
DE Human LP polypeptide #1.
PN WO200216578-A2.
PD 28-FEB-2002.
PA (ELLIL) LILLY & CO ELI.
Query Match 8.9%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 0.55;
RESULT 1177
ID AAU09883 standard; protein; 402 AA.
DE Novel human secreted protein #23.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 8.9%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 0.55;
RESULT 1178
ID ADF59259 standard; protein; 402 AA.
DE Human polypeptide sequence SEQ ID NO:1667.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.9%; Score 100.5; DB 7; Length 402;
Best Local Similarity 30.9%; Pred. No. 0.55;
RESULT 1179
ID ADF74155 standard; protein; 412 AA.
DE Human novel brain/hippocampus protein #43.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match 8.9%; Score 100.5; DB 7; Length 412;
Best Local Similarity 30.9%; Pred. No. 0.57;
RESULT 1180
ID AAR77035 standard; protein; 378 AA.
DE Cat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV VALE.
Query Match 8.9%; Score 100; DB 2; Length 378;
Best Local Similarity 24.1%; Pred. No. 0.56;
RESULT 1181
ID ABP57346 standard; protein; 402 AA.
DE Human secreted protein SECP-17 SEQ ID NO:17.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUYY/) LU Y.
Query Match 8.8%; Score 99.5; DB 6; Length 402;
Best Local Similarity 30.9%; Pred. No. 0.69;
RESULT 1182
ID ABJ56917 standard; protein; 201 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 8.8%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.31;
RESULT 1183
ID ABJ56916 standard; protein; 201 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 8.8%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.31;
RESULT 1184
ID ABJ56919 standard; protein; 600 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 8.8%; Score 99; DB 6; Length 600;
Best Local Similarity 28.0%; Pred. No. 1.3;
RESULT 1185
ID ABB70377 standard; protein; 1428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37923.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.8%; Score 99; DB 4; Length 1428;
Best Local Similarity 28.4%; Pred. No. 4.2;
RESULT 1186
ID ABB60403 standard; protein; 2112 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.7%; Score 98; DB 4; Length 2112;
Best Local Similarity 25.9%; Pred. No. 8.8;
RESULT 1187
ID AAY95559 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 3; Length 2870;
Best Local Similarity 22.4%; Pred. No. 21;
RESULT 1188
ID ADN07634 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV -1 deletion mutant protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 8; Length 2870;
Best Local Similarity 22.4%; Pred. No. 21;
RESULT 1189
ID AAY95556 standard; protein; 3178 AA.
DE Caenorhabditis elegans LOV-1 (location of vulva) protein.
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 3; Length 3178;
Best Local Similarity 22.4%; Pred. No. 24;
RESULT 1190
ID ADN07623 standard; protein; 3178 AA.
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 8; Length 3178;
Best Local Similarity 22.4%; Pred. No. 24;
RESULT 1191

ID ADO41972 standard; protein; 231 AA.
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.5%; Score 95.5; DB 8; Length 231;
Best Local Similarity 30.2%; Pred. No. 0.81;
RESULT 1192
ID ABB65987 standard; protein; 183 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 8.4%; Score 94.5; DB 4; Length 183;
Best Local Similarity 34.5%; Pred. No. 0.75;
RESULT 1193
ID ABB69806 standard; protein; 1795 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 8.4%; Score 94.5; DB 4; Length 1795;
Best Local Similarity 33.0%; Pred. No. 16;
RESULT 1194
ID AAU18060 standard; protein; 258 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 205.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1195
ID ABB10532 standard; protein; 258 AA.
DE Human cDNA SEQ ID NO: 840.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1196
ID ABB67119 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 840.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 8.3%; Score 93.5; DB 5; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1197
ID ABB31684 standard; protein; 258 AA.
DE Human novel protein SEQ ID NO 205.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 7; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1198
ID AAU17999 standard; protein; 261 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 144.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1199
ID ABB10361 standard; protein; 261 AA.
DE Human cDNA SEQ ID NO: 669.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.5;

RESULT 1200
ID ABB66948 standard; protein; 261 AA.
DE Human polypeptide SEQ ID NO 669.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 8.3%; Score 93.5; DB 5; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1201
ID ABB31623 standard; protein; 261 AA.
DE Human novel protein SEQ ID NO 144.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 7; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1202
ID ABB73157 standard; protein; 40 AA.
DE Deletion mutant of a CD44-Hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGC/) KOGERMAN P.
PA (PAEL/) PARELL T.
Query Match 8.2%; Score 92.5; DB 6; Length 40;
Best Local Similarity 54.1%; Pred. No. 0.15;
RESULT 1203
ID ADP04445 standard; protein; 1381 AA.
DE Sea squirt protein with tissue specific expression in development Seq40.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 8.2%; Score 92.5; DB 8; Length 1381;
Best Local Similarity 22.6%; Pred. No. 17;
RESULT 1204
ID AAU18036 standard; protein; 166 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 181.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.3;
RESULT 1205
ID ABB10469 standard; protein; 166 AA.
DE Human cDNA SEQ ID NO: 777.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.3;
RESULT 1206
ID ABB67056 standard; protein; 166 AA.
DE Human polypeptide SEQ ID NO 777.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 8.1%; Score 91.5; DB 5; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.3;
RESULT 1207
ID ABB31660 standard; protein; 166 AA.
DE Human novel protein SEQ ID NO 181.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 91.5; DB 7; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.3;
RESULT 1208
ID ABB69720 standard; protein; 1126 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35952.

PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 8.1%; Score 91.5; DB 4; Length 1126;
 Best Local Similarity 32.3%; Pred. No. 17;
 RESULT 1209
 ID ADG73740 standard; protein; 505 AA.
 DE Aspergillus niger Brea-109.
 PN US2003215950-A1.
 PD 20-NOV-2003.
 PA (LASU/) LASURE L L.
 PA (DAIZ/) DAI Z.
 Query Match 8.0%; Score 90.5; DB 8; Length 505;
 Best Local Similarity 27.0%; Pred. No. 7.1;
 RESULT 1210
 ID ABB69419 standard; protein; 1976 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 35049.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 8.0%; Score 90.5; DB 4; Length 1976;
 Best Local Similarity 38.5%; Pred. No. 44;
 RESULT 1211
 ID ABU36285 standard; protein; 402 AA.
 DE Protein encoded by Prokaryotic essential gene #21812.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 8.0%; Score 90; DB 6; Length 402;
 Best Local Similarity 22.4%; Pred. No. 5.9;
 RESULT 1212
 ID ADN20575 standard; protein; 1103 AA.
 DE Bacterial polypeptide #3228.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 8.0%; Score 90; DB 8; Length 1103;
 Best Local Similarity 23.5%; Pred. No. 23;
 RESULT 1213
 ID ABB65879 standard; protein; 307 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 24429.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.9%; Score 89; DB 4; Length 307;
 Best Local Similarity 31.6%; Pred. No. 5.2;
 RESULT 1214
 ID AAR69554 standard; protein; 416 AA.
 DE Human lysosomal membrane sialoglycoprotein lamp-1.
 PN WO9429342-A1.
 PD 22-DEC-1994.
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 PA (UNMI) UNIV MICHIGAN.
 Query Match 7.9%; Score 89; DB 2; Length 416;
 Best Local Similarity 23.6%; Pred. No. 7.8;
 RESULT 1215
 ID AAY52550 standard; protein; 416 AA.
 DE Human lysosomal membrane glycoprotein-1 (LAMP-1).
 PN WO9958658-A2.
 PD 18-NOV-1999.
 PA (EPTM-) EPIMUNE INC.
 Query Match 7.9%; Score 89; DB 3; Length 416;
 Best Local Similarity 23.6%; Pred. No. 7.8;
 RESULT 1216
 ID ADP65283 standard; protein; 416 AA.
 DE Human lysosomal-associated membrane protein 1.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

Query Match 7.9%; Score 89; DB 7; Length 416;
 Best Local Similarity 23.6%; Pred. No. 7.8;
 RESULT 1217
 ID ADN03755 standard; protein; 416 AA.
 DE Antipsoriatic protein sequence #74.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.9%; Score 89; DB 8; Length 416;
 Best Local Similarity 23.6%; Pred. No. 7.8;
 RESULT 1218
 ID ADP49321 standard; protein; 416 AA.
 DE Human lysosomal associated membrane protein LAMP #1.
 PN WO2004048537-A2.
 PD 10-JUN-2004.
 PA (EXEL-) EXELIXIS INC.
 Query Match 7.9%; Score 89; DB 8; Length 416;
 Best Local Similarity 23.6%; Pred. No. 7.8;
 RESULT 1219
 ID ADP23231 standard; protein; 416 AA.
 DE PRO polypeptide SEQ ID NO:325.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.9%; Score 89; DB 8; Length 416;
 Best Local Similarity 23.6%; Pred. No. 7.8;
 RESULT 1220
 ID ABO68455 standard; protein; 451 AA.
 DE Pseudomonas aeruginosa polypeptide #630.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 7.9%; Score 88.5; DB 7; Length 451;
 Best Local Similarity 20.7%; Pred. No. 9.7;
 RESULT 1221
 ID AAY52525 standard; protein; 536 AA.
 DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
 PN WO9954349-A2.
 PD 28-OCT-1999.
 PA (HESK-) HESKA CORP.
 Query Match 7.8%; Score 87.5; DB 3; Length 536;
 Best Local Similarity 23.9%; Pred. No. 15;
 RESULT 1222
 ID AAU96329 standard; protein; 536 AA.
 DE Der HMW-map polypeptide #16.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match 7.8%; Score 87.5; DB 5; Length 536;
 Best Local Similarity 23.9%; Pred. No. 15;
 RESULT 1223
 ID AAY52523 standard; protein; 555 AA.
 DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
 PN WO9954349-A2.
 PD 28-OCT-1999.
 PA (HESK-) HESKA CORP.
 Query Match 7.8%; Score 87.5; DB 3; Length 555;
 Best Local Similarity 23.9%; Pred. No. 16;
 RESULT 1224
 ID AAU96327 standard; protein; 555 AA.
 DE Der HMW-map polypeptide #14.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match 7.8%; Score 87.5; DB 5; Length 555;
 Best Local Similarity 23.9%; Pred. No. 16;
 RESULT 1225
 ID AAU96328 standard; protein; 555 AA.
 DE Der HMW-map polypeptide #15.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match 7.8%; Score 87.5; DB 5; Length 555;
 Best Local Similarity 23.9%; Pred. No. 16;
 RESULT 1226
 ID AAU96328 standard; protein; 555 AA.
 DE Der HMW-map polypeptide #15.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match 7.8%; Score 87.5; DB 5; Length 555;
 Best Local Similarity 23.9%; Pred. No. 16;
 RESULT 1227
 ID AAU96328 standard; protein; 555 AA.
 DE Der HMW-map polypeptide #15.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.

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Best Local Similarity 23.9%; Pred. No. 16;
RESULT 1226
ID AAW54844 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor 1 protein 5kb fragment.
PN US5763569-A.
PD 09-JUN-1998.
PA (NPSF-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.8%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1227
ID AAY41778 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor 1 protein sequence.
PN US5962314-A.
PD 05-OCT-1999.
PA (NPSF-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.8%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1228
ID AAW95563 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor BoPCar 1.
PN US5858684-A.
PD 12-JAN-1999.
PA (NPSF-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.8%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1229
ID AAY51825 standard; protein; 1085 AA.
DE Bovine calcium receptor BoPCar1 protein.
PN US6031003-A.
PD 29-FEB-2000.
PA (NPSF-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.8%; Score 87.5; DB 3; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1230
ID AAB47820 standard; protein; 1085 AA.
DE BoPCar1.
PN US6313146-B1.
PD 06-NOV-2001.
PA (NPSF-) NPS PHARM INC.
Query Match 7.8%; Score 87.5; DB 5; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1231
ID ADJ93194 standard; protein; 1085 AA.
DE Bovine extracellular Ca-sensing receptor.
PN WO200296946-A1.
PD 05-DEC-2002.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 7.8%; Score 87.5; DB 7; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1232
ID ADI40961 standard; protein; 1085 AA.
DE Bovine GPCR CASR.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAWA/) RAMANATHAN C S.
Query Match 7.8%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1233
ID ADI41015 standard; protein; 1085 AA.
DE Bovine GPCR CASR #2.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAWA/) RAMANATHAN C S.
Query Match 7.8%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1234
ID ADD44997 standard; protein; 235 AA.
DE Rat Protein CAA82313, SEQ ID NO 10428.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.7%; Score 87; DB 7; Length 235;
Best Local Similarity 27.8%; Pred. No. 5.7;
RESULT 1235
ID AAY29082 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9332633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1236
ID AAY29081 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9332633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1237
ID AAU25553 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTG1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1238
ID AAU25552 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTG288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1239
ID ADG17391 standard; protein; 288 AA.
DE T. gondii protein #79.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1240
ID ADG17394 standard; protein; 288 AA.
DE T. gondii protein #82.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1241
ID AAR01940 standard; protein; 417 AA.
DE Tumour necrosis factor.
PN JP01285191-A.
PD 16-NOV-1989.
PA (GREC ) GREEN CROSS CORP.
Query Match 7.7%; Score 87; DB 2; Length 417;
Best Local Similarity 23.6%; Pred. No. 12;
RESULT 1242
ID AAP01941 standard; peptide; 400 AA.
DE Sequence of preprospasmodysin.
PN DE3808456-A.
PD 28-SEP-1989.
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 7.7%; Score 86.5; DB 1; Length 400;
Best Local Similarity 30.8%; Pred. No. 13;
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RESULT 1243
ID AAR69555 standard; protein; 410 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-2.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI-) UNIV MICHIGAN.
Query Match 7.7%; Score 86.5; DB 2; Length 410;
Best Local Similarity 20.7%; Pred. No. 13;
RESULT 1244
ID AAY37234 standard; protein; 708 AA.
DE Chlamydia trachomatis cellular envelope protein.
PN WO928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 7.7%; Score 86.5; DB 2; Length 708;
Best Local Similarity 23.4%; Pred. No. 28;
RESULT 1245
ID ABM82857 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3106.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.6%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 18;
RESULT 1246
ID ABM83144 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3393.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.6%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 18;
RESULT 1247
ID ABP69313 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 1360.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.6%; Score 85.5; DB 5; Length 343;
Best Local Similarity 30.2%; Pred. No. 13;
RESULT 1248
ID AAR57350 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO9415627-A1.
PD 21-JUL-1994.
PA (GEO) GEN HOSPITAL CORP.
Query Match 7.6%; Score 85.5; DB 2; Length 354;
Best Local Similarity 26.2%; Pred. No. 14;
RESULT 1249
ID ABB78250 standard; protein; 652 AA.
DE Amino acid sequence of a human heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEO) GEN HOSPITAL CORP.
Query Match 7.6%; Score 85.5; DB 5; Length 652;
Best Local Similarity 22.4%; Pred. No. 31;
RESULT 1250
ID ABB78248 standard; protein; 841 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEO) GEN HOSPITAL CORP.
Query Match 7.6%; Score 85.5; DB 5; Length 841;
Best Local Similarity 22.4%; Pred. No. 44;
RESULT 1251
ID ADQ37103 standard; protein; 951 AA.
DE Cell proliferation-related polypeptide #118.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 7.6%; Score 85.5; DB 8; Length 951;
Best Local Similarity 26.0%; Pred. No. 52;
RESULT 1252
ID ABB78249 standard; protein; 977 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEO) GEN HOSPITAL CORP.
Query Match 7.6%; Score 85.5; DB 5; Length 977;
Best Local Similarity 22.4%; Pred. No. 53;
RESULT 1253
ID ABUS4710 standard; protein; 1784 AA.
DE Human CAL25 protein amino terminal sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 6; Length 1784;
Best Local Similarity 27.2%; Pred. No. 1.2e+02;
RESULT 1254
ID ABUS4858 standard; protein; 1794 AA.
DE Human CAL25 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 6; Length 1794;
Best Local Similarity 27.2%; Pred. No. 1.2e+02;
RESULT 1255
ID ABUS4707 standard; protein; 1821 AA.
DE Human CAL25 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 6; Length 1821;
Best Local Similarity 27.2%; Pred. No. 1.2e+02;
RESULT 1256
ID AAE34702 standard; protein; 5877 AA.
DE Human mucin (MUC-16B).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 7.6%; Score 85.5; DB 6; Length 5877;
Best Local Similarity 27.2%; Pred. No. 5.8e+02;
RESULT 1257
ID ABUS4721 standard; protein; 11721 AA.
DE Human CAL25 full length protein sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 6; Length 11721;
Best Local Similarity 27.2%; Pred. No. 1.5e+03;
RESULT 1258
ID ADP84155 standard; protein; 22157 AA.
DE Human CAL25 protein sequence SeqID 5.
PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 8; Length 22157;
Best Local Similarity 27.2%; Pred. No. 3.4e+03;
RESULT 1259
ID ABS50001 standard; protein; 569 AA.
DE Listeria monocytogenes protein #2705.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 7.6%; Score 85; DB 5; Length 569;
Best Local Similarity 22.9%; Pred. No. 29;
RESULT 1260
ID ABUS32518 standard; protein; 569 AA.
DE Protein encoded by Prokaryotic essential gene #18045.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.6%; Score 85; DB 6; Length 569;
Best Local Similarity 22.9%; Pred. No. 29;
RESULT 1261
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ID ABB5236 standard; protein; 627 AA.
 DE Lactococcus lactis protein ytfC.
 PN FR2807446-A1.
 PD 12-OCT-2001.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 Query Match 7.6%; Score 85; DB 5; Length 627;
 Best Local Similarity 21.5%; Pred. No. 33;
 RESULT 1262
 ID ADS29466 standard; protein; 627 AA.
 DE Bacterial polypeptide #18499.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 7.6%; Score 85; DB 8; Length 627;
 Best Local Similarity 21.5%; Pred. No. 33;
 RESULT 1263
 ID AAG93274 standard; protein; 631 AA.
 DE Chlamydia trachomatis PmpH(N-term) fusion protein.
 PN WO200140474-A2.
 PD 07-JUN-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 7.6%; Score 85; DB 4; Length 631;
 Best Local Similarity 27.7%; Pred. No. 33;
 RESULT 1264
 ID ABB94245 standard; protein; 631 AA.
 DE Chlamydia trachomatis protein sequence SEQ ID NO:325.
 PN WO200208267-A2.
 PD 31-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 7.6%; Score 85; DB 5; Length 631;
 Best Local Similarity 27.7%; Pred. No. 33;
 RESULT 1265
 ID ADD42755 standard; protein; 664 AA.
 DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.
 PN WO2003041560-A2.
 PD 22-MAY-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 7.6%; Score 85; DB 7; Length 664;
 Best Local Similarity 27.7%; Pred. No. 36;
 RESULT 1266
 ID AAU38901 standard; protein; 1016 AA.
 DE C. trachomatis CT872 protein.
 PN WO200181379-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 7.6%; Score 85; DB 4; Length 1016;
 Best Local Similarity 27.7%; Pred. No. 63;
 RESULT 1267
 ID ABG91037 standard; protein; 1016 AA.
 DE Chlamydia trachomatis outer membrane protein H protein.
 PN WO200262380-A2.
 PD 15-AUG-2002.
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 Query Match 7.6%; Score 85; DB 5; Length 1016;
 Best Local Similarity 27.7%; Pred. No. 63;
 RESULT 1268
 ID ADD42682 standard; protein; 1016 AA.
 DE Chlamydia trachomatis antigen protein SEQ ID NO:95.
 PN WO2003041560-A2.
 PD 22-MAY-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 7.6%; Score 85; DB 7; Length 1016;
 Best Local Similarity 27.7%; Pred. No. 63;
 RESULT 1269
 ID ADD43800 standard; protein; 1016 AA.
 DE Chlamydia trachomatis immunogenic protein, SEQ ID No 95.
 PN WO2003049762-A2.
 PD 19-JUN-2003.
 PA (CHIR-) CHIRON SPA.

Query Match 7.6%; Score 85; DB 7; Length 1016;
 Best Local Similarity 27.7%; Pred. No. 63;
 RESULT 1270
 ID ABB60387 standard; protein; 1049 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 7953.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.6%; Score 85; DB 4; Length 1049;
 Best Local Similarity 22.1%; Pred. No. 66;
 RESULT 1271
 ID ADJ66747 standard; protein; 2234 AA.
 DE Human Muc16 GST fusion protein amino acid sequence SeqID20.
 PN WO2004005470-A2.
 PD 15-JAN-2004.
 PA (IMMU-) IMMUNOGEN INC.
 Query Match 7.5%; Score 84.5; DB 8; Length 2234;
 Best Local Similarity 27.2%; Pred. No. 2e+02;
 RESULT 1272
 ID ADR72871 standard; protein; 22152 AA.
 DE Human ovarian cancer-related tumour marker CA125 protein.
 PN WO2004075713-A2.
 PD 10-SEP-2004.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Query Match 7.5%; Score 84.5; DB 8; Length 22152;
 Best Local Similarity 27.2%; Pred. No. 4.3e+03;
 RESULT 1273
 ID AAB11729 standard; protein; 216 AA.
 DE Cryptosporidium parvum Iowa isolate GP900, domain 2.
 PN US6071518-A.
 PD 06-JUN-2000.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 7.5%; Score 84; DB 3; Length 216;
 Best Local Similarity 26.7%; Pred. No. 10;
 RESULT 1274
 ID AAB11734 standard; protein; 216 AA.
 DE Cryptosporidium parvum NINC isolate GP900, domain 2.
 PN US6071518-A.
 PD 06-JUN-2000.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 7.5%; Score 84; DB 3; Length 216;
 Best Local Similarity 26.7%; Pred. No. 10;
 RESULT 1275
 ID ABJ04047 standard; protein; 216 AA.
 DE C. parvum GP900 protein fragment SEQ ID NO: 8.
 PN WO200194631-A1.
 PD 13-DEC-2001.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 7.5%; Score 84; DB 5; Length 216;
 Best Local Similarity 26.7%; Pred. No. 10;
 RESULT 1276
 ID AAB42164 standard; protein; 330 AA.
 DE Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.5%; Score 84; DB 3; Length 330;
 Best Local Similarity 27.5%; Pred. No. 18;
 RESULT 1277
 ID ABB59598 standard; protein; 330 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 5586.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.5%; Score 84; DB 4; Length 330;
 Best Local Similarity 30.6%; Pred. No. 18;
 RESULT 1278
 ID ADO61979 standard; protein; 335 AA.
 DE Transcription factor G2571, SEQ ID 446.
 PN WO2004031349-A2.
 PD 15-APR-2004.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Query Match 7.5%; Score 84; DB 8; Length 335;

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Best Local Similarity 26.4%; Pred. No. 18;
RESULT 1279
ID AAB96091 standard; protein; 1362 AA.
DE Putative P. abyssi amylpullulanase.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS ) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 7.5%; Score 84; DB 4; Length 1362;
Best Local Similarity 26.5%; Pred. No. 1.2e+02;
RESULT 1280
ID AAW48299 standard; protein; 1721 AA.
DE Cryptosporidium parvum GP900 antigen.
PN WO9806430-A1.
PD 19-FEB-1998.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 2; Length 1721;
Best Local Similarity 26.7%; Pred. No. 1.6e+02;
RESULT 1281
ID AAB11727 standard; protein; 1721 AA.
DE Portion of Cryptosporidium parvum NINC isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 3; Length 1721;
Best Local Similarity 26.7%; Pred. No. 1.6e+02;
RESULT 1282
ID ABJ04045 standard; protein; 1721 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 6.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 5; Length 1721;
Best Local Similarity 26.7%; Pred. No. 1.6e+02;
RESULT 1283
ID AAB11726 standard; protein; 1837 AA.
DE Cryptosporidium parvum Iowa isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 3; Length 1837;
Best Local Similarity 26.7%; Pred. No. 1.7e+02;
RESULT 1284
ID ABJ04044 standard; protein; 1837 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 5.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 5; Length 1837;
Best Local Similarity 26.7%; Pred. No. 1.7e+02;
RESULT 1285
ID ABUS3165 standard; protein; 143 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #25.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 143;
Best Local Similarity 30.7%; Pred. No. 6.5;
RESULT 1286
ID ABUS3163 standard; protein; 247 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #23.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 247;
Best Local Similarity 30.7%; Pred. No. 13;
RESULT 1287
ID ABUS3158 standard; protein; 260 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #18.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 260;
Best Local Similarity 30.7%; Pred. No. 14;
RESULT 1288
ID ABUS3157 standard; protein; 368 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #17.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 368;
Best Local Similarity 30.7%; Pred. No. 23;
RESULT 1289
ID ABUS3156 standard; protein; 385 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #16.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 385;
Best Local Similarity 30.7%; Pred. No. 24;
RESULT 1290
ID ABUS3159 standard; protein; 387 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #19.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 387;
Best Local Similarity 30.7%; Pred. No. 24;
RESULT 1291
ID ABUS3161 standard; protein; 387 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #21.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 393;
Best Local Similarity 26.5%; Pred. No. 25;
RESULT 1292
ID AAM50241 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase.
PN US6297055-B1.
PD 02-OCT-2001.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
Query Match 7.4%; Score 83.5; DB 4; Length 393;
Best Local Similarity 26.5%; Pred. No. 25;
RESULT 1293
ID AAU76423 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase clone wr1.pk0059.g9.
PN US2002009801-A1.
PD 24-JAN-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (OROZ/) OROZCO E R.
Query Match 7.4%; Score 83.5; DB 5; Length 393;
Best Local Similarity 26.5%; Pred. No. 25;
RESULT 1294
ID ABUS3160 standard; protein; 395 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #20.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 395;
Best Local Similarity 30.7%; Pred. No. 25;
RESULT 1295
ID ABB10349 standard; protein; 553 AA.
DE Human cDNA SEQ ID NO: 657.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 7.4%; Score 83.5; DB 4; Length 553;
Best Local Similarity 22.9%; Pred. No. 39;
RESULT 1296
ID ABP66936 standard; protein; 553 AA.
DE Human polypeptide SEQ ID NO 657.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
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PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 7.4%; Score 83.5; DB 5; Length 553;
 Best Local Similarity 22.9%; Pred. No. 39;
 RESULT 1297
 ID ABUS3144 standard; protein; 717 AA.
 DE Human testes-derived DKF2phes3_2a11 homologue #4.
 PN WO200112659-A2.
 PD 22-FEB-2001.
 PA (GERU-) GERMAN HUMAN GENOME PROJECT.
 Query Match 7.4%; Score 83.5; DB 4; Length 717;
 Best Local Similarity 30.7%; Pred. No. 56;
 RESULT 1298
 ID AAY54466 standard; protein; 788 AA.
 DE Amino acid sequence of intestinal insect mucin isoform IIM14.
 PN WO9967373-A2.
 PD 29-DEC-1999.
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
 Query Match 7.4%; Score 83.5; DB 3; Length 788;
 Best Local Similarity 26.5%; Pred. No. 63;
 RESULT 1299
 ID AAY54467 standard; protein; 807 AA.
 DE Amini acid sequence of intestinal insect mucin isoform IIM22.
 PN WO9967373-A2.
 PD 29-DEC-1999.
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
 Query Match 7.4%; Score 83.5; DB 3; Length 807;
 Best Local Similarity 26.5%; Pred. No. 65;
 RESULT 1300
 ID ABU62079 standard; protein; 4123 AA.
 DE Human jelly belly (jeb) protein.
 PN US2003054485-A1.
 PD 20-MAR-2003.
 PA (SCOT/) SCOTT M P.
 PA (WEIS/) WEISS J B.
 Query Match 7.4%; Score 83.5; DB 7; Length 4123;
 Best Local Similarity 22.7%; Pred. No. 5.7e+02;
 RESULT 1301
 ID ADH48718 standard; protein; 4219 AA.
 DE NOV1 protein sequence, SEQ ID 2.
 PN WO200268652-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.4%; Score 83.5; DB 5; Length 4219;
 Best Local Similarity 22.7%; Pred. No. 5.9e+02;
 RESULT 1302
 ID AAM24516 standard; protein; 5179 AA.
 DE C899P predicted amino acid sequence.
 PN WO200149716-A2.
 PD 12-JUL-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 7.4%; Score 83.5; DB 4; Length 5179;
 Best Local Similarity 30.7%; Pred. No. 7.8e+02;
 RESULT 1303
 ID ABP55365 standard; protein; 5179 AA.
 DE Human colon tumour protein for clone C899P SEQ ID NO:1068.
 PN WO200283070-A2.
 PD 24-OCT-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 7.4%; Score 83.5; DB 6; Length 5179;
 Best Local Similarity 30.7%; Pred. No. 7.8e+02;
 RESULT 1304
 ID ABO07258 standard; protein; 5179 AA.
 DE Human p53 modifying protein, SEQ ID 218.
 PN WO200299122-A1.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 7.4%; Score 83.5; DB 6; Length 5179;
 Best Local Similarity 30.7%; Pred. No. 7.8e+02;
 RESULT 1305
 ID ADD48091 standard; protein; 5179 AA.
 DE Human Protein NP_002448, SEQ ID NO 13789.
 PN WO2003016475-A2.

PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.4%; Score 83.5; DB 7; Length 5179;
 Best Local Similarity 30.7%; Pred. No. 7.8e+02;
 RESULT 1306
 ID ADD44998 standard; protein; 5179 AA.
 DE Human Protein Q02817, SEQ ID NO 10430.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.4%; Score 83.5; DB 7; Length 5179;
 Best Local Similarity 30.7%; Pred. No. 7.8e+02;
 RESULT 1307
 ID ADQ29695 standard; protein; 5179 AA.
 DE Human colorectal cancer-associated protein #50.
 PN EPI439393-A2.
 PD 21-JUL-2004.
 PA (FARB) BAYER HEALTHCARE LLC.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 Query Match 7.4%; Score 83.5; DB 8; Length 5179;
 Best Local Similarity 30.7%; Pred. No. 7.8e+02;
 RESULT 1308
 ID ADQ80379 standard; protein; 5179 AA.
 DE Intestinal/tracheal mucin 2 protein.
 PN WO2004063709-A2.
 PD 29-JUL-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 7.4%; Score 83.5; DB 8; Length 5179;
 Best Local Similarity 30.7%; Pred. No. 7.8e+02;
 RESULT 1309
 ID ADN95228 standard; protein; 5737 AA.
 DE Human BEC/LEC-related protein sequence SeqID150.
 PN WO2003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 7.4%; Score 83.5; DB 7; Length 5737;
 Best Local Similarity 22.7%; Pred. No. 8.9e+02;
 RESULT 1310
 ID AAR07670 standard; protein; 166 AA.
 DE Intestinal mucin deduced from clone SMUC 40.
 PN WO9012892-A.
 PD 01-NOV-1990.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 7.4%; Score 83; DB 2; Length 166;
 Best Local Similarity 29.9%; Pred. No. 8.9;
 RESULT 1311
 ID AAW75700 standard; peptide; 409 AA.
 DE Vpr protein binding HHR23B amino acid sequence.
 PN WO9835234-A1.
 PD 13-AUG-1998.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 7.4%; Score 83; DB 2; Length 409;
 Best Local Similarity 28.6%; Pred. No. 30;
 RESULT 1312
 ID AAW68186 standard; protein; 409 AA.
 DE Vpr binding protein HHR23B amino acid sequence.
 PN WO9835032-A2.
 PD 13-AUG-1998.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 7.4%; Score 83; DB 2; Length 409;
 Best Local Similarity 28.6%; Pred. No. 30;
 RESULT 1313
 ID ABU07460 standard; protein; 409 AA.
 DE Protein differentially regulated in prostate cancer #63.
 PN WO200281638-A2.
 PD 17-OCT-2002.
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 Query Match 7.4%; Score 83; DB 6; Length 409;
 Best Local Similarity 28.6%; Pred. No. 30;
 RESULT 1314

ID ADN03716 standard; protein; 409 AA.
DE Antiopieriatric protein sequence #55.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC. 7.4%; Score 83; DB 8; Length 409;
Query Match
Best Local Similarity 28.8%; Pred. No. 30;
RESULT 1315
ID ADQ65876 standard; protein; 409 AA.
DE Novel human protein sequence #849.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIO TECHNOLOGY.
Query Match
Best Local Similarity 7.4%; Score 83; DB 8; Length 409;
RESULT 1316
ID ABB61785 standard; protein; 471 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12147.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 7.4%; Score 83; DB 4; Length 471;
RESULT 1317
ID ADS43586 standard; protein; 605 AA.
DE Bacterial polypeptide #22016.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 7.4%; Score 83; DB 8; Length 605;
RESULT 1318
ID AAG34201 standard; protein; 280 AA.
DE Zea mays protein fragment SEQ ID NO: 41576.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 7.3%; Score 82.5; DB 3; Length 280;
RESULT 1319
ID AAG40817 standard; protein; 346 AA.
DE Zea mays protein fragment SEQ ID NO: 50697.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 7.3%; Score 82.5; DB 3; Length 346;
RESULT 1320
ID ADS44071 standard; protein; 825 AA.
DE Bacterial polypeptide #22501.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 7.3%; Score 82.5; DB 8; Length 825;
RESULT 1321
ID ABB71012 standard; protein; 843 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39828.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 7.3%; Score 82.5; DB 4; Length 843;
RESULT 1322
ID AAW38272 standard; protein; 1085 AA.
DE Bovine parathyroid cell calcium receptor 1 (BoPCar 1).
PN US5688938-A.

PD 18-NOV-1997.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (NPSP-) NPS PHARM INC. 7.3%; Score 82.5; DB 2; Length 1085;
Query Match
Best Local Similarity 22.4%; Pred. No. 1.2e+02;
RESULT 1323
ID ABB69011 standard; protein; 1371 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33825.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 7.3%; Score 82.5; DB 4; Length 1371;
RESULT 1324
ID AAM21657 standard; protein; 89 AA.
DE Peptide #8091 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 7.3%; Score 82; DB 4; Length 89;
RESULT 1325
ID ABB44016 standard; peptide; 89 AA.
DE Peptide #11522 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 7.3%; Score 82; DB 4; Length 89;
RESULT 1326
ID AAM37960 standard; protein; 89 AA.
DE Peptide #11997 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 7.3%; Score 82; DB 4; Length 89;
RESULT 1327
ID ABB26922 standard; protein; 89 AA.
DE Protein #8921 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 7.3%; Score 82; DB 4; Length 89;
RESULT 1328
ID AAM77746 standard; protein; 89 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 38052.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 7.3%; Score 82; DB 4; Length 89;
RESULT 1329
ID AAM65031 standard; protein; 89 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 37136.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 7.3%; Score 82; DB 4; Length 89;
RESULT 1330
ID ABB59403 standard; peptide; 89 AA.
DE Human liver peptide, SEQ ID NO 38051.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 7.3%; Score 82; DB 4; Length 89;
RESULT 1331
ID ABB46774 standard; peptide; 89 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 36439.
PN WO200186003-A2.

PD 15-NOV-2001.
PA (MOLB-) MOLECULAR DYNAMICS INC.
Query Match 7.3%; Score 82; DB 5; Length 89;
Best Local Similarity 28.9%; Pred. No. 4.9;
RESULT 1332
ID ABB67754 standard; protein; 339 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30054.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE-) PE CORP NY.
Query Match 7.3%; Score 82; DB 4; Length 339;
Best Local Similarity 25.4%; Pred. No. 29;
RESULT 1333
ID ADQ18080 standard; protein; 477 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 897.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.3%; Score 82; DB 8; Length 477;
Best Local Similarity 32.1%; Pred. No. 45;
RESULT 1334
ID ABG70759 standard; protein; 553 AA.
DE T. maritima endoglucanase protein.
PN US2002120118-A1.
PD 29-AUG-2002.
PA (SHORT-) SHORT J M.
PA (LAMD/) LAM D E.
PA (MATH/) MATHUR E J.
Query Match 7.3%; Score 82; DB 5; Length 553;
Best Local Similarity 28.2%; Pred. No. 55;
RESULT 1335
ID AAW34999 standard; protein; 628 AA.
DE Archaeobacterium ABP11a endoglucanase.
PN WO9744361-A1.
PD 27-NOV-1997.
PA (RECO-) RECOMBINANT BIOTECNOLOGY INC.
Query Match 7.3%; Score 82; DB 2; Length 628;
Best Local Similarity 28.2%; Pred. No. 66;
RESULT 1336
ID ADA55053 standard; protein; 637 AA.
DE Human protein, SEQ ID 2621.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.3%; Score 82; DB 6; Length 637;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1337
ID AAB29654 standard; protein; 667 AA.
DE Human membrane-associated protein HUMAP-11.
PN WO200065054-A2.
PD 02-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.3%; Score 82; DB 3; Length 667;
Best Local Similarity 24.2%; Pred. No. 71;
RESULT 1338
ID AAW34985 standard; protein; 841 AA.
DE Archaeobacterial thermostable endoglucanase.
PN WO9744361-A1.
PD 27-NOV-1997.
PA (RECO-) RECOMBINANT BIOTECNOLOGY INC.
Query Match 7.3%; Score 82; DB 2; Length 841;
Best Local Similarity 28.2%; Pred. No. 97;
RESULT 1339
ID AAR22234 standard; protein; 995 AA.
DE Sequence encoded by ILTV gp60 gene.
PN WO9203554-A.
PD 05-MAR-1992.
PA (WEBS-) WEBSTER A PTY LTD.
Query Match 7.3%; Score 82; DB 2; Length 995;
Best Local Similarity 31.7%; Pred. No. 1.2e+02;
RESULT 1340
ID ADM47185 standard; protein; 1671 AA.

DE Neurexin III-alpha membrane-bound type I precursor like NOVX 3a protein.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.3%; Score 82; DB 7; Length 1671;
Best Local Similarity 24.2%; Pred. No. 2.4e+02;
RESULT 1341
ID AAB09826 standard; protein; 346 AA.
DE Endoglucanase protein sequence 6.
PN WO200024879-A1.
PD 04-MAY-2000.
PA (MEIJ-) MEIJI SEIKA KAISHA LTD.
Query Match 7.2%; Score 81.5; DB 3; Length 346;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1342
ID AAO15057 standard; protein; 346 AA.
DE Phycomyces nitens endoglucanase-related protein.
PN WO200242474-A1.
PD 30-MAY-2002.
PA (MEIJ-) MEIJI SEIKA KAISHA LTD.
Query Match 7.2%; Score 81.5; DB 5; Length 346;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1343
ID ABO8065 standard; protein; 346 AA.
DE P. nitens CP99002 PCEI protein.
PN WO200238754-A1.
PD 16-MAY-2002.
PA (MEIJ-) MEIJI SEIKA KAISHA LTD.
Query Match 7.2%; Score 81.5; DB 5; Length 346;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1344
ID ADA37114 standard; protein; 346 AA.
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO:6.
PN WO2003052105-A1.
PD 26-JUN-2003.
PA (MEIJ-) MEIJI SEIKA KAISHA LTD.
Query Match 7.2%; Score 81.5; DB 6; Length 346;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1345
ID ABU23564 standard; protein; 386 AA.
DE Protein encoded by Prokaryotic essential gene #9091.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 81.5; DB 6; Length 386;
Best Local Similarity 22.0%; Pred. No. 38;
RESULT 1346
ID ABO58564 standard; protein; 800 AA.
DE Human genome derived single exon protein #4798.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 7.2%; Score 81.5; DB 8; Length 800;
Best Local Similarity 35.8%; Pred. No. 1e+02;
RESULT 1347
ID AAY59288 standard; protein; 957 AA.
DE Human MUC11 polypeptide.
PN WO200004142-A1.
PD 27-JAN-2000.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
Query Match 7.2%; Score 81.5; DB 3; Length 957;
Best Local Similarity 29.0%; Pred. No. 1.3e+02;
RESULT 1348
ID AAM24513 standard; protein; 957 AA.
DE C900P predicted amino acid sequence.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 81.5; DB 4; Length 957;
Best Local Similarity 29.0%; Pred. No. 1.3e+02;

RESULT 1349
ID ABP5362 standard; protein; 957 AA.
DE Human colon tumour protein for clone C900P SEQ ID NO:1065.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP. 7.2%; Score 81.5; DB 6; Length 957;
Query Match Best Local Similarity 29.0%; Pred. No. 1.3e+02;
RESULT 1350
ID ADC31682 standard; protein; 1205 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1764.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSQ INC. 7.2%; Score 81.5; DB 7; Length 1205;
Query Match Best Local Similarity 29.0%; Pred. No. 1.7e+02;
RESULT 1351
ID ABB69973 standard; protein; 1354 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36711.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY. 7.2%; Score 81.5; DB 4; Length 1354;
Query Match Best Local Similarity 21.9%; Pred. No. 2e+02;
RESULT 1352
ID AAY93912 standard; protein; 289 AA.
DE A human hyaluronan-binding protein, designated OE-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match Best Local Similarity 24.4%; Pred. No. 29;
RESULT 1353
ID ABB64749 standard; protein; 294 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21039.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY. 7.2%; Score 81; DB 3; Length 289;
Query Match Best Local Similarity 22.0%; Pred. No. 30;
RESULT 1354
ID AAR60563 standard; protein; 862 AA.
DE Yeast 2.6 KB agglutination gene FLO1S.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB-) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGERILABORATORIUM.
Query Match Best Local Similarity 21.8%; Pred. No. 1.3e+02;
RESULT 1355
ID AAR58754 standard; protein; 894 AA.
DE S. cerevisiae FLO1.
PN WO9418330-A1.
PD 18-AUG-1994.
PA (UNIL-) UNILEVER PLC.
PA (UNIL-) UNILEVER NV. 7.2%; Score 81; DB 2; Length 894;
Query Match Best Local Similarity 21.8%; Pred. No. 1.3e+02;
RESULT 1356
ID AAR47578 standard; protein; 894 AA.
DE Flocculation protein of Saccharomyces cerevisiae.
PN WO9401567-A1.
PD 20-JAN-1994.
PA (UNIL-) UNILEVER PLC.
PA (UNIL-) UNILEVER NV. 7.2%; Score 81; DB 2; Length 894;
Query Match Best Local Similarity 21.8%; Pred. No. 1.3e+02;
RESULT 1357
ID ADS44054 standard; protein; 1128 AA.
DE Bacterial polypeptide #22484.
PN US2003233675-A1.
PD 18-DEC-2003.

PA (CAOY-) CAO Y. 7.2%; Score 81; DB 8; Length 1128;
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match Best Local Similarity 22.8%; Pred. No. 1.8e+02;
RESULT 1358
ID AAR60562 standard; protein; 1537 AA.
DE Yeast 4.7 KB agglutination gene FLO1L.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB-) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGERILABORATORIUM.
Query Match Best Local Similarity 21.8%; Pred. No. 2.7e+02;
RESULT 1359
ID ADP87475 standard; protein; 1537 AA.
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.
PN WO2004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match Best Local Similarity 21.8%; Pred. No. 2.7e+02;
RESULT 1360
ID ADNI8745 standard; protein; 1537 AA.
DE Bacterial polypeptide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match Best Local Similarity 21.8%; Pred. No. 2.7e+02;
RESULT 1361
ID ADRI8921 standard; protein; 1569 AA.
DE Human mucin glycoprotein, MUC6.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF-) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match Best Local Similarity 25.5%; Pred. No. 2.8e+02;
RESULT 1362
ID ADNI8882 standard; protein; 1609 AA.
DE Bacterial polypeptide #1535.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match Best Local Similarity 22.4%; Pred. No. 2.9e+02;
RESULT 1363
ID ADRI8914 standard; protein; 2240 AA.
DE Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF-) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match Best Local Similarity 25.5%; Pred. No. 4.5e+02;
RESULT 1364
ID ADRI8913 standard; protein; 2258 AA.
DE Human mucin-like protein, SCS0004, variant SEQ ID 3.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF-) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match Best Local Similarity 25.5%; Pred. No. 4.5e+02;
RESULT 1365
ID ADS44054 standard; protein; 1128 AA.
DE Bacterial polypeptide #22484.
PN US2003233675-A1.
PD 18-DEC-2003.

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ID ADRL8915 standard; protein; 2264 AA.
DE His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.2%; Score 81; DB 8; Length 2264;
Best Local Similarity 25.5%; Pred. No. 4.5e+02;
RESULT 1366
ID ABB69480 standard; protein; 2977 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35232.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 7.2%; Score 81; DB 4; Length 2977;
Best Local Similarity 18.8%; Pred. No. 6.5e+02;
RESULT 1367
ID ABP07042 standard; protein; 128 AA.
DE Human ORFX protein sequence SEQ ID NO:14066.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 7.2%; Score 80.5; DB 5; Length 128;
Best Local Similarity 33.8%; Pred. No. 11;
RESULT 1368
ID ADD46369 standard; protein; 148 AA.
DE Rat Protein CAA34901, SEQ ID NO 12049.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
Query Match 7.2%; Score 80.5; DB 7; Length 148;
Best Local Similarity 23.5%; Pred. No. 13;
RESULT 1369
ID AAU50934 standard; protein; 176 AA.
DE Propionibacterium acnes immunogenic protein #11830.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 80.5; DB 4; Length 176;
Best Local Similarity 27.8%; Pred. No. 17;
RESULT 1370
ID ABM47453 standard; protein; 176 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12129.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 80.5; DB 6; Length 176;
Best Local Similarity 27.8%; Pred. No. 17;
RESULT 1371
ID ABU26248 standard; protein; 323 AA.
DE Protein encoded by Prokaryotic essential gene #11775.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 80.5; DB 6; Length 323;
Best Local Similarity 27.1%; Pred. No. 38;
RESULT 1372
ID ABP28528 standard; protein; 540 AA.
DE Streptococcus polypeptide SEQ ID NO 6232.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
Query Match 7.2%; Score 80.5; DB 5; Length 540;
Best Local Similarity 22.5%; Pred. No. 75;
RESULT 1373
ID ABB57757 standard; protein; 1167 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 63.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 7.2%; Score 80.5; DB 4; Length 1167;
Best Local Similarity 28.2%; Pred. No. 2.1e+02;
RESULT 1374
ID AAR77036 standard; protein; 52 AA.
DE Human brain-enriched hyaluronan binding protein PIR1 domain.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA ) UNIV YALE.
Query Match 7.1%; Score 80; DB 2; Length 52;
Best Local Similarity 35.0%; Pred. No. 3.7;
RESULT 1375
ID ABP63646 standard; protein; 89 AA.
DE Human ORF16.
PN US2002082206-A1.
PD 27-JUN-2002.
PA (LEAC/) LEACH M D.
PA (MEHR/) MEHRABAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.
PA (LAWD/) LAW D.
Query Match 7.1%; Score 80; DB 5; Length 89;
Best Local Similarity 32.6%; Pred. No. 7.6;
RESULT 1376
ID ABO79758 standard; protein; 95 AA.
DE Pseudomonas aeruginosa polypeptide #11933.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.1%; Score 80; DB 7; Length 95;
Best Local Similarity 28.3%; Pred. No. 8.3;
RESULT 1377
ID ADRO9088 standard; protein; 272 AA.
DE Human protein useful for treating neurological disease Seq 2594.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.1%; Score 80; DB 8; Length 272;
Best Local Similarity 23.4%; Pred. No. 34;
RESULT 1378
ID ADF58702 standard; protein; 351 AA.
DE Human polypeptide sequence SEQ ID NO:1110.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 80; DB 7; Length 351;
Best Local Similarity 23.4%; Pred. No. 47;
RESULT 1379
ID ABB66171 standard; protein; 449 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25305.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 7.1%; Score 80; DB 4; Length 449;
Best Local Similarity 23.9%; Pred. No. 66;
RESULT 1380
ID AAY01077 standard; protein; 473 AA.
DE H. insolens Cel16A fungal cellulase protien sequence.
PN WO9501544-A1.
PD 14-JAN-1999.
PA (NOVO ) NOVO-NORDISK AS.
Query Match 7.1%; Score 80; DB 2; Length 473;
Best Local Similarity 28.1%; Pred. No. 71;
RESULT 1381
ID ADN19351 standard; protein; 725 AA.
DE Bacterial polypeptide #2004.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 80; DB 8; Length 725;
Best Local Similarity 27.2%; Pred. No. 1.2e+02;
RESULT 1382
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ID ABU09610 standard; protein; 729 AA.
DE Mouse retinoic acid-regulated nuclear matrix-associated protein.
PN US2003003485-A1.
PD 02-JAN-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 7.1%; Score 80; DB 6; Length 729;
Best Local Similarity 20.8%; Pred. No. 1.3e+02;
RESULT 1383
ID ABG23210 standard; protein; 791 AA.
DE Novel human diagnostic protein #23201.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 80; DB 4; Length 791;
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1384
ID ADS12299 standard; protein; 791 AA.
DE Human therapeutic contig protein - SEQ ID 2536.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.1%; Score 80; DB 8; Length 791;
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1385
ID AAG70752 standard; protein; 881 AA.
DE S cerevisiae apoptosis associated protein YJL070C.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC-) JANSSEN PHARM NV.
Query Match 7.1%; Score 80; DB 4; Length 881;
Best Local Similarity 23.6%; Pred. No. 1.6e+02;
RESULT 1386
ID ABU54861 standard; protein; 10431 AA.
DE Human CA125 amino terminal extension.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.1%; Score 80; DB 6; Length 10431;
Best Local Similarity 22.3%; Pred. No. 4.4e+03;
RESULT 1387
ID ABUS3162 standard; protein; 277 AA.
DE Human testes-derived DKFzpthes3_2a11 homologue #22.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.1%; Score 79.5; DB 4; Length 277;
Best Local Similarity 29.4%; Pred. No. 39;
RESULT 1388
ID ABG01510 standard; protein; 320 AA.
DE Novel human diagnostic protein #1501.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 79.5; DB 4; Length 320;
Best Local Similarity 25.7%; Pred. No. 47;
RESULT 1389
ID ABO62076 standard; protein; 324 AA.
DE Klebsiella pneumoniae polypeptide seqid 8593.
PN US610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.1%; Score 79.5; DB 7; Length 324;
Best Local Similarity 21.3%; Pred. No. 48;
RESULT 1390
ID ADJ76313 standard; protein; 363 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1565.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.1%; Score 79.5; DB 8; Length 363;
Best Local Similarity 25.2%; Pred. No. 56;
RESULT 1391
ID ABG07923 standard; protein; 366 AA.

DE Novel human diagnostic protein #7914.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 79.5; DB 4; Length 366;
Best Local Similarity 25.7%; Pred. No. 56;
RESULT 1392
ID ABUS3155 standard; protein; 692 AA.
DE Human testes-derived DKFzpthes3_2a11 homologue #15.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.1%; Score 79.5; DB 4; Length 692;
Best Local Similarity 29.4%; Pred. No. 1.3e+02;
RESULT 1393
ID ABB63128 standard; protein; 796 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16176.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 7.1%; Score 79.5; DB 4; Length 796;
Best Local Similarity 26.3%; Pred. No. 1.6e+02;
RESULT 1394
ID ABB49326 standard; protein; 860 AA.
DE Listeria monocytogenes protein #2030.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match 7.1%; Score 79.5; DB 5; Length 860;
Best Local Similarity 20.3%; Pred. No. 1.8e+02;
RESULT 1395
ID ABUS2996 standard; protein; 860 AA.
DE Protein encoded by Prokaryotic essential gene #18523.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 79.5; DB 6; Length 860;
Best Local Similarity 20.3%; Pred. No. 1.8e+02;
RESULT 1396
ID ABB71072 standard; protein; 875 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40008.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 7.1%; Score 79.5; DB 4; Length 875;
Best Local Similarity 29.5%; Pred. No. 1.8e+02;
RESULT 1397
ID AAW00634 standard; protein; 985 AA.
DE ILTV glycoprotein g60.
PN WO9508622-A1.
PD 30-MAR-1995.
PA (SYTR-) SYNTRO CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 985;
Best Local Similarity 30.9%; Pred. No. 2.1e+02;
RESULT 1398
ID AAW06786 standard; protein; 985 AA.
DE ILTV glycoprotein g60.
PN WO9629396-A1.
PD 26-SEP-1996.
PA (SYTR-) SYNTRO CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 985;
Best Local Similarity 30.9%; Pred. No. 2.1e+02;
RESULT 1399
ID AAY41092 standard; protein; 1114 AA.
DE Peptide Seq ID No: 34 of WO9945111.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 1114;
Best Local Similarity 20.8%; Pred. No. 2.5e+02;
RESULT 1400
ID AAB15730 standard; protein; 1114 AA.
DE Protein encoded by cDNA generated from RACE3.3 and clone 3.3 sequences.

PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 3; Length 1114;
Best Local Similarity 20.8%; Pred. No. 2.5e+02;
RESULT 1401
ID AAY41086 standard; protein; 1123 AA.
DE Human lectomedin-beta polypeptide.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 1123;
Best Local Similarity 20.8%; Pred. No. 2.5e+02;
RESULT 1402
ID AAB15724 standard; protein; 1123 AA.
DE Human lectomedin-beta.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 3; Length 1123;
Best Local Similarity 20.8%; Pred. No. 2.5e+02;
RESULT 1403
ID AAY41085 standard; protein; 1177 AA.
DE Human lectomedin-lalpa.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 1177;
Best Local Similarity 20.8%; Pred. No. 2.7e+02;
RESULT 1404
ID AAB15723 standard; protein; 1177 AA.
DE Human lectomedin-lalpa.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 3; Length 1177;
Best Local Similarity 20.8%; Pred. No. 2.7e+02;
RESULT 1405
ID ADD46682 standard; protein; 1318 AA.
DE Human Protein CAC19796, SEQ ID NO 12367.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 79.5; DB 7; Length 1318;
Best Local Similarity 20.8%; Pred. No. 3.1e+02;
RESULT 1406
ID ADE55337 standard; protein; 1318 AA.
DE Human Protein CAC19796, SEQ ID NO 1151.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 79.5; DB 7; Length 1318;
Best Local Similarity 20.8%; Pred. No. 3.1e+02;
RESULT 1407
ID AAY41087 standard; protein; 1403 AA.
DE Human lectomedin-igamma polypeptide.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1408
ID AAB15725 standard; protein; 1403 AA.
DE Human lectomedin-igamma cDNA.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 3; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1409
ID ABP81675 standard; protein; 1403 AA.

DE Human latrophilin-2 protein SEQ ID NO:526.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 7.1%; Score 79.5; DB 6; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1410
ID ADD89067 standard; protein; 1403 AA.
DE TAT254.
PN WO2003057160-A2.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 79.5; DB 7; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1411
ID ADN95548 standard; protein; 1403 AA.
DE Human BEC/LEC-related protein sequence SeqID471.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.1%; Score 79.5; DB 7; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1412
ID ADO29115 standard; protein; 1403 AA.
DE Human novel GPCR LEC1, SEQ ID NO:214.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 7.1%; Score 79.5; DB 8; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1413
ID AAU30676 standard; protein; 1425 AA.
DE Novel human secreted protein #1167.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 79.5; DB 4; Length 1425;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1414
ID ADC26275 standard; protein; 1459 AA.
DE Human NOV22 protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.1%; Score 79.5; DB 7; Length 1459;
Best Local Similarity 20.8%; Pred. No. 3.5e+02;
RESULT 1415
ID ABB59325 standard; protein; 1486 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 4767.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.1%; Score 79.5; DB 4; Length 1486;
Best Local Similarity 24.2%; Pred. No. 3.6e+02;
RESULT 1416
ID ADM97582 standard; protein; 1488 AA.
DE Human calcium-independent alpha-latrotoxin receptor.
PN WO2004031235-A1.
PD 15-APR-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 7.1%; Score 79.5; DB 8; Length 1488;
Best Local Similarity 20.8%; Pred. No. 3.6e+02;
RESULT 1417
ID ABP43908 standard; protein; 4315 AA.
DE MUC5B partial gene protein.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 79.5; DB 5; Length 4315;
Best Local Similarity 33.0%; Pred. No. 1.5e+03;
RESULT 1418
ID ADL23265 standard; protein; 5703 AA.

DE Human MUC5B.
 PN WO2004019041-A1.
 PD 04-MAR-2004.
 PA (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.
 PA (PACK/) PACKER N H.
 PA (KARL/) KARLSSON N.
 PA (SCHU/) SCHULZ B L.
 Query Match 7.1%; Score 79.5; DB 8; Length 5703;
 Best Local Similarity 33.0%; Pred. No. 2.2e+03;
 RESULT 1419
 ID AAB11743 standard; protein; 175 AA.
 DE C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:17.
 PN US6071518-A.
 PD 06-JUN-2000.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 7.0%; Score 79; DB 3; Length 175;
 Best Local Similarity 24.2%; Pred. No. 24;
 RESULT 1420
 ID ABJ04056 standard; protein; 175 AA.
 DE C parvum GP900 protein fragment SEQ ID NO: 17.
 PN WO200194631-A1.
 PD 13-DEC-2001.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 7.0%; Score 79; DB 5; Length 175;
 Best Local Similarity 24.2%; Pred. No. 24;
 RESULT 1421
 ID ABB69342 standard; protein; 195 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 34818.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.0%; Score 79; DB 4; Length 195;
 Best Local Similarity 29.1%; Pred. No. 27;
 RESULT 1422
 ID ADO66739 standard; protein; 213 AA.
 DE Novel human protein sequence #1712.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 7.0%; Score 79; DB 8; Length 213;
 Best Local Similarity 25.9%; Pred. No. 31;
 RESULT 1423
 ID AAU93021 standard; protein; 352 AA.
 DE Arabidopsis transcription factor #59.
 PN WO200215675-A1.
 PD 28-FEB-2002.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 PA (PILG/) PILGRIM M.
 PA (CREE/) CREELMAN R.
 PA (DUBE/) DUBELL A J.
 PA (HEAR/) HEARD J.
 PA (JIAN/) JIANG C.
 PA (KEDD/) KEDDIE J.
 PA (ADAM/) ADAM L.
 PA (REUB/) REUBER J L.
 PA (RIEC/) RIECHMANN J L.
 PA (YUGG/) YU G.
 PA (PINE/) PINEDA O.
 Query Match 7.0%; Score 79; DB 5; Length 352;
 Best Local Similarity 27.1%; Pred. No. 60;
 RESULT 1424
 ID ADA15555 standard; protein; 352 AA.
 DE A. thaliana protein, SEQ ID NO:110.
 PN US2003061637-A1.
 PD 27-MAR-2003.
 PA (JIAN/) JIANG C.
 PA (BROU/) BROUN P.
 PA (RIEC/) RIECHMANN J L.
 PA (PINE/) PINEDA O.
 PA (ZHAN/) ZHANG J.
 PA (YUGG/) YU G.
 PA (PILG/) PILGRIM M.
 PA (KEDD/) KEDDIE J.
 PA (HEAR/) HEARD J.
 PA (FROM/) FROMM M E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMAHA R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 Query Match 7.0%; Score 79; DB 8; Length 352;
 Best Local Similarity 27.1%; Pred. No. 60;
 RESULT 1425
 ID ADD30080 standard; protein; 352 AA.
 DE Plant yield-related protein from clone G671.
 PN WO2003013227-A2.
 PD 20-FEB-2003.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Query Match 7.0%; Score 79; DB 7; Length 352;
 Best Local Similarity 27.1%; Pred. No. 60;
 RESULT 1426
 ID ADE31453 standard; protein; 352 AA.
 DE Plant yield related protein from clone G671.
 PN WO2003013228-A2.
 PD 20-FEB-2003.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Query Match 7.0%; Score 79; DB 7; Length 352;
 Best Local Similarity 27.1%; Pred. No. 60;
 RESULT 1427
 ID ADI43589 standard; protein; 352 AA.
 DE Plant transcription factor #667.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAR/) HAAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 Query Match 7.0%; Score 79; DB 8; Length 352;
 Best Local Similarity 27.1%; Pred. No. 60;
 RESULT 1428
 ID ADO02037 standard; protein; 352 AA.
 DE Thalecress transcription factor protein #225.
 PN US2004045049-A1.
 PD 04-MAR-2004.
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROMM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMAHA R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 Query Match 7.0%; Score 79; DB 8; Length 352;
 Best Local Similarity 27.1%; Pred. No. 60;
 RESULT 1429
 ID ABU07483 standard; protein; 410 AA.

DE Protein differentially regulated in prostate cancer #86.
 PN WO200281638-A2.
 PD 17-OCT-2002.
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 Query Match 7.0%; Score 79; DB 6; Length 410;
 Best Local Similarity 20.5%; Pred. No. 73;
 RESULT 1430
 ID ADE58847 standard; protein; 410 AA.
 DE Human Protein P13473, SEQ ID NO 4735.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.0%; Score 79; DB 7; Length 410;
 Best Local Similarity 20.5%; Pred. No. 73;
 RESULT 1431
 ID ADL14997 standard; protein; 410 AA.
 DE Human lysosome associated protein 2 protein for cancer treatment.
 PN WO2003068268-A2.
 PD 21-AUG-2003.
 PA (BIOI-) BIOINVENT INT AB.
 Query Match 7.0%; Score 79; DB 7; Length 410;
 Best Local Similarity 20.5%; Pred. No. 73;
 RESULT 1432
 ID ADN95768 standard; protein; 410 AA.
 DE Human BSC/LEC-related protein sequence SeqID692.
 PN WO2003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 7.0%; Score 79; DB 7; Length 410;
 Best Local Similarity 20.5%; Pred. No. 73;
 RESULT 1433
 ID ADP23470 standard; protein; 410 AA.
 DE Human lysosomal associated membrane protein LAMP #2.
 PN WO2004048537-A2.
 PD 10-JUN-2004.
 PA (EXEL-) EXELIXIS INC.
 Query Match 7.0%; Score 79; DB 8; Length 410;
 Best Local Similarity 20.5%; Pred. No. 73;
 RESULT 1434
 ID ADP23470 standard; protein; 410 AA.
 DE PRO polypeptide SEQ ID NO:648.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.0%; Score 79; DB 8; Length 410;
 Best Local Similarity 20.5%; Pred. No. 73;
 RESULT 1435
 ID AAO29892 standard; protein; 411 AA.
 DE Human organelle-associated protein (ORGA)-5.
 PN WO2003044171-A2.
 PD 30-MAY-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 7.0%; Score 79; DB 6; Length 411;
 Best Local Similarity 20.5%; Pred. No. 74;
 RESULT 1436
 ID ADK68630 standard; protein; 599 AA.
 DE HSP65-MUC1 antigen CTL epitope related protein.
 PN CN1368384-A.
 PD 11-SEP-2002.
 PA (DIWE-) DIWEIHUAYU BIO TECHNOLOGY CO LTD BEIJING.
 Query Match 7.0%; Score 79; DB 7; Length 599;
 Best Local Similarity 19.0%; Pred. No. 1.2e+02;
 RESULT 1437
 ID AAR88466 standard; protein; 629 AA.
 DE Drosophila scavenger receptor class CI.
 PN WO9600288-A2.
 PD 04-JAN-1996.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 7.0%; Score 79; DB 2; Length 629;
 Best Local Similarity 22.2%; Pred. No. 1.3e+02;
 RESULT 1438

ID ABB59507 standard; protein; 629 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 5313.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.0%; Score 79; DB 4; Length 629;
 Best Local Similarity 22.2%; Pred. No. 1.3e+02;
 RESULT 1439
 ID ABB67438 standard; protein; 629 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 29106.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.0%; Score 79; DB 4; Length 629;
 Best Local Similarity 29.2%; Pred. No. 1.3e+02;
 RESULT 1440
 ID ABG33057 standard; protein; 629 AA.
 DE Fruit fly scavenger receptor type CI (dsr-CI).
 PN US6429289-B1.
 PD 06-AUG-2002.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 7.0%; Score 79; DB 5; Length 629;
 Best Local Similarity 22.2%; Pred. No. 1.3e+02;
 RESULT 1441
 ID AAE21524 standard; protein; 629 AA.
 DE Drosophila melanogaster scavenger receptor class CI (dsr-CI).
 PN US6350859-B1.
 PD 26-FEB-2002.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 7.0%; Score 79; DB 5; Length 629;
 Best Local Similarity 22.2%; Pred. No. 1.3e+02;
 RESULT 1442
 ID ADQ97694 standard; protein; 786 AA.
 DE Mouse cancer associated sequence MP10-029, SEQ ID 671.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 7.0%; Score 79; DB 8; Length 786;
 Best Local Similarity 20.6%; Pred. No. 1.7e+02;
 RESULT 1443
 ID ABB91667 standard; protein; 980 AA.
 DE Herbicidially active polypeptide SEQ ID NO 878.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 7.0%; Score 79; DB 5; Length 980;
 Best Local Similarity 21.0%; Pred. No. 2.3e+02;
 RESULT 1444
 ID ADE58456 standard; protein; 1031 AA.
 DE Rat Protein AAK52670, SEQ ID NO 4331.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.0%; Score 79; DB 7; Length 1031;
 Best Local Similarity 22.0%; Pred. No. 2.5e+02;
 RESULT 1445
 ID ADE58468 standard; protein; 1031 AA.
 DE Rat Protein AAK52670, SEQ ID NO 4343.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.0%; Score 79; DB 7; Length 1031;
 Best Local Similarity 22.0%; Pred. No. 2.5e+02;
 RESULT 1446
 ID ADE58460 standard; protein; 1031 AA.
 DE Rat Protein AAK52670, SEQ ID NO 4335.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.0%; Score 79; DB 7; Length 1031;
 Best Local Similarity 22.0%; Pred. No. 2.5e+02;
 RESULT 1447
 ID ADE58460 standard; protein; 1031 AA.
 DE Rat Protein AAK52670, SEQ ID NO 4335.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.0%; Score 79; DB 7; Length 1031;
 Best Local Similarity 22.0%; Pred. No. 2.5e+02;
 RESULT 1448

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Best Local Similarity 22.0%; Pred. No. 2.5e+02;
RESULT 1447
ID ADE58464 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4339.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 7.0%; Score 79; DB 7; Length 1031;
Pred. No. 2.5e+02;
RESULT 1448
ID ADE58472 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4347.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 7.0%; Score 79; DB 7; Length 1031;
Pred. No. 2.5e+02;
RESULT 1449
ID ADE58476 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4351.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 7.0%; Score 79; DB 7; Length 1031;
Pred. No. 2.5e+02;
RESULT 1450
ID ABB64889 standard; protein; 2616 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21459.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NV.
Query Match
Best Local Similarity 7.0%; Score 79; DB 4; Length 2616;
Pred. No. 8.7e+02;
RESULT 1451
ID AAB11740 standard; protein; 130 AA.
DE C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:14.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC ) UNIV CALIFORNIA.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 3; Length 130;
Pred. No. 18;
RESULT 1452
ID ABJ04053 standard; protein; 130 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 14.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC ) UNIV CALIFORNIA.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 5; Length 130;
Pred. No. 18;
RESULT 1453
ID ADQ30914 standard; protein; 252 AA.
DE Avian pneumovirus (Colorado) protein SeqID36.
PN WO2004050843-A2.
PD 17-JUN-2004.
PA (UYMA-) UNIV MARYLAND BALTIMORE.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 8; Length 252;
Pred. No. 43;
RESULT 1454
ID AAY75301 standard; protein; 286 AA.
DE Neisseria gonorrhoeae ORF 645 protein sequence SEQ ID NO:2076.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 3; Length 286;
Pred. No. 51;
RESULT 1455
ID ADO29463 standard; protein; 410 AA.
DE Mouse GPCR GPCR5B, SEQ ID NO:565.
PN WO2004040000-A2.

PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 8; Length 410;
Pred. No. 82;
RESULT 1456
ID AAW25156 standard; protein; 562 AA.
DE HIV-1 Rev/HTLV-1 Rex activation domain binding protein.
PN WO9706257-A1.
PD 20-FEB-1997.
PA (UYDU-) UNIV DUKE.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 2; Length 562;
Pred. No. 1.2e+02;
RESULT 1457
ID AAW83285 standard; protein; 562 AA.
DE Human h-RAB.
PN WO9846744-A1.
PD 22-OCT-1998.
PA (EUON-) IST EURO DI ONCOLOGIA SRL.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 2; Length 562;
Pred. No. 1.2e+02;
RESULT 1458
ID ADM05676 standard; protein; 569 AA.
DE Human protein of the invention SEQ ID NO:4361.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 7; Length 569;
Pred. No. 1.3e+02;
RESULT 1459
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 3; Length 590;
Pred. No. 1.3e+02;
RESULT 1460
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 6; Length 590;
Pred. No. 1.3e+02;
RESULT 1461
ID ADA23287 standard; protein; 653 AA.
DE Human SECX polypeptide, SEC5 #1.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 6; Length 653;
Pred. No. 1.5e+02;
RESULT 1462
ID AAB23033 standard; protein; 694 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-1.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 3; Length 694;
Pred. No. 1.7e+02;
RESULT 1463
ID AAB94736 standard; protein; 858 AA.
DE Human protein sequence SEQ ID NO:15772.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 4; Length 858;
Pred. No. 2.2e+02;
RESULT 1464
ID AAU10540 standard; protein; 1478 AA.
DE Rat CIRL-2 variant BC (YSG2) polypeptide.
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PN WO200175440-A2.
PD 11-OCT-2001.
PA (WELF-) WELFIDE CORP.
Query Match 7.0%; Score 78.5; DB 5; Length 1478;
Best Local Similarity 19.6%; Pred. No. 4.5e+02;
RESULT 1465
ID ADD46680 standard; protein; 1478 AA.
DE Rat Protein AAC62654, SEQ ID NO 12365.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1478;
Best Local Similarity 19.6%; Pred. No. 4.5e+02;
RESULT 1466
ID ADE55162 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 967.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1488;
Best Local Similarity 19.6%; Pred. No. 4.6e+02;
RESULT 1467
ID ADE55174 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 979.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1488;
Best Local Similarity 19.6%; Pred. No. 4.6e+02;
RESULT 1468
ID ADE55170 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 975.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1488;
Best Local Similarity 19.6%; Pred. No. 4.6e+02;
RESULT 1469
ID ADE55166 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 971.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1488;
Best Local Similarity 19.6%; Pred. No. 4.6e+02;
RESULT 1470
ID ABB63883 standard; protein; 2040 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18441.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 7.0%; Score 78.5; DB 4; Length 2040;
Best Local Similarity 22.0%; Pred. No. 7e+02;
RESULT 1471
ID ABR63235 standard; protein; 2055 AA.
DE Glucanase sequence from strain KG15.
PN WO2003008618-A2.
PD 30-JAN-2003.
PA (NEDE ) NEDERLANDSE ORG TOEGEPAST.
Query Match 7.0%; Score 78.5; DB 6; Length 2055;
Best Local Similarity 26.2%; Pred. No. 7e+02;
RESULT 1472
ID ABM70225 standard; protein; 2466 AA.
DE Photorhabdus luminescens protein sequence #3322.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match 6.9%; Score 78; DB 8; Length 287;
Best Local Similarity 24.2%; Pred. No. 57;
RESULT 1479
ID ABU05689 standard; protein; 293 AA.
DE M. tuberculosis and M. leprae marker protein #340.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP ) INST PASTEUR.
Query Match 6.9%; Score 78; DB 2; Length 116;
Best Local Similarity 23.3%; Pred. No. 17;
RESULT 1474
ID AAW74523 standard; protein; 252 AA.
DE Cloned duplicate of human aggrecan G1-B domain.
PN EP861903-A1.
PD 02-SEP-1998.
PA (LANS/) LANSING M.
PA (UHLE/) UHLENKUEKEN J.
PA (SCHM/) SCHMIDT G.
Query Match 6.9%; Score 78; DB 2; Length 116;
Best Local Similarity 23.3%; Pred. No. 17;
RESULT 1475
ID AAY00274 standard; protein; 268 AA.
DE Human secreted protein encoded by gene 17.
PN WO9906423-A1.
PD 11-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 78; DB 2; Length 268;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1476
ID ADD90303 standard; protein; 268 AA.
DE Novel human secreted protein seq id 118.
PN US2003199683-A1.
PD 23-OCT-2003.
PA (RUBE/) RUBEN S M.
PA (FENG/) FENG P.
PA (LAFU/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (KYAW/) KYAW H.
PA (LIYU/) LI Y.
PA (ZENG/) ZENG Z.
PA (CART/) CARTER K C.
PA (ENDR/) ENDRESS G A.
PA (WEIY/) WEI Y.
PA (FANP/) FAN P.
PA (ROSE/) ROSEN C A.
Query Match 6.9%; Score 78; DB 7; Length 268;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1477
ID ADG90122 standard; protein; 268 AA.
DE Human protein from secreted protein gene 17.
PN US2003166541-A1.
PD 04-SEP-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 78; DB 7; Length 268;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1478
ID ADP07513 standard; protein; 287 AA.
DE Partial cell-recognition and cell-damage protein seqid 4.
PN JP2004129608-A.
PD 30-APR-2004.
PA (UYKY-) UNIV KYUSHU.
PA (FUKU-) FUKUOKA KEN.
Query Match 6.9%; Score 78; DB 8; Length 287;
Best Local Similarity 24.2%; Pred. No. 57;
RESULT 1479
ID ABU05689 standard; protein; 293 AA.
DE M. tuberculosis and M. leprae marker protein #340.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP ) INST PASTEUR.

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Query Match 6.9%; Score 78; DB 5; Length 293;
Best Local Similarity 31.3%; Pred. No. 59;
RESULT 1480
ID ADP07511 standard; protein; 338 AA.
DE B. thuringiensis cell-recognition and cell-damage protein seqid 2.
PN JP2004129608-A.
PD 30-APR-2004.
PA (UYKY-) UNIV KYUSHU.
PA (FUKU-) FUKUOKA KEN.
Query Match 6.9%; Score 78; DB 8; Length 338;
Best Local Similarity 24.2%; Pred. No. 71;
RESULT 1481
ID ADC23743 standard; protein; 400 AA.
DE B. juncea chitinase (BjCHI1).
PN US2003097682-A1.
PD 22-MAY-2003.
PA (CHYE/) CHYE M L.
PA (ZHAO/) ZHAO K.
Query Match 6.9%; Score 78; DB 7; Length 400;
Best Local Similarity 25.3%; Pred. No. 89;
RESULT 1482
ID ADN46313 standard; protein; 510 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID191.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.9%; Score 78; DB 8; Length 510;
Best Local Similarity 25.5%; Pred. No. 1.2e+02;
RESULT 1483
ID ABG66756 standard; protein; 1296 AA.
DE Human novel polypeptide #91.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 78; DB 5; Length 1296;
Best Local Similarity 28.8%; Pred. No. 4.3e+02;
RESULT 1484
ID ABG66702 standard; protein; 1296 AA.
DE Human novel polypeptide #37.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 78; DB 5; Length 1296;
Best Local Similarity 28.8%; Pred. No. 4.3e+02;
RESULT 1485
ID ADI17257 standard; protein; 1955 AA.
DE NOVX protein homologue SeqID 733.
PN WO200268643-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 78; DB 5; Length 1955;
Best Local Similarity 22.9%; Pred. No. 7.4e+02;
RESULT 1486
ID ABG60750 standard; protein; 2162 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9042.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.9%; Score 78; DB 4; Length 2162;
Best Local Similarity 21.3%; Pred. No. 8.4e+02;
RESULT 1487
ID ADO28932 standard; protein; 2590 AA.
DE Mouse novel GPCR PGRI7, SEQ ID NO:31.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.9%; Score 78; DB 8; Length 2590;
Best Local Similarity 21.4%; Pred. No. 1.1e+03;
RESULT 1488
ID ABP76679 standard; protein; 1938 AA.
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 3.
PN WO200268436-A1.
PD 06-SEP-2002.

PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 6.9%; Score 78; DB 6; Length 19938;
Best Local Similarity 27.2%; Pred. No. 1.6e+04;
RESULT 1489
ID AAM50239 standard; protein; 497 AA.
DE Rice tyrosine decarboxylase.
PN US6297055-B1.
PD 02-OCT-2001.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match 6.9%; Score 77.5; DB 4; Length 497;
Best Local Similarity 23.6%; Pred. No. 1.3e+02;
RESULT 1490
ID AAU76421 standard; protein; 497 AA.
DE Rice tyrosine decarboxylase clone r186.pk0031.bs.
PN US2002009801-A1.
PD 24-JAN-2002.
PA (FALC/) FALCO S C.
PA (FAMC/) FAMODU O O.
PA (OROZ/) OROZCO E R.
Query Match 6.9%; Score 77.5; DB 5; Length 497;
Best Local Similarity 23.6%; Pred. No. 1.3e+02;
RESULT 1491
ID AAW12713 standard; protein; 562 AA.
DE hRIP, a protein critical for HIV replication.
PN WO9701648-A1.
PD 16-JAN-1997.
PA (UYNA-) UNIV MASSACHUSETTS MEDICAL CENT.
Query Match 6.9%; Score 77.5; DB 2; Length 562;
Best Local Similarity 25.0%; Pred. No. 1.6e+02;
RESULT 1492
ID ADO00991 standard; protein; 562 AA.
DE Human homologue of Fruit fly AD-related protein CG3365.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIPE-) LIPE SCI DEV CORP.
Query Match 6.9%; Score 77.5; DB 8; Length 562;
Best Local Similarity 25.0%; Pred. No. 1.6e+02;
RESULT 1493
ID ADP55222 standard; protein; 562 AA.
DE Human PRO protein sequence SEQ ID NO:1198.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.9%; Score 77.5; DB 8; Length 562;
Best Local Similarity 25.0%; Pred. No. 1.6e+02;
RESULT 1494
ID ABB63033 standard; protein; 583 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15891.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.9%; Score 77.5; DB 4; Length 583;
Best Local Similarity 23.3%; Pred. No. 1.6e+02;
RESULT 1495
ID AAU38948 standard; protein; 583 AA.
DE Drosophila G-protein coupled receptor, GCPR #26.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.9%; Score 77.5; DB 4; Length 583;
Best Local Similarity 23.3%; Pred. No. 1.6e+02;
RESULT 1496
ID ADC35826 standard; protein; 583 AA.
DE Drosophila G-protein coupled receptor seq id 28.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match 6.9%; Score 77.5; DB 7; Length 583;
Best Local Similarity 23.3%; Pred. No. 1.6e+02;
RESULT 1497
ID ADM47277 standard; protein; 620 AA.
DE Protocadherin like NOVX 26a protein.
PN WO2003083039-A2.

PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 77.5; DB 7; Length 620;
Best Local Similarity 22.1%; Pred. No. 1.8e+02;
RESULT 1498
ID AAU33234 standard; protein; 644 AA.
DE Novel human secreted protein #3725.
PN WO20017949-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 77.5; DB 4; Length 644;
Best Local Similarity 25.0%; Pred. No. 1.9e+02;
RESULT 1499
ID ABB60849 standard; protein; 826 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9339.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 6.9%; Score 77.5; DB 4; Length 826;
Best Local Similarity 21.1%; Pred. No. 2.6e+02;
RESULT 1500
ID ADD01209 standard; protein; 874 AA.
DE Human nucleic acid-associated protein NAAP-47 SEQ ID NO:47.
PN WO2003054219-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.9%; Score 77.5; DB 7; Length 874;
Best Local Similarity 26.4%; Pred. No. 2.8e+02;

GenCore version 5.1.1.6
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 OM protein - protein search, using sw model
 Run on: October 5, 2005, 17:19:28 ; Search time 137.744 Seconds
 (without alignments)
 1197.068 Million cell updates/sec
 Title: US-10-063-510-6
 Perfect score: 1657
 Sequence: 1 MARCSFVLLTSTWTRLL.....NPESKSPSKTTRVCLEAEV 322
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 1612378 seqs, 512079187 residues
 Total number of hits satisfying chosen parameters: 1612378
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries
 Database : Uniprot_03: +
 1: uniprot_sprot: +
 2: uniprot_trembl: +
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	ID		
1	1657	100.0	322	2	Q9UNF4	homo sapien
2	1643	99.2	322	2	Q8TC18	homo sapien
3	1638	98.9	322	2	Q9Y5Y7	homo sapien
4	1174	70.9	322	2	Q6UC88	bos taurus
5	1103	66.6	318	2	Q8BHC0	bos taurus
6	1095	66.1	318	2	Q9NEE4	mus musculus
7	726.5	43.8	201	2	Q7YS22	mus musculus
8	241	14.5	441	2	Q6QM56	scrofa
9	233.5	14.1	362	1	CD44_CRIGR	cricketulus
10	229.5	13.9	437	2	Q6P8A2	cricketulus
11	227	13.7	364	2	Q70509	cricketulus
12	222.5	13.4	362	1	CD44_FAPHA	cricketulus
13	222	13.4	503	1	CD44_RAT	cricketulus
14	219.5	13.2	780	2	Q08779	cricketulus
15	219	13.2	265	2	Q98SR5	cricketulus
16	217.5	13.1	398	2	Q902L8	cricketulus
17	212.5	12.8	431	1	CD44_MESAU	cricketulus
18	210	12.7	778	1	CD44_MOUSE	cricketulus
19	208.5	12.6	366	1	CD44_BOVIN	cricketulus
20	206.5	12.5	168	2	Q902L6	cricketulus
21	204	12.3	361	2	Q86T72	cricketulus
22	203.5	12.3	364	2	Q97569	cricketulus
23	203.5	12.3	396	2	Q9W6S4	cricketulus
24	203	12.3	742	2	Q9UJ36	cricketulus
25	202.5	12.2	351	1	CD44_CANFA	cricketulus
26	202	12.2	361	2	Q8N694	cricketulus
27	202	12.2	742	1	CD44_HUMAN	cricketulus
28	201	12.1	580	2	Q80X37	cricketulus
29	199.5	12.0	493	2	Q86Z27	cricketulus
30	199	12.0	338	2	Q9H5A4	cricketulus
31	197	11.9	719	2	Q9H5A5	cricketulus

32	196	11.8	294	2	Q92493	homo sapien
33	191.5	11.6	676	2	Q9H5A7	homo sapien
34	191	11.5	271	2	Q9H5A3	homo sapien
35	191	11.5	470	2	Q9H5A6	homo sapien
36	186	11.2	359	1	CD44_HORSE	equus caball
37	150	9.1	537	1	PGCA_FIG	scrofa
38	149.5	9.0	2109	2	P97987	gallus gall
39	148.5	9.0	2109	2	PGCA_CHICK	gallus gall
40	145.5	8.8	494	2	Q9BGH3	scrofa
41	145.5	8.8	3562	1	PGCV_CHICK	gallus gall
42	145	8.8	277	1	TS66_HUMAN	homo sapien
43	144	8.7	275	1	TS66_MOUSE	mus musculus
44	143	8.6	2149	2	Q6XL68	bos taurus
45	143	8.6	2364	1	PGCA_BOVIN	bos taurus
46	143	8.6	2365	2	Q6XL67	bos taurus
47	140.5	8.5	2571	1	SNB1_MOUSE	mus musculus
48	139.5	8.4	2333	1	PGCA_CANFA	canis famil
49	137	8.3	276	1	TS66_RABIT	oryctolagus
50	136	8.2	2559	1	SNB2_MOUSE	mus musculus
51	133	8.0	514	2	Q62913	rattus norv
52	133	8.0	1431	1	SNB2_RAT	rattus norv
53	133	8.0	2551	1	SNB2_HUMAN	homo sapien
54	132.5	8.0	721	2	Q6PID9	homo sapien
55	131.5	7.9	2124	1	PGCA_RAT	rattus norv
56	131	7.9	911	1	PGCB_HUMAN	homo sapien
57	131	7.9	2132	1	PGCA_MOUSE	mus musculus
58	130.5	7.9	883	1	PGCB_MOUSE	mus musculus
59	130.5	7.9	883	1	PGCB_RAT	rattus norv
60	130.5	7.9	883	2	Q80WT7	mus musculus
61	130.5	7.9	1152	2	Q90WM2	scrofa
62	130.5	7.9	2415	1	PGCA_HUMAN	homo sapien
63	130.5	7.9	2570	1	SNB1_HUMAN	homo sapien
64	128.5	7.8	912	1	PGCB_BOVIN	bos taurus
65	126	7.6	3358	1	PGCV_MOUSE	mus musculus
66	122	7.4	394	1	PGCA_RABIT	oryctolagus
67	121.5	7.3	360	1	HPL3_HUMAN	homo sapien
68	121	7.3	516	2	Q8IWX2	homo sapien
69	120.5	7.3	1570	2	Q75Z13	brachydanio
70	119.5	7.2	411	2	Q702X4	human herpe
71	119	7.2	359	2	Q72X17	scrofa
72	118.5	7.2	3396	1	PGCV_HUMAN	homo sapien
73	118	7.1	341	1	HPL2_MOUSE	mus musculus
74	117.5	7.1	397	2	Q702X3	human herpe
75	117	7.1	340	1	HPL2_HUMAN	homo sapien
76	116	7.0	368	2	Q8BS97	mus musculus
77	116	7.0	2738	1	PGCV_RAT	rattus norv
78	115	6.9	370	2	Q7M2W7	scrofa
79	115	6.9	394	2	Q6DCI6	scrofa
80	115	6.9	3381	1	PGCV_BOVIN	bos taurus
81	114.5	6.9	1257	1	PGCN_RAT	rattus norv
82	114	6.9	610	2	Q9N3C0	caenorhabdi
83	113.5	6.8	1290	2	Q9W6E1	gallus gall
84	113	6.8	341	1	HPL2_RAT	rattus norv
85	113	6.8	892	1	LDL2_XENLA	scrofa
86	112.5	6.8	417	1	PGCB_FELCA	felis silve
87	112	6.8	210	2	Q8C9U7	mus musculus
88	112	6.8	390	1	VGL1_HHV11	human herpe
89	112	6.8	390	2	Q702X7	human herpe
90	111.5	6.7	402	1	ODP2_MYCPN	mycoplasma
91	111	6.7	354	2	Q86W61	homo sapien
92	110	6.6	363	2	Q6NV41	brachydanio
93	109	6.6	816	2	Q70474	rattus norv
94	109	6.6	1321	1	PGCN_HUMAN	homo sapien
95	108.5	6.5	397	2	Q702X6	human herpe
96	108	6.5	354	1	HPL1_HUMAN	homo sapien
97	108	6.5	359	1	HPL3_MOUSE	mus musculus
98	108	6.5	624	2	Q19780	caenorhabdi
99	107.5	6.5	665	2	Q7Q4E5	anopheles g
100	107.5	6.5	739	2	O02360	caenorhabdi
101	107	6.5	354	1	HPL1_RAT	rattus norv
102	107	6.5	355	1	HPL1_CHICK	gallus gall
103	107	6.5	356	1	HPL1_MOUSE	mus musculus
104	107	6.5	862	2	Q9UF98	homo sapien

105	107	6.5	1268	1	PGCN_MOUSE	P55066	mus musculus	178	97.5	5.9	1403	2	Q81MM4	Q81mm4	drosophila
106	107	6.5	1268	2	Q6P1E3	Q6pie3	mus musculus	179	97	5.9	316	2	Q702Y6	Q9u9j0	toxocara ca
107	107	6.5	1795	2	Q76894	Q76894	drosophila	180	97	5.9	404	2	Q702Y6	Q702y6	human herpe
108	105.5	6.4	374	2	Q92209	Q92209	cricetulus	181	97	5.9	604	2	Q6E9K8	Q6e9k8	listeria mo
109	105.5	6.4	573	2	Q8CUD9	Q8cjd9	rattus norv	182	97	5.9	604	2	Q6E9X2	Q6e9x2	listeria mo
110	105.5	6.4	830	2	Q6CAY0	Q6cay0	yarrowia li	183	97	5.9	604	2	Q6EAI6	Q6eai6	listeria mo
111	105	6.3	354	1	HPL1_BOVIN	P55252	bos taurus	184	96.5	5.8	303	2	Q8R3W0	Q8r3w0	mus musculu
112	105	6.3	463	2	Q7RNE3	Q7rne3	plasmodium	185	96.5	5.8	385	2	Q9N666	Q9n666	drosophila
113	105	6.3	612	2	Q6CD44	Q6cd44	yarrowia li	186	96.5	5.8	385	2	Q9NHU6	Q9nhu6	drosophila
114	104.5	6.3	862	1	PGCV_MACNE	Q28858	macaca neme	187	96.5	5.8	397	2	Q702Y5	Q702y5	human herpe
115	104	6.3	139	2	Q95370	Q95370	homo sapien	188	96.5	5.8	465	1	YHU6_YEAST	P38845	saccharomyc
116	104	6.3	354	1	HPL1_HORSE	Q28381	equus cabal	189	96.5	5.8	604	2	Q8GNS1	Q8gns1	listeria mo
117	104	6.3	354	1	HPL1_PIG	P10859	sus scrofa	190	96.5	5.8	731	1	NOG2_CRYBA	Q6t9j8	cryptococcu
118	104	6.3	627	2	Q8MP19	Q8mpl9	dictyosteli	191	96.5	5.8	961	2	Q92223	Q92223	emericella
119	104	6.3	1716	2	Q917Q8	Q917q8	drosophila	192	96.5	5.8	1031	2	Q925N8	Q925n8	mus musculu
120	104	6.3	1912	2	Q9V859	Q9v859	drosophila	193	96.5	5.8	1031	2	Q9D071	Q9d071	m mus musculu
121	103.5	6.2	288	2	Q6QPC9	Q6qpc9	simian aden	194	96	5.8	429	2	Q76430	Q76430	caenorhabdi
122	103.5	6.2	952	2	Q86AH0	Q86ah0	dictyosteli	195	96	5.8	449	2	Q71UN8	Q71un8	caenorhabdi
123	103.5	6.2	1254	2	Q94185	Q94185	caenorhabdi	196	96	5.8	481	2	Q9XUF4	Q9xuf4	caenorhabdi
124	103	6.2	80	2	Q86UZ1	Q86uz1	homo sapien	197	96	5.8	555	2	Q95X13	Q95x13	caenorhabdi
125	102.5	6.2	182	2	Q810D8	Q810d8	drosophila	198	96	5.8	556	2	Q6DEK7	Q6dek7	brachydantio
126	102.5	6.2	183	2	Q9VT37	Q9vt37	drosophila	199	96	5.8	604	2	Q6E9R2	Q6e9r2	listeria mo
127	102.5	6.2	497	2	Q8QVC4	Q8qvc4	eyach virus	200	96	5.8	604	2	Q6E9R8	Q6e9r8	listeria mo
128	102.5	6.2	553	2	Q8F932	Q8f932	leptospira	201	96	5.8	604	2	Q6E9R8	Q6e9r8	listeria mo
129	102.5	6.2	557	2	Q72VI3	Q72vi3	leptospira	202	96	5.8	604	2	Q6E9R8	Q6e9r8	listeria mo
130	102.5	6.2	699	2	Q8QVE9	Q8qve9	eyach virus	203	96	5.8	625	2	Q6V6E1	Q6v6e1	drosophila
131	102	6.2	391	2	Q753G3	Q753g3	ashbya goss	204	96	5.8	1088	1	NCAL_XENLA	P16170	xenopus lae
132	102	6.2	404	2	Q702X0	Q702x0	human herpe	205	95.5	5.8	376	1	MID2_YEAST	P36027	saccharomyc
133	102	6.2	404	2	Q702Y3	Q702y3	human herpe	206	95.5	5.8	385	2	Q9NHU5	Q9nhu5	drosophila
134	101.5	6.1	380	2	Q02343	Q02343	caenorhabdi	207	95.5	5.8	385	2	Q9NHU7	Q9nhu7	drosophila
135	101.5	6.1	768	2	Q60279	Q60279	homo sapien	208	95.5	5.8	1259	2	Q869X4	Q869x4	dictyosteli
136	101.5	6.1	1853	2	Q7KT96	Q7kt96	drosophila	209	95.5	5.8	5374	2	Q99ND0	Q99nd0	mus musculu
137	101.5	6.1	1893	2	Q9NKC9	Q9nkc9	drosophila	210	95	5.7	273	2	Q61002	Q61002	mus musculu
138	101	6.1	700	2	Q8TG00	Q8tg00	aspergillus	211	95	5.7	390	2	Q702W9	Q702w9	human herpe
139	101	6.1	708	2	Q18175	Q18175	caenorhabdi	212	95	5.7	424	2	Q9FGW0	Q9fgw0	arabidopsis
140	101	6.1	2535	2	Q755B8	Q755b8	ashbya goss	213	95	5.7	538	2	Q69379	Q69379	listeria mo
141	100.5	6.1	402	1	HPL4_HUMAN	Q86uw8	homo sapien	214	95	5.7	604	2	Q6EAD8	Q6ead8	listeria mo
142	100.5	6.1	411	2	Q702X9	Q702x9	human herpe	215	95	5.7	604	2	Q9RQ13	Q9rq13	listeria mo
143	100.5	6.1	1121	2	Q72884	Q72884	candida alb	216	95	5.7	639	2	Q8E904	Q8e904	listeria mo
144	100	6.0	403	2	Q702W8	Q702w8	human herpe	217	95	5.7	639	2	Q6E982	Q6e982	listeria mo
145	100	6.0	404	2	Q702W6	Q702w6	human herpe	218	95	5.7	639	2	Q6E9Q6	Q6e9q6	listeria mo
146	100	6.0	404	2	Q702Y0	Q702y0	human herpe	219	95	5.7	639	2	Q8GNR2	Q8gnr2	listeria mo
147	100	6.0	486	2	Q8FRY2	Q8fry2	corynebacte	220	95	5.7	753	2	Q6PPF4	Q6ppf4	brachydantio
148	100	6.0	1240	1	YQJ3_CAEEL	Q09550	caenorhabdi	221	95	5.7	1203	2	Q6C028	Q6c028	yarrowia li
149	99.5	6.0	478	2	Q7YX15	Q7yx15	caenorhabdi	222	94.5	5.7	345	2	Q691Y8	Q691y8	anolis sagr
150	99.5	6.0	1092	1	NC42_XENLA	P36335	xenopus lae	223	94.5	5.7	383	2	Q702X5	Q702x5	human herpe
151	99	6.0	178	2	Q8FQU3	Q8fq3	corynebacte	224	94.5	5.7	383	2	Q702Y4	Q702y4	human herpe
152	99	6.0	410	1	GC5B_MOUSE	Q923z0	mus musculu	225	94.5	5.7	395	2	Q702Z0	Q702z0	human herpe
153	99	6.0	604	2	Q689B8	Q6e9b8	listeria mo	226	94.5	5.7	519	2	Q7YTR7	Q7ytr7	caenorhabdi
154	99	6.0	896	2	Q20253	Q20253	caenorhabdi	227	94.5	5.7	1066	2	Q76NW3	Q76nw3	dictyosteli
155	99	6.0	1100	2	Q8CCT8	Q8cct8	mus musculu	228	94.5	5.7	1079	2	Q9N4S7	Q9n4s7	caenorhabdi
156	99	6.0	5376	1	ZAN_MOUSE	Q88799	mus musculu	229	94.5	5.7	1390	2	Q17602	Q17602	caenorhabdi
157	98.5	5.9	204	2	Q9N528	Q9n528	caenorhabdi	230	94.5	5.7	1942	2	Q8GIZ7	Q8giz7	lactobacill
158	98.5	5.9	346	2	Q7S973	Q7s973	neurospora	231	94.5	5.7	3370	2	Q8I1N9	Q8i1n9	plasmodiun
159	98.5	5.9	397	2	Q702W7	Q702w7	human herpe	232	94	5.7	639	2	Q6E8W8	Q6e8w8	listeria mo
160	98.5	5.9	397	2	Q702X1	Q702x1	human herpe	233	94	5.7	639	2	Q6E922	Q6e922	listeria mo
161	98.5	5.9	425	2	Q702W3	Q702w3	human herpe	234	94	5.7	639	2	Q6E9G6	Q6e9g6	listeria mo
162	98.5	5.9	578	2	Q632X6	Q632x6	mus musculu	235	94	5.7	639	2	Q6EA26	Q6ea26	listeria mo
163	98.5	5.9	1126	2	Q9VGK5	Q9vgk5	drosophila	236	94	5.7	639	2	Q6EA68	Q6ea68	listeria mo
164	98.5	5.9	1203	2	Q6ZQ56	Q6zq56	mus musculu	237	94	5.7	639	2	Q6EAF0	Q6eaf0	listeria mo
165	98.5	5.9	1378	1	YS89_CAEEL	Q09624	caenorhabdi	238	94	5.7	639	2	Q8GNR8	Q8gnr8	listeria mo
166	98	5.9	384	2	Q9DW41	Q9dw41	rat cytomeg	239	94	5.7	769	2	Q00816	Q00816	toxoplasma
167	98	5.9	390	2	Q702W4	Q702w4	human herpe	240	94	5.7	776	2	Q7Q5E1	Q7q5e1	anopheles g
168	98	5.9	604	2	Q6E9T6	Q6e9t6	listeria mo	241	94	5.7	989	2	Q83U76	Q83u76	chlamydia t
169	98	5.9	604	2	Q8GNR1	Q8gnr1	listeria mo	242	94	5.7	989	2	Q84FU9	Q84fu9	chlamydia t
170	98	5.9	604	2	Q8GNR7	Q8gnr7	listeria mo	243	94	5.7	1241	1	PER_DROPS	P12348	drosophila
171	98	5.9	771	2	Q22783	Q22783	caenorhabdi	244	94	5.7	1241	2	Q75JCO	Q75jco	dictyosteli
172	98	5.9	2112	2	Q9VEL9	Q9vel9	drosophila	245	93.5	5.6	296	2	Q6P9X9	Q6p9x9	rattus norv
173	97.5	5.9	260	2	Q7PR65	Q7pr65	anopheles g	246	93.5	5.6	359	2	Q43656	Q43656	homo sapien
174	97.5	5.9	298	2	Q9Z0F0	Q9z0f0	rattus norv	247	93.5	5.6	383	2	Q702W5	Q702w5	human herpe
175	97.5	5.9	318	2	Q86HN3	Q86hn3	dictyosteli	248	93.5	5.6	385	2	Q9NHU8	Q9nhu8	drosophila
176	97.5	5.9	385	2	Q9NHU9	Q9nhu9	drosophila	249	93.5	5.6	498	2	Q6FWR9	Q6fwr9	candida gia
177	97.5	5.9	909	1	LDL1_XENLA	Q99087	xenopus lae	250	93.5	5.6	607	2	Q8GNS0	Q8gns0	listeria mo

251	93.5	5.6	626	2	Q9NDD1	Q9ndd1 leishmania	324	91	5.5	174	2	Q7YTP1	Q7ytp1 caenorhabdi
252	93	5.6	261	2	Q70CC2	Q70cc2 eimeria ten	325	91	5.5	198	2	Q7X3M4	Q7x3m4 listeria mo
253	93	5.6	311	2	O46019	O46019 caenorhabdi	326	91	5.5	246	2	Q9UAV4	Q9uav4 caenorhabdi
254	93	5.6	364	2	Q96D42	Q96d42 homo sapien	327	91	5.5	450	2	Q8CV85	Q8cv85 oceanobacil
255	93	5.6	385	2	O8T817	O8t817 drosophila	328	91	5.5	488	2	Q09586	Q09586 caenorhabdi
256	93	5.6	385	2	O8T819	Q8t819 drosophila	329	91	5.5	596	2	Q6PIT0	Q6pit0 xenopus tro
257	93	5.6	405	2	Q66HZ2	Q66hz2 brachydanio	330	91	5.5	620	2	Q8SVR3	Q8svr3 encephalito
258	93	5.6	629	2	Q24017	Q24017 drosophila	331	91	5.5	639	2	Q6SE94	Q6se94 listeria mo
259	93	5.6	639	2	O6E8X4	O6e8x4 listeria mo	332	91	5.5	701	2	Q6EAI0	Q6eai0 listeria mo
260	93	5.6	639	2	O8GNR5	O8gnr5 listeria mo	333	91	5.5	701	2	Q8ZMG4	Q8zmg4 pyrobaculum
261	93	5.6	639	2	O8GNR6	O8gnr6 listeria mo	334	91	5.5	705	2	Q7PY77	Q7py77 anopheles g
262	93	5.6	673	2	Q7QJB6	Q7qjb6 anopheles g	335	91	5.5	730	2	Q8GAZ8	Q8gaz8 dictyosteli
263	93	5.6	916	2	Q7YZ10	Q7yz10 monosiga br	336	91	5.5	1398	2	Q869T5	Q869t5 dictyosteli
264	93	5.6	930	2	O8YBL5	O8ybl5 aeropyrum p	337	91	5.5	2162	2	Q09515	Q09515 caenorhabdi
265	93	5.6	1349	2	O8WMQ4	Q8wmq4 homo sapien	338	91	5.5	4262	2	Q685J2	Q685j2 homo sapien
266	92.5	5.6	247	2	O8MKY7	O8mkv7 drosophila	339	91	5.5	4493	2	Q685J3	Q685j3 homo sapien
267	92.5	5.6	248	2	Q9NED0	Q9ned0 leishmania	340	90.5	5.5	385	2	Q9NHV0	Q9nhv0 drosophila
268	92.5	5.6	296	2	Q923D3	Q923d3 mus musculu	341	90.5	5.5	385	2	Q9NHV3	Q9nhv3 drosophila
269	92.5	5.6	300	1	JAM1_MOUSE	O8h792 mus musculu	342	90.5	5.5	408	2	Q6UDF5	Q6udf5 psittacid h
270	92.5	5.6	385	2	Q9NHV2	O9nhv2 drosophila	343	90.5	5.5	461	2	Q6C2X8	Q6c2x8 yarrowia li
271	92.5	5.6	400	1	HPL4_MOUSE	O80wm4 mus musculu	344	90.5	5.5	575	1	CH61_CUCMA	O05045 cucurbita m
272	92.5	5.6	446	2	O8EMV3	O8emv3 oceanobacil	345	90.5	5.5	662	1	MUC1_XENLA	O05049 xenopus lae
273	92.5	5.6	569	2	O9KGV9	O9kgv9 listeria mo	346	90.5	5.5	690	2	Q66S18	Q66s18 oikopleura
274	92.5	5.6	604	2	O6EAE4	Q6eae4 listeria mo	347	90.5	5.5	966	2	Q9U3P1	Q9u3p1 caenorhabdi
275	92.5	5.6	623	2	O57602	Q57602 ictalurus p	348	90.5	5.5	1084	2	Q86LA6	Q86la6 dictyosteli
276	92.5	5.6	708	2	Q73H41	Q73h41 wolbachia p	349	90.5	5.5	1175	2	Q9VRL7	Q9vrl7 drosophila
277	92.5	5.6	784	2	Q7S3V6	Q7s3v6 neurospora	350	90.5	5.5	1711	1	N214_DROME	Q9w1x4 drosophila
278	92.5	5.6	927	2	Q21811	Q21811 caenorhabdi	351	90.5	5.5	1976	2	Q9V9I8	Q9v9i8 drosophila
279	92.5	5.6	1636	1	BUD3_YEAST	P25558 saccharomyc	352	90.5	5.5	2300	2	Q7SFP6	Q7sfp6 neurospora
280	92.5	5.6	2338	2	Q7S9S3	Q7s9s3 ashbya goss	353	90	5.4	388	1	VE2_HPV27	P36789 human papil
281	92	5.6	347	2	Q8SYW5	O8syw5 drosophila	354	90	5.4	540	2	Q7SF17	Q7sf17 neurospora
282	92	5.6	429	2	P79046	P79046 humicola gr	355	90	5.4	604	2	Q6E9Q0	Q6e9q0 listeria mo
283	92	5.6	500	2	Q864U4	O864u4 bos taurus	356	90	5.4	626	2	O8IQJ5	O8iqj5 drosophila
284	92	5.6	604	2	Q9JNA2	O9jna2 listeria mo	357	90	5.4	629	2	Q9V3H7	Q9v3h7 drosophila
285	92	5.6	634	2	O6EA92	Q6ea92 listeria mo	358	90	5.4	639	2	Q6E8S6	Q6e8s6 listeria mo
286	92	5.6	649	2	Q6CF32	Q6cf33 yarrowia li	359	90	5.4	877	2	Q9H3Q6	Q9h3q6 homo sapien
287	92	5.6	659	2	Q9SXZ2	O9sxz2 caenorhabdi	360	90	5.4	878	2	Q9H3Q7	Q9h3q7 homo sapien
288	92	5.6	741	2	O6CH88	O6ch88 yarrowia li	361	90	5.4	948	2	O86AV9	O86av9 dictyosteli
289	92	5.6	846	2	O01699	O01699 caenorhabdi	362	90	5.4	957	2	O14651	O14651 homo sapien
290	92	5.6	907	2	O6CTD8	O6ctd8 kluyveromyc	363	90	5.4	965	2	Q22286	Q22286 caenorhabdi
291	92	5.6	966	1	SSN6_YEAST	P14922 saccharomyc	364	90	5.4	1217	1	Q9UKW9	Q9ukw9 homo sapien
292	92	5.6	1720	2	Q8I486	Q8i486 plasmodium	365	90	5.4	1367	1	AMYH_YEAST	P08640 saccharomyc
293	92	5.6	2829	2	P70039	P70039 xenopus lae	366	90	5.4	1367	2	Q6LCS8	Q6lcs8 saccharomyc
294	91.5	5.5	161	2	Q6CEP23	O6cp23 kluyveromyc	367	90	5.4	1593	2	Q8SX82	Q8sx82 drosophila
295	91.5	5.5	198	2	Q7WRT1	O7wrt1 listeria mo	368	90	5.4	2282	2	Q9NK56	Q9nk56 drosophila
296	91.5	5.5	198	2	Q7X384	O7x384 listeria mo	369	90	5.4	2871	2	Q8IM87	Q8im87 drosophila
297	91.5	5.5	300	2	O8VC39	O8vc39 mus musculu	370	90	5.4	2871	2	Q9V483	Q9v483 drosophila
298	91.5	5.5	305	2	O8RI83	O8ri83 mus musculu	371	89.5	5.4	195	2	Q9QX82	Q9qx82 rattus norv
299	91.5	5.5	338	2	Q6EAH4	Q6eah4 listeria mo	372	89.5	5.4	224	2	Q9CRT7	Q9crt7 mus musculu
300	91.5	5.5	383	2	Q702X8	O702x8 human herpe	373	89.5	5.4	303	2	Q9D116	Q9d116 mus musculu
301	91.5	5.5	385	2	Q9NHV1	O9nhv1 drosophila	374	89.5	5.4	305	2	O8VBM0	O8vbm0 mus musculu
302	91.5	5.5	411	1	LMP2_RAT	P17046 rattus norv	375	89.5	5.4	319	2	Q9D0D7	Q9dd07 mus musculu
303	91.5	5.5	411	2	Q6P6W1	Q6p6w1 rattus norv	376	89.5	5.4	319	2	Q9D4W4	Q9d4w4 m mus muscu
304	91.5	5.5	497	2	O8QVC5	Q8qvc5 eyach virus	377	89.5	5.4	326	2	Q7SCW5	Q7scw5 neurospora
305	91.5	5.5	538	2	Q76H84	Q76h84 streptococc	378	89.5	5.4	350	2	Q7Q1R0	Q7q1r0 anopheles g
306	91.5	5.5	573	2	Q69380	O69380 listeria mo	379	89.5	5.4	440	2	O9P566	O9p566 neurospora
307	91.5	5.5	604	2	Q6E8U4	Q6e8u4 listeria mo	380	89.5	5.4	443	2	Q6P111	Q6p111 brachydanio
308	91.5	5.5	604	2	O8GNR3	O8gnr3 listeria mo	381	89.5	5.4	455	2	Q7VNN0	Q7vnn0 haemophilus
309	91.5	5.5	627	2	Q7RWT2	Q7rwt2 neurospora	382	89.5	5.4	456	2	Q25242	Q25242 lucilia cup
310	91.5	5.5	633	2	Q9JMY6	Q9jmy6 listeria mo	383	89.5	5.4	471	2	Q9VMG7	Q9vmg7 drosophila
311	91.5	5.5	639	1	ACTA_LISMO	P33379 listeria mo	384	89.5	5.4	480	2	Q25241	Q25241 lucilia cup
312	91.5	5.5	639	2	Q6E8V0	Q6e8v0 listeria mo	385	89.5	5.4	492	2	O6CGC6	O6cgc6 yarrowia li
313	91.5	5.5	639	2	Q6E914	Q6e914 listeria mo	386	89.5	5.4	510	2	Q6SCJ8	Q6scj8 aspergillus
314	91.5	5.5	639	2	Q6E9X8	Q6e9x8 listeria mo	387	89.5	5.4	604	2	Q6E9W0	Q6e9w0 listeria mo
315	91.5	5.5	639	2	Q6EA56	Q6ea56 listeria mo	388	89.5	5.4	634	2	Q7IT11	Q7it11 momordica c
316	91.5	5.5	639	2	Q6EAA4	Q6eaa4 listeria mo	389	89.5	5.4	659	2	Q86A18	Q86a18 dictyosteli
317	91.5	5.5	639	2	O8GNR9	O8gnr9 listeria mo	390	89.5	5.4	1145	2	O8JKT0	Q8jkt0 heliothis z
318	91.5	5.5	639	2	O8GNR2	O8gnr2 listeria mo	391	89.5	5.4	1368	2	Q23821	Q23821 caenorhabdi
319	91.5	5.5	681	1	VGP_MABVP	P35254 marburg vir	392	89.5	5.4	1403	2	Q9NHN6	Q9nhn6 drosophila
320	91.5	5.5	681	2	Q71WM1	Q71wm1 lake victor	393	89	5.4	307	1	SGS3_DROME	P02840 drosophila
321	91.5	5.5	860	2	Q7RZN3	Q7rzn3 neurospora	394	89	5.4	369	2	Q91E39	Q91e39 phocid herp
322	91.5	5.5	1148	2	O6CBJ2	O6cbj2 yarrowia li	395	89	5.4	416	1	LMP1_HUMAN	P11279 homo sapien
323	91.5	5.5	1167	2	Q7RWQ7	Q7rwq7 neurospora	396	89	5.4	417	2	O8WU33	Q8wu33 homo sapien

397	89	5.4	421	2	Q6KCA6	Q6kca6 candida dub	470	87.5	5.3	283	2	Q9FKU2	Q9fkku2 arabidopsis
398	89	5.4	472	2	Q14887	Q14887 homo sapien	471	87.5	5.3	338	2	Q6CY50	Q6cy50 kluyveromyc
399	89	5.4	482	2	Q6BSZ9	Q6bez9 debaryomyc	472	87.5	5.3	366	2	Q6FSI8	Q6fei8 candida gla
400	89	5.4	503	2	Q19269	Q19269 caenorhabdi	473	87.5	5.3	383	2	Q702Y9	Q702y9 human herbe
401	89	5.4	603	2	Q6CE49	Q6ce49 yarrowia li	474	87.5	5.3	442	2	Q7S223	Q7sz23 neurospora
402	89	5.4	666	2	Q7QXK0	Q7qxx0 giardia lam	475	87.5	5.3	462	2	Q8TUE0	Q8tue0 methanosarc
403	89	5.4	714	2	Q9NGW9	Q9ngw9 dictyosteli	476	87.5	5.3	498	2	Q6FVC8	Q6fvc8 candida gla
404	89	5.4	828	2	Q8IRC1	Q8irc1 drosophila	477	87.5	5.3	555	2	Q9U6R7	Q9u6r7 dermatophag
405	89	5.4	846	2	Q9VZ10	Q9vzi0 drosophila	478	87.5	5.3	623	2	Q6T547	Q6t547 listeria mo
406	89	5.4	882	2	Q917T2	Q917t2 drosophila	479	87.5	5.3	634	2	Q7RWB0	Q7rwb0 neurospora
407	89	5.4	887	2	Q6NQY4	Q6ngy4 drosophila	480	87.5	5.3	639	2	Q6T548	Q6t548 listeria mo
408	89	5.4	893	2	Q8IRCO	Q8irc0 drosophila	481	87.5	5.3	648	2	Q44189	Q44189 caenorhabdi
409	89	5.4	951	2	Q9FVX8	Q9fvx8 oryza sativ	482	87.5	5.3	653	2	Q8NK55	Q8nk55 candida alb
410	89	5.4	978	2	Q8IRB9	Q8irb9 drosophila	483	87.5	5.3	717	2	Q8NAJ6	Q8naj6 homo sapien
411	89	5.4	1483	2	Q7KWU3	Q7kwu3 dictyosteli	484	87.5	5.3	752	2	Q8MNE2	Q8mne2 dictyosteli
412	89	5.4	1708	2	Q7XWZ9	Q7xwz9 oryza sativ	485	87.5	5.3	785	2	Q7QQI5	Q7qqi5 giardia lam
413	89	5.4	2273	2	Q6JHU2	Q6jhu2 burkholderi	486	87.5	5.3	825	2	Q9LZA6	Q9lza6 arabidopsis
414	89	5.4	6994	2	Q17343	Q17343 caenorhabdi	487	87.5	5.3	867	2	Q90X49	Q90x49 brachydanio
415	89	5.4	6994	2	Q17490	Q17490 caenorhabdi	488	87.5	5.3	906	2	Q8UUV1	Q8uvu1 xenopus lae
416	88.5	5.3	193	2	Q23366	Q23366 arabidopsis	489	87.5	5.3	971	2	Q6W3C4	Q6w3c4 caenorhabdi
417	88.5	5.3	264	2	Q80XS5	Q80xs5 mus musculu	490	87.5	5.3	989	2	Q19930	Q19930 caenorhabdi
418	88.5	5.3	321	2	Q25939	Q25939 plasmodium	491	87.5	5.3	997	1	VGNM_APMV	P38485 andean poea
419	88.5	5.3	448	2	Q6AQD8	Q6aqd8 desulfotale	492	87.5	5.3	1085	1	CASR_BOVIN	P35384 bos taurus
420	88.5	5.3	481	2	Q9VMK3	Q9vmk3 drosophila	493	87.5	5.3	1091	1	NCA1_CHICK	P13590 gallus gall
421	88.5	5.3	518	2	Q8NJS3	Q8njs3 candida alb	494	87.5	5.3	1129	2	Q6CB75	Q6cb75 yarrowia li
422	88.5	5.3	569	2	Q71X10	Q71x10 listeria mo	495	87.5	5.3	1370	2	Q6C3B8	Q6c3b8 yarrowia li
423	88.5	5.3	582	2	Q81R74	Q81r74 drosophila	496	87.5	5.3	1799	2	Q7KUI0	Q7kui0 drosophila
424	88.5	5.3	596	1	AIUP_MOUSE	Q99nb8 mus musculu	497	87.5	5.3	1802	1	HKRI_YEAST	P41809 saccharomyc
425	88.5	5.3	598	2	Q9JMY5	Q9jmy5 listeria mo	498	87.5	5.3	2817	2	Q97K42	Q97k42 clostridium
426	88.5	5.3	615	2	Q9M6E8	Q9m6e8 phaseolus v	499	87.5	5.3	9234	2	Q7KTP5	Q7ktp5 drosophila
427	88.5	5.3	653	2	Q81JX0	Q81jx0 plasmodium	500	87	5.3	167	2	Q65742	Q65742 cicer ariet
428	88.5	5.3	699	2	Q6CSM7	Q6cm7 kluyveromyc	501	87	5.3	235	2	Q63349	Q63349 rattus norv
429	88.5	5.3	721	2	Q97UG7	Q97ug7 sulfolobus	502	87	5.3	259	2	Q70CD5	Q70cd5 eimeria tan
430	88.5	5.3	722	2	Q59644	Q59644 sulfolobus	503	87	5.3	362	2	Q6CGU2	Q6cgu2 yarrowia li
431	88.5	5.3	722	2	Q6FTP4	Q6ftp4 candida gla	504	87	5.3	363	2	Q91YK8	Q91yk8 mus musculu
432	88.5	5.3	901	2	Q9H195	Q9h195 homo sapien	505	87	5.3	379	2	Q823B1	Q823b1 chlamydophi
433	88.5	5.3	980	2	Q84FU6	Q84fu6 chlamydia t	506	87	5.3	385	2	Q8T8J9	Q8t8j9 drosophila
434	88.5	5.3	980	2	Q84FU7	Q84fu8 chlamydia t	507	87	5.3	442	2	Q758Q5	Q758q5 ashbya goss
435	88.5	5.3	981	2	Q84FU8	Q84fu7 chlamydia t	508	87	5.3	453	2	Q9U301	Q9u301 caenorhabdi
436	88.5	5.3	1101	1	GUNC_CELFI	P14090 cellulomona	509	87	5.3	639	2	Q6E8S0	Q6e8s0 listeria mo
437	88	5.3	103	2	Q9VTB3	Q9vtb3 sus scrofa	510	87	5.3	661	2	Q13444	Q13444 cladosporiu
438	88	5.3	161	2	Q9CVT7	Q9cvt7 mus musculu	511	87	5.3	689	2	Q724Q0	Q724q0 listeria mo
439	88	5.3	259	2	Q9N3B9	Q9n3b9 caenorhabdi	512	87	5.3	752	2	Q9YC61	Q9yc61 aeropyrum p
440	88	5.3	319	2	Q7QJAO	Q7qja0 anopheles g	513	87	5.3	841	2	Q6AX88	Q6ax88 xenopus lae
441	88	5.3	345	2	Q690W2	Q690w2 anolis sagr	514	87	5.3	905	2	Q86SU9	Q86su9 homo sapien
442	88	5.3	347	2	Q9TZV4	Q9tzv4 plasmodium	515	87	5.3	991	2	Q83UW2	Q83uw2 chlamydia t
443	88	5.3	362	2	Q9TZV3	Q9tzv3 plasmodium	516	87	5.3	991	2	Q84FV0	Q84fv0 chlamydia t
444	88	5.3	382	2	Q6C971	Q6c971 yarrowia li	517	87	5.3	991	1	PMPH_CHLTR	Q84fv1 chlamydia t
445	88	5.3	385	2	Q8T8I2	Q8t8i2 drosophila	518	87	5.3	1016	1	Q91AU3	Q91au3 legionella
446	88	5.3	385	2	Q8T8I4	Q8t8i4 drosophila	519	87	5.3	1048	2	Q91AU3	Q91au3 schizosacch
447	88	5.3	385	2	Q8T8I6	Q8t8i6 drosophila	520	87	5.3	1082	1	YK02_SCHPO	Q9hdy9 schizosacch
448	88	5.3	385	2	Q8T8J0	Q8t8j0 drosophila	521	87	5.3	1506	2	P79927	P79927 xenopus lae
449	88	5.3	385	2	Q8T8J1	Q8t8j1 drosophila	522	87	5.3	1537	1	FLO1_YEAST	P32768 saccharomyc
450	88	5.3	385	2	Q8T8K3	Q8t8k3 drosophila	523	86.5	5.2	197	2	Q9Z317	Q9z317 mus musculu
451	88	5.3	447	2	Q6CCR1	Q6ccr1 yarrowia li	524	86.5	5.2	249	2	Q9R0L9	Q9r0l9 mus musculu
452	88	5.3	449	2	Q6CWZ6	Q6cwz6 kluyveromyc	525	86.5	5.2	260	2	Q6BVX5	Q6bvx5 debaryomyc
453	88	5.3	456	2	Q9U2W2	Q9u2w2 caenorhabdi	526	86.5	5.2	319	2	Q8BP27	Q8bp27 mus musculu
454	88	5.3	564	2	Q01627	Q01627 caenorhabdi	527	86.5	5.2	390	2	Q8BP27	Q8bp27 mus musculu
455	88	5.3	577	2	Q6FSJ1	Q6fsj1 candida gla	528	86.5	5.2	400	1	MUAI_XENLA	Q10667 xenopus lae
456	88	5.3	588	2	Q813F9	Q813f9 bacillus ce	529	86.5	5.2	401	2	Q6BV71	Q6bv71 debaryomyc
457	88	5.3	601	2	Q6V6S2	Q6v6s2 drosophila	530	86.5	5.2	442	2	Q7M8Z3	Q7m8z3 wolinnella s
458	88	5.3	602	2	Q8YV91	Q8yv91 anabaena sp	531	86.5	5.2	451	2	Q6DF68	Q6df68 xenopus tro
459	88	5.3	604	2	Q6E916	Q6e916 listeria mo	532	86.5	5.2	461	2	Q21004	Q21004 caenorhabdi
460	88	5.3	616	2	Q8R0X0	Q8r0x0 mus musculu	533	86.5	5.2	461	2	Q21004	Q21004 xenopus lae
461	88	5.3	656	2	Q8BUE7	Q8bue7 mus musculu	534	86.5	5.2	484	1	PAP2_XENLA	P51005 xenopus lae
462	88	5.3	716	2	Q9NYE4	Q9nye4 homo sapien	535	86.5	5.2	493	2	Q23330	Q23330 caenorhabdi
463	88	5.3	761	2	Q22271	Q22271 arabidopsis	536	86.5	5.2	503	1	WSC2_YEAST	P53832 saccharomyc
464	88	5.3	995	2	Q91638	Q91638 xenopus lae	537	86.5	5.2	601	2	Q6V6S4	Q6v6s4 drosophila
465	88	5.3	1051	2	Q6CLJ9	Q6clj9 yarrowia li	538	86.5	5.2	604	2	Q8E8Z8	Q8e8z8 listeria mo
466	88	5.3	1630	1	MSFI_PLAFK	P04932 plasmodium	539	86.5	5.2	604	2	Q8E928	Q8e928 listeria mo
467	88	5.3	1790	2	Q81816	Q81816 aplysia cal	540	86.5	5.2	639	2	Q6E952	Q6e952 listeria mo
468	88	5.3	5703	1	MUSB_HUMAN	Q9hc84 homo sapien	541	86.5	5.2	639	2	Q6E976	Q6e976 listeria mo
469	87.5	5.3	147	2	Q61043	Q61043 trypanosoma	542	86.5	5.2	639	2	Q8GNR0	Q8gnr0 listeria mo

543	86.5	5.2	687	2	Q6NHU1	Q6nhul corynebacte	616	85.5	5.2	2448	2	Q8WMQ5	Q8wmq5 homo sapien
544	86.5	5.2	740	1	GAG_SMRVH	P21411 squirrel mo	617	85.5	5.2	3346	2	Q822X0	Q822x0 chlamydomphi
545	86.5	5.2	788	2	O18510	O18510 trichoplusi	618	85.5	5.2	6995	2	Q86RK2	Q86rk2 homo sapien
546	86.5	5.2	790	2	Q8TBZ7	Q8tbz7 homo sapien	619	85	5.1	172	2	Q8VC95	Q8vc95 mus musculus
547	86.5	5.2	807	2	O18511	O18511 trichoplusi	620	85	5.1	255	2	Q86HS8	Q86hs8 dictyosteli
548	86.5	5.2	838	2	Q7UNP4	Q7unp4 rhodopirell	621	85	5.1	265	2	Q9GZE5	Q9gze5 caenorhabdi
549	86.5	5.2	941	2	Q9LTH0	Q9lth0 arabidopsis	622	85	5.1	300	2	Q95XH5	Q95xh5 caenorhabdi
550	86.5	5.2	1300	2	Q6BZP6	Q6bzip6 yarrowia li	623	85	5.1	317	2	Q8BEK4	Q8bek4 cowpox viru
551	86.5	5.2	1546	2	Q80SS4	Q80ss4 mus musculus	624	85	5.1	326	2	Q9VM89	Q9vm89 drosophila
552	86.5	5.2	1579	2	Q99MP1	Q99mp1 mus musculus	625	85	5.1	477	2	Q7MR34	Q7mr34 wolinelia s
553	86.5	5.2	1683	2	Q810D4	Q810d4 mus musculus	626	85	5.1	503	2	Q8VCF0	Q8vcf0 mus musculus
554	86.5	5.2	1684	2	Q9WTO5	Q9wt05 mus musculus	627	85	5.1	510	2	Q8NJT3	Q8njt3 kluyveromyc
555	86.5	5.2	1822	2	Q7ROW4	Q7row4 giardia lam	628	85	5.1	510	2	Q6CUX5	Q6cux5 kluyveromyc
556	86.5	5.2	1844	2	Q22579	Q22579 caenorhabdi	629	85	5.1	573	2	Q8H7K9	Q8h7k9 oryza sativ
557	86.5	5.2	1851	2	Q9ESP3	Q9esp3 rattus norv	630	85	5.1	576	2	Q66G04	Q66g04 saccharomyc
558	86.5	5.2	2781	2	Q9UIG2	Q9uig2 homo sapien	631	85	5.1	599	2	Q6C2K2	Q6c2k2 yarrowia li
559	86	5.2	345	2	Q6UJM5	Q6ujm5 diploactyl	632	85	5.1	601	2	Q6V6S1	Q6v6s1 drosophila
560	86	5.2	347	2	Q9TZV5	Q9tzv5 plasmodium	633	85	5.1	627	1	PKNB_LACLA	Q9cst5 lactococcus
561	86	5.2	372	2	Q9TZV6	Q9tzv6 plasmodium	634	85	5.1	629	2	Q7ZTW7	Q7ztw7 brachydanio
562	86	5.2	385	2	Q8T8K4	Q8t8k4 drosophila	635	85	5.1	639	2	Q6E9T0	Q6e9t0 listeria mo
563	86	5.2	390	2	Q96TSS	Q96tss phlebia rad	636	85	5.1	782	2	Q8GX37	Q8gx37 arabidopsis
564	86	5.2	390	2	Q70LM3	Q70lm3 phlebia rad	637	85	5.1	852	2	Q6CIA5	Q6cia5 yarrowia li
565	86	5.2	434	2	Q872V2	Q872v2 neurospora	638	85	5.1	860	1	VG12_BPB03	Q37893 bacterioph
566	86	5.2	450	2	O18984	Q18984 cercopithe	639	85	5.1	911	2	Q7RWL1	Q7kw11 dictyosteli
567	86	5.2	476	2	Q03396	Q03396 plasmodium	640	85	5.1	989	2	Q9M1E4	Q9mie4 arabidopsis
568	86	5.2	477	2	Q66YC5	Q66yc5 homo sapien	641	85	5.1	990	2	Q91803	Q91803 xenopus lae
569	86	5.2	495	2	Q6AK33	Q6ak33 desulfotale	642	85	5.1	993	2	Q83TJ6	Q83tj6 chlamydia t
570	86	5.2	551	1	PODX_RABIT	Q28645 oryctolagus	643	85	5.1	1013	2	Q6CKC8	Q6ckc8 kluyveromyc
571	86	5.2	604	2	Q6E9N2	Q6e9n2 listeria mo	644	85	5.1	1049	2	Q960E6	Q960e6 drosophila
572	86	5.2	604	2	Q8GNQ9	Q8gnq9 listeria mo	645	85	5.1	1049	2	Q96V6L1	Q9v6l1 drosophila
573	86	5.2	639	2	Q6E8R4	Q6e8r4 listeria mo	646	85	5.1	1170	2	Q95011	Q95011 caenorhabdi
574	86	5.2	639	2	Q7S009	Q7s009 neurospora	647	85	5.1	1225	2	Q9VR49	Q9vr49 drosophila
575	86	5.2	734	2	Q869R9	Q869r9 dictyosteli	648	85	5.1	1354	2	Q9VKA7	Q9vka7 drosophila
576	86	5.2	750	2	Q9HFZ4	Q9hfz4 candida alb	649	85	5.1	1779	2	O52374	Q52374 calicellul
577	86	5.2	780	2	Q9LK78	Q9lk78 arabidopsis	650	85	5.1	3150	2	Q7PMD5	Q7pmd5 anopheles g
578	86	5.2	799	2	Q75FI7	Q75fi7 leptospira	651	85	5.1	1732	2	Q95YM2	Q95ym2 procambus
579	86	5.2	799	2	Q8EXF5	Q8exf5 leptospira	652	84.5	5.1	220	2	Q9EQG0	Q9eqg0 mus musculus
580	86	5.2	843	2	Q7XJ06	Q7xj06 oryza sativ	653	84.5	5.1	313	2	Q8BEJ1	Q8bej1 skunkpox vi
581	86	5.2	866	2	Q80XL8	Q80xl8 mus musculus	654	84.5	5.1	345	2	Q691T8	Q691t8 anolis sagr
582	86	5.2	1080	1	UBP8_MOUSE	Q80u87 mus musculus	655	84.5	5.1	378	2	Q6FNP6	Q6fnp6 candida gla
583	86	5.2	1266	2	Q6CAR3	Q6car3 yarrowia li	656	84.5	5.1	423	2	Q6CTJ9	Q6ctj9 kluyveromyc
584	86	5.2	1324	2	Q8MMQ2	Q8mmq2 dictyosteli	657	84.5	5.1	456	2	Q8R5M8	Q8r5m8 mus musculus
585	86	5.2	1674	2	Q80Z18	Q80z18 mus musculus	658	84.5	5.1	463	2	Q9JX25	Q9jx25 neisseria m
586	86	5.2	1785	2	Q25685	Q25685 plasmodium	659	84.5	5.1	493	1	TNR8_RAT	P97525 rattus norv
587	85.5	5.2	193	2	Q8LB00	Q8lb00 arabidopsis	660	84.5	5.1	532	2	Q6P7V2	Q6p7v2 mus musculus
588	85.5	5.2	206	2	Q6TVK4	Q6tvk4 orf virus	661	84.5	5.1	540	1	CH60_STRAP	Q8k420 streptococc
589	85.5	5.2	224	2	Q8KKT9	Q8kkt9 rhizobium e	662	84.5	5.1	562	1	NUPL_HUMAN	P52594 homo sapien
590	85.5	5.2	269	2	Q9U9J2	Q9u9j2 toxocara ca	663	84.5	5.1	570	2	Q6GMZ9	Q6gmz9 xenopus lae
591	85.5	5.2	271	2	Q6DG19	Q6dg19 brachydanio	664	84.5	5.1	622	2	Q6V6E2	Q6v6e2 drosophila
592	85.5	5.2	345	2	Q691X0	Q691x0 anolis sagr	665	84.5	5.1	624	2	Q675N0	Q675n0 cornus suet
593	85.5	5.2	370	2	Q7KRX4	Q7krx4 drosophila	666	84.5	5.1	636	2	Q66HZ5	Q66hz5 brachydanio
594	85.5	5.2	378	1	FBSH_MOUSE	Q8r089 mus musculus	667	84.5	5.1	657	2	Q86ID0	Q86id0 dictyosteli
595	85.5	5.2	379	2	Q81050	Q8i050 drosophila	668	84.5	5.1	658	1	SHK1_SCHPO	P50527 schizosacch
596	85.5	5.2	390	2	Q81GQ0	Q8i9g0 drosophila	669	84.5	5.1	709	2	O16783	O16783 caenorhabdi
597	85.5	5.2	429	2	Q95Y50	Q95y50 caenorhabdi	670	84.5	5.1	753	2	Q9VCQ7	Q9vcq7 drosophila
598	85.5	5.2	575	1	CH62_CUCMA	Q05046 cucurbita m	671	84.5	5.1	773	2	Q8TGH3	Q8tgh3 malassezia
599	85.5	5.2	595	2	Q7R2J1	Q7r2j1 giardia lam	672	84.5	5.1	803	1	IF2_COXBU	Q83bel coxiellia bu
600	85.5	5.2	622	2	Q6V6D8	Q6v6d8 drosophila	673	84.5	5.1	806	2	Q960Q0	Q960q0 drosophila
601	85.5	5.2	622	2	Q6V6E4	Q6v6e4 drosophila	674	84.5	5.1	814	2	Q6C247	Q6c247 yarrowia li
602	85.5	5.2	623	2	Q99QR8	Q99qr8 bradyrhizob	675	84.5	5.1	931	2	Q877B7	Q877b7 aspergillus
603	85.5	5.2	625	2	Q9LCJ8	Q9lcj8 staphylococ	676	84.5	5.1	934	2	Q64Y17	Q64y17 bacterioides
604	85.5	5.2	649	2	Q49445	Q49445 arabidopsis	677	84.5	5.1	1047	2	Q874L3	Q874l3 candida alb
605	85.5	5.2	734	2	Q7S939	Q7s939 neurospora	678	84.5	5.1	1102	2	Q08964	Q08964 saccharomyc
606	85.5	5.2	781	2	Q96JM7	Q96jm7 homo sapien	679	84.5	5.1	1103	2	Q6CA70	Q6ca70 yarrowia li
607	85.5	5.2	786	2	Q21027	Q21027 caenorhabdi	680	84.5	5.1	1161	1	DAN4_YEAST	P47179 saccharomyc
608	85.5	5.2	841	2	Q6RBJ4	Q6rbj4 brachydanio	681	84.5	5.1	1355	2	Q8GAM1	Q8gam1 dictyosteli
609	85.5	5.2	843	2	Q9VYH8	Q9vyh8 drosophila	682	84.5	5.1	1743	2	Q81IL9	Q81il9 plasmodium
610	85.5	5.2	863	2	Q851G7	Q851g7 oryza sativ	683	84.5	5.1	1878	2	Q6CPZ4	Q6cpz4 kluyveromyc
611	85.5	5.2	895	2	Q80973	Q80973 arabidopsis	684	84.5	5.1	1984	2	Q08562	Q08562 rattus norv
612	85.5	5.2	935	2	Q6RBJ3	Q6rbj3 brachydanio	685	84.5	5.1	2180	2	Q9VAS8	Q9vas8 drosophila
613	85.5	5.2	977	2	Q6RBJ2	Q6rbj2 brachydanio	686	84.5	5.1	2378	2	Q7N7Y6	Q7n7y6 photorhabdu
614	85.5	5.2	981	2	Q6GG19	Q6gg19 xenopus lae	687	84.5	5.1	2481	2	Q99QR6	Q99qr6 staphylococ
615	85.5	5.2	1052	2	Q91G49	Q91g49 chilo iride	688	84.5	5.1	2481	2	Q7A4B1	Q7a4b1 staphylococ

689	84.5	5.1	2761	2	Q19522	Q19522 caenorhabdi	762	83.5	5.0	812	2	Q86AW3	Q86aw3 dictyosteli
690	84.5	5.1	3443	2	Q8JZM8	Q8jzm8 mus musculu	763	83.5	5.0	838	2	Q90YMI	Q90ym1 brachydanio
691	84.5	5.1	22152	2	Q8WXL7	Q8wxi7 homo sapien	764	83.5	5.0	935	2	Q9VGN4	Q9vgn4 drosophila
692	84	5.1	262	2	P74577	P74577 synechocyst	765	83.5	5.0	967	2	Q08294	Q08294 saccharomyc
693	84	5.1	309	2	Q63549	Q63549 rattus norv	766	83.5	5.0	976	2	Q9A531	Q9a531 caulobacter
694	84	5.1	335	2	Q9C7W2	Q9c7w2 arabidopsis	767	83.5	5.0	1001	2	Q05164	Q05164 saccharomyc
695	84	5.1	359	1	MTD MEDSA	Q82515 medicago sa	768	83.5	5.0	1043	2	Q97E41	Q97e41 clostridium
696	84	5.1	385	2	Q8T8I3	Q8t8i3 drosophila	769	83.5	5.0	1286	2	Q9TXR6	Q9txr6 caenorhabdi
697	84	5.1	385	2	Q8T8I5	Q8t8i5 drosophila	770	83.5	5.0	1607	2	Q6CDM9	Q6cdm9 yarrowia li
698	84	5.1	385	2	Q8T8K2	Q8t8k2 drosophila	771	83.5	5.0	1713	2	Q8TGE1	Q8tgel saccharomyc
699	84	5.1	385	2	Q8T8L0	Q8t8l0 drosophila	772	83.5	5.0	2764	2	Q7Z7D6	Q7z7d6 homo sapien
700	84	5.1	420	2	Q8N7W9	Q8n7w9 homo sapien	773	83.5	5.0	3026	2	Q8ILS9	Q8ils9 plasmodium
701	84	5.1	420	2	Q8N7H1	Q8n7h1 anabaena sp	774	83.5	5.0	3175	1	RPOA_EAV	P19811 equine arte
702	84	5.1	456	1	NX3B_BOVIN	Q28143 bos taurus	775	83.5	5.0	3371	1	Q864S8	Q864s8 felis silve
703	84	5.1	464	2	Q9VX42	Q9vx42 drosophila	776	83.5	5.0	3179	1	MUC2_HUMAN	Q02817 homo sapien
704	84	5.1	475	2	Q8FQJ1	Q8fqj1 corynebacte	777	83	5.0	197	2	Q8UL62	Q8jl62 choristoneu
705	84	5.1	487	2	Q8E1P9	Q8e1p9 streptococc	778	83	5.0	217	2	Q7PER9	Q7per9 anopheles g
706	84	5.1	487	2	Q8E764	Q8e764 streptococc	779	83	5.0	221	1	RL1_SULAC	P35024 sulfolobus
707	84	5.1	543	2	Q14879	Q14879 homo sapien	780	83	5.0	291	2	Q6QPG5	Q6qpg5 simian aden
708	84	5.1	625	2	Q7PRT5	Q7prt5 anopheles g	781	83	5.0	309	2	Q6IEI3	Q6iel3 oryza sativ
709	84	5.1	636	1	ENV_MCFP	P15073 mink cell f	782	83	5.0	309	2	Q7XNY3	Q7xny3 oryza sativ
710	84	5.1	639	2	Q6E934	Q6e934 listeria mo	783	83	5.0	314	2	Q9H8R7	Q9h8r7 homo sapien
711	84	5.1	641	2	Q6AJU8	Q6aju8 desulfotale	784	83	5.0	316	2	Q8TD14	Q8td14 homo sapien
712	84	5.1	648	2	Q95QX0	Q95qx0 caenorhabdi	785	83	5.0	329	2	Q7QB72	Q7qb72 anopheles g
713	84	5.1	730	2	Q6CPU9	Q6cpu9 kluyveromyc	786	83	5.0	337	2	Q7Z5K8	Q7z5k8 homo sapien
714	84	5.1	793	2	Q8VAG7	Q8vag7 listeria mo	787	83	5.0	345	2	Q691Y6	Q691y6 anolis sagr
715	84	5.1	827	2	Q61WN3	Q61wn3 ustilago ma	788	83	5.0	346	2	Q8SHB2	Q8shb2 rhapholeon
716	84	5.1	864	1	YCI8_HUMAN	Q9ulk2 homo sapien	789	83	5.0	378	2	Q8SXS5	Q8sxs5 drosophila
717	84	5.1	880	2	Q7YU85	Q7yu85 drosophila	790	83	5.0	382	2	Q9XZ28	Q9xzz8 litomosoid
718	84	5.1	933	2	Q6ZM25	Q6zms5 homo sapien	791	83	5.0	385	2	Q8T8K5	Q8t8k5 drosophila
719	84	5.1	961	1	BNCL_MOUSE	Q95914 mus musculu	792	83	5.0	409	1	R23B_HUMAN	P54727 homo sapien
720	84	5.1	996	1	LRP8_MOUSE	Q924x6 mus musculu	793	83	5.0	419	2	Q8TD11	Q8td11 homo sapien
721	84	5.1	1021	2	Q6CXI2	Q6cxy2 kluyveromyc	794	83	5.0	422	2	Q8TD13	Q8td13 homo sapien
722	84	5.1	1075	1	FLOS_YEAST	P38894 saccharomyc	795	83	5.0	463	2	Q42665	Q42665 schizosacch
723	84	5.1	1153	2	Q6ALQ0	Q6alq0 drosophila	796	83	5.0	485	2	Q9V8B0	Q9v8b0 drosophila
724	84	5.1	1331	1	MANB_CALSA	P22533 caldocellum	797	83	5.0	559	2	Q9VN36	Q9vn36 drosophila
725	84	5.1	1343	2	Q9G0V6	Q9g0v6 drosophila	798	83	5.0	601	1	ALUP_HUMAN	Q9nrr5 homo sapien
726	84	5.1	1343	2	Q9W2G6	Q9w2g6 drosophila	799	83	5.0	605	1	WSC4_YEAST	P38739 saccharomyc
727	84	5.1	1362	2	Q9V294	Q9v294 pyrococcus	800	83	5.0	639	2	Q8E8Z2	Q8e8z2 listeria mo
728	84	5.1	1362	2	Q86AM2	Q86am2 dictyosteli	801	83	5.0	653	1	NUMB_MOUSE	Q9qzs3 mus musculu
729	84	5.1	1645	2	Q9U263	Q9u263 caenorhabdi	802	83	5.0	661	2	Q9V8S2	Q9v8s2 drosophila
730	84	5.1	1832	2	Q96503	Q96503 cryptospori	803	83	5.0	737	1	KNS1_YEAST	P32350 saccharomyc
731	84	5.1	2215	2	Q8II26	Q8iiz6 plasmodium	804	83	5.0	738	1	VU47_HHV62	P52549 human herpe
732	83.5	5.0	216	2	Q28501	Q28501 macaca mula	805	83	5.0	762	2	Q86AG3	Q86ag3 dictyosteli
733	83.5	5.0	274	2	Q9EX24	Q9ex24 streptomyce	806	83	5.0	769	2	Q17921	Q17921 caenorhabdi
734	83.5	5.0	279	2	Q14888	Q14888 homo sapien	807	83	5.0	786	2	Q9FDM5	Q9fdm5 streptococc
735	83.5	5.0	292	2	Q86688	Q86688 bacillus me	808	83	5.0	797	1	VGLX_BHV1B	P28968 equine herp
736	83.5	5.0	306	2	Q88V34	Q88v34 lactobacill	809	83	5.0	826	2	Q8VLE0	Q8dle0 equid herpe
737	83.5	5.0	306	2	Q9QVLA	Q9qv14 mus musculu	810	83	5.0	867	2	Q8V0L5	Q8v0l5 equid herpe
738	83.5	5.0	352	2	Q22685	Q22685 arabidopsis	811	83	5.0	858	2	Q9H8D9	Q9h8d9 homo sapien
739	83.5	5.0	352	2	Q8LPH6	Q8lph6 arabidopsis	812	83	5.0	866	2	Q39781	Q39781 equid herpe
740	83.5	5.0	385	2	Q8T8L3	Q8t8l3 drosophila	813	83	5.0	866	2	Q6S6W0	Q6s6w0 equid herpe
741	83.5	5.0	385	2	Q83NC5	Q83nc5 tropheryma	814	83	5.0	867	2	Q39782	Q39782 equid herpe
742	83.5	5.0	405	2	Q95XV0	Q95xv0 caenorhabdi	815	83	5.0	963	1	L8P8_HUMAN	Q14114 homo sapien
743	83.5	5.0	446	2	Q6CQ08	Q6cq08 kluyveromyc	816	83	5.0	1002	2	Q6CBD5	Q6cbd5 yarrowia li
744	83.5	5.0	446	2	Q9V849	Q9v849 kluyveromyc	817	83	5.0	1030	2	Q7QV30	Q7qv30 giardia lam
745	83.5	5.0	446	2	Q95QJ6	Q95qj6 caenorhabdi	818	83	5.0	1126	2	Q8S6U1	Q8seu1 streptococc
746	83.5	5.0	448	2	Q83FT5	Q83fts tropheryma	819	83	5.0	1183	2	Q8GCD1	Q8gcd1 chloroflexu
747	83.5	5.0	465	2	Q84DR0	Q84dr0 listeria mo	820	83	5.0	1212	2	Q6QR81	Q6qrr81 homo sapien
748	83.5	5.0	476	2	Q7SEJ2	Q7sej2 neurospora	821	83	5.0	1265	2	Q9P2G7	Q9p2g7 homo sapien
749	83.5	5.0	476	2	Q6AYP5	Q6ayp5 rattus norv	822	83	5.0	1686	2	Q7RZE6	Q7rze6 neurospora
750	83.5	5.0	486	1	TNR8_MOUSE	Q84dr1 listeria mo	823	83	5.0	2162	2	Q8N3U0	Q8n3u0 homo sapien
751	83.5	5.0	498	1	TNR8_MOUSE	Q60846 mus musculu	824	83	5.0	2210	2	Q7Z3E7	Q7z3e7 homo sapien
752	83.5	5.0	498	2	Q6C977	Q6c977 yarrowia li	825	83	5.0	2478	2	Q9LCH2	Q9lch2 staphylococ
753	83.5	5.0	506	2	Q7PR64	Q7pr64 anopheles g	826	83	5.0	2478	2	Q9RL69	Q9rl69 staphylococ
754	83.5	5.0	516	2	Q7YVC5	Q7yvc5 cryptospori	827	82.5	5.0	197	2	Q26878	Q26878 trypanosoma
755	83.5	5.0	623	2	Q7XND3	Q7xnd3 oryza sativ	828	82.5	5.0	231	2	Q86LC2	Q86lc2 zoanthus sp
756	83.5	5.0	641	2	Q86SD2	Q86sd2 ciona satis	829	82.5	5.0	252	2	Q6GZ06	Q6gz06 avian pneum
757	83.5	5.0	669	2	Q7EZY9	Q7ezy9 oryza sativ	830	82.5	5.0	258	2	Q7SGP8	Q7sgp8 neurospora
758	83.5	5.0	674	2	Q6APL0	Q6api0 desulfotale	831	82.5	5.0	286	2	Q7SAZ7	Q7saz7 neurospora
759	83.5	5.0	743	2	Q7PQ19	Q7pq19 anopheles g	832	82.5	5.0	290	1	LECR_CLAUJ	Q39527 lecrastis
760	83.5	5.0	791	2	Q66VC3	Q66vc3 equid herpe	833	82.5	5.0	308	2	Q7XA59	Q7xa59 lilium long
761	83.5	5.0	800	2	Q8TFG4	Q8tfg4 schizosacch	834	82.5	5.0	326	2	Q9NFX5	Q9nfx5 ceratitis c

835	82.5	5.0	345	2	Q690V6	Q690v6 anolis sagr	908	82	4.9	529	2	Q7PV84	Q7pv84 anopheles g
836	82.5	5.0	345	2	Q690V7	Q690v7 anolis sagr	909	82	4.9	538	2	Q75JS0	Q75j80 dictyosteli
837	82.5	5.0	345	2	Q690X3	Q690x3 anolis sagr	910	82	4.9	544	2	Q8IG67	Q8ig67 caenorhabdi
838	82.5	5.0	345	2	Q691U6	Q691u6 anolis sagr	911	82	4.9	584	1	CEJ1 CAEEL	Q17802 caenorhabdi
839	82.5	5.0	345	2	Q691Z2	Q691z2 anolis sagr	912	82	4.9	584	2	Q9UL73	Q9ult3 homo sapien
840	82.5	5.0	345	2	Q692A4	Q692a4 anolis sagr	913	82	4.9	599	2	Q9V680	Q9ve80 drosophila
841	82.5	5.0	345	2	Q692C2	Q692c2 anolis sagr	914	82	4.9	601	2	Q9V6S0	Q9ve60 drosophila
842	82.5	5.0	383	1	VE2 HPV57	P22155 human papil	915	82	4.9	630	2	Q6V6YH6	Q6v6yh6 sulfolobus
843	82.5	5.0	389	2	Q64BB8	Q64bb8 uncultured	916	82	4.9	641	2	Q83363	Q83363 murine leuk
844	82.5	5.0	389	2	Q6GX00	Q6gxx0 swine hepat	917	82	4.9	670	2	Q9VWM0	Q9vwm0 gibbon ape
845	82.5	5.0	389	2	Q6GX22	Q6gxx2 swine hepat	918	82	4.9	673	2	Q91VK6	Q91vk6 mus musculu
846	82.5	5.0	389	2	Q6GX33	Q6gxx3 swine hepat	919	82	4.9	693	2	Q27394	Q27394 caenorhabdi
847	82.5	5.0	400	2	Q9SQF7	Q9sqf7 brassica ju	920	82	4.9	720	1	NUP2 YEAST	P32499 saccharomyc
848	82.5	5.0	416	2	Q9K8G4	Q9k8g4 bacillus ha	921	82	4.9	746	2	Q82GM0	Q82gm0 streptomyce
849	82.5	5.0	452	2	Q6CE56	Q6ce56 yarrowia li	922	82	4.9	761	2	Q9C9S3	Q9c9s3 arabidopsis
850	82.5	5.0	456	1	Y883 HAEIN	P44917 haemophilus	923	82	4.9	771	2	Q86NN7	Q86nn7 drosophila
851	82.5	5.0	464	2	Q9C247	Q9c247 neurospora	924	82	4.9	789	2	Q9VY98	Q9vy98 drosophila
852	82.5	5.0	508	2	Q6VNX4	Q6vnx4 drosophila	925	82	4.9	824	2	Q6CY28	Q6cy28 kluyveromyc
853	82.5	5.0	540	1	CH60 STRA3	O8cx22 streptococc	926	82	4.9	846	2	Q57577	Q57577 cynops pyrr
854	82.5	5.0	540	1	CH60 STRA5	O8cx00 streptococc	927	82	4.9	847	2	Q6ZQ82	Q6zq82 mus musculu
855	82.5	5.0	540	2	Q7UPM2	Q7upm2 rhodopirell	928	82	4.9	894	2	Q7FL10	Q7fl10 arabidopsis
856	82.5	5.0	569	2	Q9SL10	Q9sl10 arabidopsis	929	82	4.9	894	2	Q9C8I6	Q9c8i6 arabidopsis
857	82.5	5.0	607	2	Q8GNR4	Q8gnr4 listeria mo	930	82	4.9	911	2	Q8GWK9	Q8gwk9 arabidopsis
858	82.5	5.0	624	2	Q675N1	Q675n1 cornus suet	931	82	4.9	911	2	Q9SAL8	Q9sal8 arabidopsis
859	82.5	5.0	635	2	Q66065	Q66065 fibrobacter	932	82	4.9	926	1	YIY8 SCHPO	Q9uu15 schizosacch
860	82.5	5.0	639	2	Q6E910	Q6e910 listeria mo	933	82	4.9	926	2	Q7LDM3	Q7ldm3 homo sapien
861	82.5	5.0	639	2	Q6E940	Q6e940 listeria mo	934	82	4.9	943	1	YL61 SCHPO	Q8tf99 schizosacch
862	82.5	5.0	686	2	Q8NVE4	Q8nve4 staphylococ	935	82	4.9	957	2	Q9UKN0	Q9ukn0 homo sapien
863	82.5	5.0	698	2	Q74LM8	Q74lm8 lactobacili	936	82	4.9	963	2	Q99MX4	Q99mx4 glaucomya v
864	82.5	5.0	711	2	Q7YX9	Q7yxx9 cryptospori	937	82	4.9	971	2	Q6A036	Q6a036 mus musculu
865	82.5	5.0	726	1	NF11 YEAST	Q12216 saccharomyc	938	82	4.9	972	2	Q7CZHI	Q7czhi agrobacteri
866	82.5	5.0	728	2	Q7NB51	Q7nb51 mycoplasma	939	82	4.9	977	2	Q8UFQ8	Q8ufq8 agrobacteri
867	82.5	5.0	782	2	Q6CNV3	Q6cnv3 kluyveromyc	940	82	4.9	1019	2	Q9V6L9	Q9v6l9 homo sapien
868	82.5	5.0	790	1	AD30 HUMAN	Q9ukf2 homo sapien	941	82	4.9	1021	1	BUB1 YEAST	P41695 saccharomyc
869	82.5	5.0	808	2	Q81123	Q81123 caenorhabdi	942	82	4.9	1023	2	Q7M009	Q7m009 simian cyc
870	82.5	5.0	825	2	Q03088	Q03088 saccharomyc	943	82	4.9	1074	2	Q8C0P8	Q8c0p8 mus musculu
871	82.5	5.0	848	2	Q6GP20	Q6gp20 xenopus lae	944	82	4.9	1083	2	Q06108	Q06108 saccharomyc
872	82.5	5.0	871	1	POB1 SCHPO	Q74653 schizosacch	945	82	4.9	1099	2	Q7TUJ6	Q7tuj6 prochloroco
873	82.5	5.0	876	2	Q6XLI5	Q6xli5 brachydanio	946	82	4.9	1100	1	TCG1 MOUSE	Q8cgf7 mus musculu
874	82.5	5.0	988	2	Q8UVU2	Q8uvu2 xenopus lae	947	82	4.9	1126	2	Q9EQJ9	Q9eqj9 mus musculu
875	82.5	5.0	993	2	Q92JCS	Q92jcs rickettsia	948	82	4.9	1127	2	Q94248	Q94248 caenorhabdi
876	82.5	5.0	1091	2	Q7SDT8	Q7sd8t neurospora	949	82	4.9	1170	2	Q89ZE1	Q89zel mus musculu
877	82.5	5.0	1163	2	Q7PY32	Q7py32 anopheles g	950	82	4.9	1339	2	Q35788	Q35788 rattus norv
878	82.5	5.0	1206	1	FM14 MOUSE	Q05859 mus musculu	951	82	4.9	1423	2	Q6CRU1	Q6cru1 kluyveromyc
879	82.5	5.0	1258	2	Q86IA2	Q86ia2 dictyosteli	952	82	4.9	1564	2	Q95VZ5	Q95vz5 drosophila
880	82.5	5.0	1261	2	Q7R2F4	Q7r2f4 giardia lam	953	82	4.9	1672	1	PMPB CHLMU	Q9pj22 chlamydia m
881	82.5	5.0	1371	2	Q9VU22	Q9vu22 drosophila	954	82	4.9	1854	2	Q7ZA78	Q7za78 candida alb
882	82.5	5.0	1460	1	PMPC CHLMU	Q9pjy1 chlamydia m	955	82	4.9	2981	2	Q6CEB2	Q6ceb2 yarrowia li
883	82.5	5.0	1468	1	FMN1 MOUSE	Q05860 mus musculu	956	82	4.9	3146	2	Q9VUB5	Q9vub5 drosophila
884	82.5	5.0	1472	2	Q6V9R4	Q6v9r4 strongyloce	957	82	4.9	3529	2	Q9GP30	Q9gp30 theileria p
885	82.5	5.0	1478	1	LHN2 BOVIN	Q97817 bos taurus	958	82	4.9	26926	2	Q10466	Q10466 homo sapien
886	82.5	5.0	1969	1	Q7SEZ5	P08ez5 neurospora	959	81.5	4.9	171	1	NUOE BUCBP	Q89au3 buchnera ap
887	82.5	5.0	2311	1	KROS CHICK	Q08941 gallus gall	960	81.5	4.9	234	2	Q6FXA6	Q6fxa6 candida gla
888	82.5	5.0	3295	2	Q6GGT3	Q6ggt3 rattus norv	961	81.5	4.9	235	2	Q9M182	Q9m182 arabidopsis
889	82	4.9	208	2	Q8IWS2	Q8iws2 homo sapien	962	81.5	4.9	245	2	Q7SBI6	Q7abi6 neurospora
890	82	4.9	208	2	Q8N131	Q8n131 homo sapien	963	81.5	4.9	273	2	Q6JK85	Q6jk85 neodiprion
891	82	4.9	236	2	Q9LM00	Q9lm00 pinus taeda	964	81.5	4.9	345	2	Q690T8	Q690t8 anolis sagr
892	82	4.9	250	2	Q8FSI6	Q8fsi6 corynebacte	965	81.5	4.9	345	2	Q690U2	Q690u2 anolis sagr
893	82	4.9	255	2	Q811N1	Q811n1 drosophila	966	81.5	4.9	345	2	Q890U5	Q890u5 anolis sagr
894	82	4.9	260	2	Q27007	Q27007 methanobact	967	81.5	4.9	345	2	Q690U6	Q690u6 anolis sagr
895	82	4.9	282	2	Q9FSR0	Q9fsr0 oryza sativ	968	81.5	4.9	345	2	Q690U8	Q690u8 anolis sagr
896	82	4.9	323	2	Q9W1I7	Q9w1i7 drosophila	969	81.5	4.9	345	2	Q690V1	Q690v1 anolis sagr
897	82	4.9	328	2	Q8T8J5	Q8t8j5 drosophila	970	81.5	4.9	345	2	Q690W8	Q690w8 anolis sagr
898	82	4.9	339	2	Q9VUX8	Q9vux8 drosophila	971	81.5	4.9	345	2	Q690X6	Q690x6 anolis sagr
899	82	4.9	345	2	Q690W9	Q690w9 anolis sagr	972	81.5	4.9	345	2	Q690X8	Q690x8 anolis sagr
900	82	4.9	345	2	Q691G8	Q691g8 anolis sagr	973	81.5	4.9	345	2	Q691Q6	Q691q6 anolis sagr
901	82	4.9	385	2	Q8T8K9	Q8t8k9 drosophila	974	81.5	4.9	345	2	Q691T7	Q691t7 anolis sagr
902	82	4.9	385	2	Q8T8L2	Q8t8l2 drosophila	975	81.5	4.9	345	2	Q691U4	Q691u4 anolis sagr
903	82	4.9	389	2	Q76573	Q76573 caenorhabdi	976	81.5	4.9	345	2	Q691Y0	Q691y0 anolis sagr
904	82	4.9	410	1	LMP2 HUMAN	P13473 homo sapien	977	81.5	4.9	345	2	Q691Y1	Q691y1 anolis sagr
905	82	4.9	411	2	Q6QJG8	Q6qjg8 homo sapien	978	81.5	4.9	368	2	Q864C4	Q864c4 delphinus d
906	82	4.9	477	1	MYPH HUMAN	Q13203 homo sapien	979	81.5	4.9	369	2	O65249	O65249 arabidopsis
907	82	4.9	483	2	Q9W4M2	Q9w4m2 drosophila	980	81.5	4.9	386	2	Q97G38	Q97g38 clostridium

981	81.5	4.9	388	2	Q7Q1W8	Q7q1w8 anopheles g	1054	81	4.9	831	2	Q6BMH2	Q6bmh2 debaromyce
982	81.5	4.9	390	2	Q6PND6	Q6pnd6 emericeella	1055	81	4.9	855	1	CLOC_MOUSE	Q08785 mus musculus
983	81.5	4.9	410	2	Q9UD93	Q9ud93 homo sapien	1056	81	4.9	857	2	QSZQD6	Q6zqd6 mus musculus
984	81.5	4.9	412	2	Q9P603	Q9p603 neurospora	1057	81	4.9	904	2	Q8IWC1	Q8iwc1 homo sapien
985	81.5	4.9	432	2	Q6NUR0	Q6nur0 homo sapien	1058	81	4.9	911	2	Q7Q143	Q7q143 anopheles g
986	81.5	4.9	432	2	Q7Y0E4	Q7y0e4 oryza sativ	1059	81	4.9	941	2	Q7Z5R7	Q7z5r7 homo sapien
987	81.5	4.9	438	2	Q6INH8	Q6inh8 xenopus lae	1060	81	4.9	948	2	Q8NDA4	Q8nda4 homo sapien
988	81.5	4.9	463	2	Q9K1H4	Q9k1h4 neisseria m	1061	81	4.9	1047	2	Q24019	Q24019 drosophila
989	81.5	4.9	551	2	Q7E436	Q7e436 neurospora	1062	81	4.9	1128	1	BEM3_YEAST	Q32873 saccharomyc
990	81.5	4.9	567	2	Q6PR51	Q6fr51 candida gla	1063	81	4.9	1163	2	Q86ARI	Q8ear1 dictyosteli
991	81.5	4.9	599	2	Q9U3W0	Q9u3w0 drosophila	1064	81	4.9	1169	1	YK82_YEAST	P36170 saccharomyc
992	81.5	4.9	636	1	YR6E_YEAST	P53882 saccharomyc	1065	81	4.9	1223	2	Q6ZS17	Q6zsl7 homo sapien
993	81.5	4.9	687	1	SRB4_YEAST	P32569 saccharomyc	1066	81	4.9	1322	1	FLO9_YEAST	P39712 saccharomyc
994	81.5	4.9	687	2	Q6B1B4	Q6b1b4 saccharomyc	1067	81	4.9	1502	2	Q8IS10	Q8is10 dictyosteli
995	81.5	4.9	838	2	Q7OC91	Q7oc91 anopheles g	1068	81	4.9	1569	2	Q8W4X9	Q8w4x9 homo sapien
996	81.5	4.9	846	2	Q6ZKY0	Q6zky0 oryza sativ	1069	81	4.9	1609	1	FIG2_YEAST	P25653 saccharomyc
997	81.5	4.9	860	1	MUTS_LISIN	Q92bv3 listeria in	1070	81	4.9	1625	2	Q6MVD4	Q6mvd4 neurospora
998	81.5	4.9	869	2	Q01262	Q01262 caenorhabdi	1071	81	4.9	1657	2	Q76NT8	Q76nt8 dictyosteli
999	81.5	4.9	873	2	Q9W468	Q9w468 drosophila	1072	81	4.9	1709	2	Q86L43	Q86l43 dictyosteli
1000	81.5	4.9	880	1	PHTF_DROME	Q7v9a8 drosophila	1073	81	4.9	1800	2	Q8IEI9	Q8ie19 plasmodium
1001	81.5	4.9	913	2	Q7NP28	Q7np28 gloebacter	1074	81	4.9	2060	2	Q8MZK8	Q8mzk8 homo sapien
1002	81.5	4.9	917	2	Q7RA65	Q7ra65 plasmodium	1075	81	4.9	2282	1	ZAN_RABIT	P57999 cryotolagus
1003	81.5	4.9	976	2	Q6NTV5	Q6ntv5 xenopus lae	1076	81	4.9	2727	2	Q6NR00	Q6nr00 drosophila
1004	81.5	4.9	980	1	SLK3_MOUSE	Q810b9 mus musculus	1077	81	4.9	2727	2	Q9VL06	Q9vl06 drosophila
1005	81.5	4.9	980	2	Q9WA13	Q9ma13 arabidopsis	1078	81	4.9	2977	2	Q9VAP9	Q9vap9 drosophila
1006	81.5	4.9	1142	2	Q6CCL7	Q6ccl7 yarrowia li	1079	81	4.9	5017	2	Q63DF3	Q63df3 bacillus ce
1007	81.5	4.9	1151	1	FOG2_MOUSE	Q8ech7 mus musculus	1080	80.5	4.9	148	1	SY02_RAT	P14844 rattus norv
1008	81.5	4.9	1206	1	BUN2_DROME	Q24523 drosophila	1081	80.5	4.9	165	2	Q26877	Q26877 trypanosoma
1009	81.5	4.9	1216	1	YPX5_CABEL	Q09277 caenorhabdi	1082	80.5	4.9	242	2	Q86RS8	Q86rs8 caenorhabdi
1010	81.5	4.9	1320	2	Q9GKF5	Q9gkf5 homo sapien	1083	80.5	4.9	326	2	Q7SCU5	Q7scj5 neurospora
1011	81.5	4.9	1419	1	ALAI1_CANAL	Q13368 candida alb	1084	80.5	4.9	334	2	Q6VAV6	Q6vav6 anopheles g
1012	81.5	4.9	1445	1	PTPG_HUMAN	P23470 homo sapien	1085	80.5	4.9	345	2	Q8WD11	Q8wd11 anolis sagr
1013	81.5	4.9	1481	2	Q6BWS6	Q6bws6 debaromyce	1086	80.5	4.9	345	2	Q690T5	Q690t5 anolis sagr
1014	81.5	4.9	1500	2	Q6AUV2	Q6auv2 oryza sativ	1087	80.5	4.9	345	2	Q690U7	Q690u7 anolis sagr
1015	81.5	4.9	1536	2	Q86AL7	Q86al7 dictyosteli	1088	80.5	4.9	345	2	Q690U0	Q690u0 anolis sagr
1016	81.5	4.9	2063	2	Q7RQL1	Q7rgl1 plasmodium	1089	80.5	4.9	345	2	Q690U1	Q690u1 anolis sagr
1017	81.5	4.9	2282	2	Q6SNP9	Q6snp9 mus musculus	1090	80.5	4.9	345	2	Q690U3	Q690u3 anolis sagr
1018	81.5	4.9	2338	2	Q629N6	Q629n6 burkholderi	1091	80.5	4.9	345	2	Q690V2	Q690v2 anolis sagr
1019	81	4.9	184	2	Q7BPK1	Q7bpk1 anopheles g	1092	80.5	4.9	345	2	Q690W5	Q690w5 anolis sagr
1020	81	4.9	218	2	Q7Z3K1	Q7z3k1 homo sapien	1093	80.5	4.9	345	2	Q691G5	Q691g5 anolis sagr
1021	81	4.9	267	2	Q6FXC3	Q6fxc3 candida gla	1094	80.5	4.9	345	2	Q691M1	Q691m1 anolis sagr
1022	81	4.9	301	2	Q924G0	Q924g0 cratogeomys	1095	80.5	4.9	345	2	Q691R1	Q691r1 anolis sagr
1023	81	4.9	315	2	Q7VXK1	Q7vxk1 drosophila	1096	80.5	4.9	345	2	Q691U7	Q691u7 anolis sagr
1024	81	4.9	349	2	Q7XEC9	Q7xec9 oryza sativ	1097	80.5	4.9	345	2	Q692A0	Q692a0 anolis sagr
1025	81	4.9	355	2	Q9NP13	Q9np13 homo sapien	1098	80.5	4.9	345	2	Q692A2	Q692a2 anolis sagr
1026	81	4.9	370	2	Q9FN39	Q9fn39 arabidopsis	1099	80.5	4.9	345	2	Q692A3	Q692a3 anolis sagr
1027	81	4.9	370	2	Q9YIT4	Q9yyt4 mouse endog	1100	80.5	4.9	356	2	Q6CNP5	Q6cnp5 kluyveromyc
1028	81	4.9	384	2	Q702Z1	Q702z1 human herpe	1101	80.5	4.9	358	2	Q8MRL6	Q8mrl6 drosophila
1029	81	4.9	385	2	Q8T8J7	Q8t8j7 drosophila	1102	80.5	4.9	364	2	Q62799	Q62799 tursiops tr
1030	81	4.9	385	2	Q8T8K0	Q8t8k0 drosophila	1103	80.5	4.9	366	2	Q75AD7	Q75ad7 ashbya goss
1031	81	4.9	411	2	Q8DVK6	Q8dvx6 streptococc	1104	80.5	4.9	388	2	Q6CRL0	Q6crl0 kluyveromyc
1032	81	4.9	413	2	Q53974	Q53974 streptococc	1105	80.5	4.9	391	1	VZ2_HPV2A	P25482 human papil
1033	81	4.9	422	1	SYT2_RAT	P29101 rattus norv	1106	80.5	4.9	395	2	Q6CAU7	Q6cau7 yarrowia li
1034	81	4.9	428	2	Q7SPW2	Q7spw2 human betar	1107	80.5	4.9	399	2	Q6SX73	Q6sx73 human cytom
1035	81	4.9	431	1	MNS1_MACFA	Q95kg7 macaca fasc	1108	80.5	4.9	402	2	Q9N503	Q9n503 caenorhabdi
1036	81	4.9	437	2	Q7XPL0	Q7xpl0 oryza sativ	1109	80.5	4.9	410	1	LWP2_CRIGR	P49130 cricetus
1037	81	4.9	446	2	Q9U137	Q9u137 leishmania	1110	80.5	4.9	441	2	Q9U2W3	Q9u2w3 caenorhabdi
1038	81	4.9	489	2	Q95Q80	Q95q80 caenorhabdi	1111	80.5	4.9	478	2	Q61122	Q61122 dictyosteli
1039	81	4.9	495	2	Q6MRG4	Q6mr94 bdellovibri	1112	80.5	4.9	487	2	Q96601	Q96601 plasmodium
1040	81	4.9	497	2	Q8MY24	Q8my24 homo sapien	1113	80.5	4.9	540	1	CH60_STRAG	Q9ame7 streptococc
1041	81	4.9	503	2	Q95Q82	Q95q82 caenorhabdi	1114	80.5	4.9	541	2	O15681	O15681 toxoplasma
1042	81	4.9	562	2	Q8IEJ5	Q8iej5 plasmodium	1115	80.5	4.9	543	2	Q20720	Q20720 caenorhabdi
1043	81	4.9	626	2	Q8IGQ7	Q8igq7 drosophila	1116	80.5	4.9	547	2	Q8IV81	Q8iv81 homo sapien
1044	81	4.9	634	1	HWF1_CANAL	P46597 candida alb	1117	80.5	4.9	552	2	Q89JG4	Q89jg4 oryza sativ
1045	81	4.9	637	2	Q7TSS5	Q7tss5 rattus norv	1118	80.5	4.9	573	2	Q8T0R9	Q8t0r9 drosophila
1046	81	4.9	642	2	Q75JG6	Q75jg6 dictyosteli	1119	80.5	4.9	581	2	Q7R0Z5	Q7r0z5 giardia lam
1047	81	4.9	651	1	VU47_HHV6U	Q06093 human herpe	1120	80.5	4.9	591	2	Q6K4S0	Q6k4s0 oryza sativ
1048	81	4.9	668	2	Q6FWR2	Q6fwr2 candida gla	1121	80.5	4.9	592	2	Q23036	Q23036 caenorhabdi
1049	81	4.9	670	2	Q70653	Q70653 gibbon ape	1122	80.5	4.9	595	1	DNAK_MYCHO	Q9ze10 mycoplasma
1050	81	4.9	683	2	O24424	O24424 papaver som	1123	80.5	4.9	595	2	TNR8_HUMAN	T28908 homo sapien
1051	81	4.9	683	2	Q9SK94	Q9sk94 arabidopsis	1124	80.5	4.9	658	2	Q8MQZ8	Q8mqz8 drosophila
1052	81	4.9	759	2	O05143	O05143 ruminococcu	1125	80.5	4.9	668	2	Q75CS6	Q75cs6 ashbya goss
1053	81	4.9	802	2	Q7YVP9	Q7yvp9 trypanosoma	1126	80.5	4.9	672	2	Q7SFD8	Q7sfd8 neurospora

1127	80.5	4.9	676	2	Q9VB94	Q9vb94 drosophila	1200	80	4.8	683	2	Q8MRH5	Q8mrh5 drosophila
1128	80.5	4.9	706	2	Q9VNZ5	Q9vnz5 drosophila	1201	80	4.8	688	1	SLP2_CLOTH	Q06953 clostridium
1129	80.5	4.9	747	2	Q7S8F0	Q7s8f0 neurospora	1202	80	4.8	698	2	Q8JUG8	Q8jkg8 heliothis z
1130	80.5	4.9	754	2	Q7NB52	Q7nb52 mycoplasma	1203	80	4.8	725	1	AGAL_YEAST	P32223 saccharomyc
1131	80.5	4.9	758	2	Q9T214	Q9t214 caenorhabdi	1204	80	4.8	729	2	Q8OWY2	Q8owt2 mus musculu
1132	80.5	4.9	760	2	Q6RJF7	Q6rjf7 homo sapien	1205	80	4.8	732	2	Q8OWY1	Q8owt1 mus musculu
1133	80.5	4.9	765	2	Q7S127	Q7s127 oryza sativ	1206	80	4.8	733	2	Q811D2	Q811d2 mus musculu
1134	80.5	4.9	805	2	Q6C980	Q6c980 yarrowia li	1207	80	4.8	743	2	Q95RK9	Q95rk9 drosophila
1135	80.5	4.9	832	2	Q8KOC2	Q8koc2 mus musculu	1208	80	4.8	743	2	Q6G0S0	Q960s0 drosophila
1136	80.5	4.9	860	2	Q712R7	Q712r7 listeria mo	1209	80	4.8	747	2	Q8CCZ1	Q8ccz1 mus musculu
1137	80.5	4.9	879	2	Q91SD0	Q91sd0 canine heyrp	1210	80	4.8	772	2	Q82YF8	Q82yf8 streptomyc
1138	80.5	4.9	918	1	GLK1_HUMAN	P39086 homo sapien	1211	80	4.8	782	2	Q7R2Z3	Q7r2z3 giardia lam
1139	80.5	4.9	919	2	Q76EQ4	Q76eq4 streptococc	1212	80	4.8	787	2	Q9VEY6	Q9vey6 drosophila
1140	80.5	4.9	921	1	SFRB_HUMAN	Q12872 homo sapien	1213	80	4.8	789	2	Q7PDP0	Q7pdp0 plasmodium
1141	80.5	4.9	962	1	Q7PFG9	Q7pfg9 anopheles g	1214	80	4.8	849	2	P87107	P87107 saccharomyc
1142	80.5	4.9	983	2	Q8G204	Q8g204 arabidopsia	1215	80	4.8	870	2	Q824X2	Q824x2 chlamydomophi
1143	80.5	4.9	989	1	ALS3_CANAL	Q74623 candida alb	1216	80	4.8	873	2	Q9NYU3	Q9nyu3 homo sapien
1144	80.5	4.9	1119	2	Q92E44	Q9ze44 rickettsia	1217	80	4.8	881	1	PRY3_YEAST	P47033 saccharomyc
1145	80.5	4.9	1124	2	Q86AL9	Q86al9 dictyosteli	1218	80	4.8	882	2	Q9VA36	Q9va36 drosophila
1146	80.5	4.9	1155	2	Q7KR63	Q7kr63 drosophila	1219	80	4.8	902	2	Q8Q7H5	Q8q7h5 human immun
1147	80.5	4.9	1159	1	RRPO_ROTGI	P35942 rotavirus (1220	80	4.8	916	2	Q9W4A6	Q9w4a6 drosophila
1148	80.5	4.9	1163	1	COAA_BACTF	Q9x597 bacillus th	1221	80	4.8	933	2	Q61RA7	Q61ra7 xenopus lae
1149	80.5	4.9	1179	2	Q9JK71	Q9jk71 rattus norv	1222	80	4.8	979	2	Q6BTQ3	Q6btq3 debaryomyce
1150	80.5	4.9	1184	2	Q6F3A8	Q6f3a8 oryza sativ	1223	80	4.8	982	2	Q6CGV5	Q6cgv5 yarrowia li
1151	80.5	4.9	1245	2	Q7Q947	Q7q947 anopheles g	1224	80	4.8	1008	2	Q6FM15	Q6fm15 candida gla
1152	80.5	4.9	1297	2	Q8SSS5	Q8sss5 dictyosteli	1225	80	4.8	1012	1	PPOL_MOUSE	P11103 mus musculu
1153	80.5	4.9	1342	2	Q8A0H1	Q8a0h1 bacteroides	1226	80	4.8	1047	2	Q9VZH2	Q9vzh2 drosophila
1154	80.5	4.9	1367	2	Q9SPB6	Q9sfb6 arabidopsia	1227	80	4.8	1150	2	Q9HBC4	Q9hbc4 homo sapien
1155	80.5	4.9	1372	2	Q8SX99	Q8sx99 drosophila	1228	80	4.8	1153	2	Q9V6J8	Q9v6j8 drosophila
1156	80.5	4.9	1372	2	Q9VNA6	Q9vna6 drosophila	1229	80	4.8	1168	2	Q9VZE8	Q9vze8 drosophila
1157	80.5	4.9	1743	2	Q811M4	Q811m4 plasmodium	1230	80	4.8	1197	2	Q6CDS2	Q6cds2 yarrowia li
1158	80.5	4.9	1752	2	Q869Q7	Q869q7 dictyosteli	1231	80	4.8	1207	2	Q81174	Q81174 drosophila
1159	80.5	4.9	1984	2	Q7QRS1	Q7qrs1 giardia lam	1232	80	4.8	1209	2	Q6SZU2	Q6szu2 mus musculu
1160	80.5	4.9	2162	2	Q7OPP2	Q7opp2 drosophila	1233	80	4.8	1226	2	Q9NZB6	Q9nzb6 homo sapien
1161	80.5	4.9	2225	2	Q4S881	Q4s881 caenorhabdi	1234	80	4.8	1240	2	Q7TQM8	Q7tqm8 mus musculu
1162	80.5	4.9	3218	2	Q9W3V6	Q9w3v6 drosophila	1235	80	4.8	1248	2	Q8BWH3	Q8bwh3 mus musculu
1163	80	4.8	103	2	Q46380	Q46380 oryctolagus	1236	80	4.8	1325	2	Q9BKV7	Q9bkv7 leishmania
1164	80	4.8	153	1	FIT2_YEAST	Q08906 saccharomyc	1237	80	4.8	1469	2	Q7S353	Q7s353 neurospora
1165	80	4.8	174	2	Q64EZ1	Q64ez1 tenebrio mo	1238	80	4.8	1486	2	Q9SRE5	Q9sre5 drosophila
1166	80	4.8	177	1	ARG1_YEAST	P07249 saccharomyc	1239	80	4.8	1486	2	Q967Y2	Q967y2 drosophila
1167	80	4.8	231	2	Q9CY44	Q9cy44 mus musculu	1240	80	4.8	1486	2	Q7KR7	Q7krp7 drosophila
1168	80	4.8	242	2	Q9VDN0	Q9vdn0 drosophila	1241	80	4.8	1582	2	Q7KR7	Q7krp7 drosophila
1169	80	4.8	250	2	Q9HFS1	Q9hfs1 candida alb	1242	80	4.8	1693	1	SAS_DROME	Q04164 drosophila
1170	80	4.8	251	2	Q674L5	Q674l5 human respi	1243	80	4.8	1721	2	Q8SSQ0	Q8ssq0 dictyosteli
1171	80	4.8	257	2	Q77KZ8	Q77kz8 bovine resp	1244	80	4.8	1761	2	Q7KTF6	Q7ktf6 drosophila
1172	80	4.8	257	2	Q9XS25	Q9xs25 bovine resp	1245	80	4.8	1845	2	Q86JH8	Q86jh8 dictyosteli
1173	80	4.8	261	1	EMCN_HUMAN	Q9ulc0 homo sapien	1246	80	4.8	2154	2	Q8WZ51	Q8wz51 homo sapien
1174	80	4.8	272	2	Q6ZSN5	Q6zen5 homo sapien	1247	80	4.8	2616	1	NDL_DROME	P98159 drosophila
1175	80	4.8	283	2	Q6CIR8	Q6cir8 kluyveromyc	1248	80	4.8	2828	2	Q6MMK5	Q6mmk5 bdellovibri
1176	80	4.8	301	2	Q6L4D1	Q6l4d1 oryza sativ	1249	80	4.8	3410	2	Q7TN00	Q7tn00 rattus norv
1177	80	4.8	325	2	Q25936	Q25936 plasmodium	1250	80	4.8	3493	2	Q39734	Q39734 sweet potat
1178	80	4.8	329	2	Q8JFF6	Q8jff6 xenopus lae	1251	80	4.8	10791	2	Q7U7M8	Q7u7m8 synecococc
1179	80	4.8	334	2	Q6VAM0	Q6vaw0 anopheles g	1252	80	4.8	26926	2	Q8WZB3	Q8wzb3 homo sapien
1180	80	4.8	345	2	Q6Z224	Q6z224 caenorhabdi	1253	80	4.8	34350	2	Q8WZ42	Q8wz42 homo sapien
1181	80	4.8	345	2	Q9X0W7	Q9x0w7 anolis sagr	1254	79.5	4.8	80	2	Q7MSR8	Q7msr8 wolinnella s
1182	80	4.8	359	2	Q9XZT0	Q9xzt0 drosophila	1255	79.5	4.8	123	2	O15773	O15773 trypanosoma
1183	80	4.8	374	2	Q9GNC5	Q9gnc5 homo sapien	1256	79.5	4.8	129	2	Q5UNH4	Q5unh4 ictalurus p
1184	80	4.8	415	2	Q8YR34	Q8yr34 anabaena sp	1257	79.5	4.8	151	2	Q75QC1	Q75qc1 locus japon
1185	80	4.8	449	2	Q9VKS4	Q9vks4 drosophila	1258	79.5	4.8	152	2	Q8IG73	Q8ig73 caenorhabdi
1186	80	4.8	451	2	Q9S144	Q9s144 cercopithe	1259	79.5	4.8	161	2	Q61GP4	Q61gp4 drosophila
1187	80	4.8	468	1	VAS1_BOVIN	P40682 bos taurus	1260	79.5	4.8	165	1	H1_TETPY	P12305 tetrahymena
1188	80	4.8	472	2	Q8KWT3	Q8kwt3 bacillus su	1261	79.5	4.8	194	2	Q9Y9W0	Q9y9w0 aeropyrum p
1189	80	4.8	473	2	Q21052	Q21052 caenorhabdi	1262	79.5	4.8	199	2	Q6C3G4	Q6c3g4 yarrowia li
1190	80	4.8	486	2	Q53630	Q53630 staphylococ	1263	79.5	4.8	213	2	Q8ZU27	Q8zu27 homo sapien
1191	80	4.8	486	2	Q6GGT1	Q6ggt1 staphylococ	1264	79.5	4.8	232	2	Q69EW2	Q69ew2 streptococc
1192	80	4.8	521	2	Q04383	Q04383 saccharomyc	1265	79.5	4.8	257	2	Q9N5S7	Q9n5s7 caenorhabdi
1193	80	4.8	549	2	Q7VHX1	Q7vbx1 mus musculu	1266	79.5	4.8	269	2	Q7TTU8	Q7ttu8 synecococc
1194	80	4.8	555	2	Q7REM0	Q7rem0 plasmodium	1267	79.5	4.8	272	2	Q8A3G1	Q8a3g1 bacteroides
1195	80	4.8	600	2	Q8C692	Q8c692 mus musculu	1268	79.5	4.8	299	2	Q8EH39	Q8eh39 respiratory
1196	80	4.8	634	2	Q8JFF5	Q8jff5 xenopus lae	1269	79.5	4.8	316	2	Q8BEK1	Q8bek1 cowpox viru
1197	80	4.8	650	2	Q9U0U5	Q9uu05 schizosacch	1270	79.5	4.8	326	2	Q6CV42	Q6cv42 kluyveromyc
1198	80	4.8	657	2	Q6AM00	Q6am00 desulfotale	1271	79.5	4.8	328	2	Q9TXC7	Q9txc7 drosophila
1199	80	4.8	667	1	CYL1_BOVIN	P35662 bos taurus	1272	79.5	4.8	333	2	Q6VAV7	Q6vav7 anopheles g

1273	79.5	4.8	344	2	Q691Z8	Q691z8 anolis sagr	1346	79.5	4.8	1441	2	Q8S628	Q8s628 oryza sativ
1274	79.5	4.8	345	2	Q690W1	Q690w1 anolis sagr	1347	79.5	4.8	1441	2	Q8GU94	Q8gu94 oryza sativ
1275	79.5	4.8	345	2	Q690X0	Q690x0 anolis sagr	1348	79.5	4.8	1443	2	Q9Y8F2	Q9y8f2 candida alb
1276	79.5	4.8	345	2	Q691G9	Q691g9 anolis sagr	1349	79.5	4.8	1444	2	Q94KE2	Q94ke2 arabidopsis
1277	79.5	4.8	345	2	Q691U8	Q691u8 anolis sagr	1350	79.5	4.8	1445	2	Q94HN8	Q94hn8 oryza sativ
1278	79.5	4.8	345	2	Q692A8	Q692a8 anolis sagr	1351	79.5	4.8	1445	2	Q7XGK2	Q7xgk2 oryza sativ
1279	79.5	4.8	354	2	Q25402	Q25402 litomoeide	1352	79.5	4.8	1459	1	LHN2_HUMAN	Q95490 homo sapien
1280	79.5	4.8	373	2	Q76810	Q76810 litomoeide	1353	79.5	4.8	1532	2	Q9LJW1	Q9ljlw1 arabidopsis
1281	79.5	4.8	384	2	Q882D3	Q882d3 anopheles g	1354	79.5	4.8	1532	2	Q6PMR4	Q6pmr4 swine hepat
1282	79.5	4.8	385	2	Q8T8L4	Q8t8l4 drosophila	1355	79.5	4.8	1806	2	Q869R4	Q869r4 dictyosteli
1283	79.5	4.8	403	2	Q8MVA9	Q8mva9 ixodes scap	1356	79.5	4.8	1873	2	Q6S003	Q6s003 dictyosteli
1284	79.5	4.8	425	2	Q7RSR5	Q7rsr5 plasmodium	1357	79.5	4.8	2359	2	Q81519	Q81519 plasmodium
1285	79.5	4.8	429	2	Q93ZM7	Q93zm7 arabidopsis	1358	79.5	4.8	2623	2	Q6WRI0	Q6wri0 homo sapien
1286	79.5	4.8	433	2	Q88VCO	Q88vc0 lactobacill	1359	79.5	4.8	3365	2	Q6XHA7	Q6xha7 dictyosteli
1287	79.5	4.8	457	2	Q81VS6	Q81vs6 homo sapien	1360	79.5	4.8	3550	2	Q66GT4	Q66gt4 rattus norv
1288	79.5	4.8	461	1	TR1B_HUMAN	P20333 h tumor nec	1361	79.5	4.8	5017	2	Q6HKW5	Q6hkw5 bacillus th
1289	79.5	4.8	480	2	Q84DS4	Q84ds4 listeria mo	1362	79.5	4.8	6458	2	Q7QZA9	Q7qza9 dirosophila
1290	79.5	4.8	480	2	Q84DS5	Q84ds5 listeria mo	1363	79.5	4.8	2015	2	Q81Q18	Q81q18 drosophila
1291	79.5	4.8	495	2	Q9CV82	Q9cv82 mus musculu	1364	79	4.8	146	2	Q6FIU3	Q6fiu3 candida gla
1292	79.5	4.8	504	2	Q8VYJ6	Q8vyj6 arabidopsis	1365	79	4.8	195	2	Q94VJ3	Q94vj3 drosophila
1293	79.5	4.8	509	1	AIOL_HUMAN	Q9ukt9 homo sapien	1366	79	4.8	202	2	Q7XLD8	Q7xld8 oryza sativ
1294	79.5	4.8	510	2	Q9JUS7	Q9j577 chlamydia p	1367	79	4.8	204	2	Q7M5K8	Q7m5k8 smian aden
1295	79.5	4.8	510	2	Q9JUS9	Q9j577 chlamydia p	1368	79	4.8	211	2	Q6DF90	Q6df90 xenopus lae
1296	79.5	4.8	511	2	Q8UYA8	Q8uya8 human herpe	1369	79	4.8	214	1	H11_HUMAN	Q02539 homo sapien
1297	79.5	4.8	511	2	Q8UZ60	Q8uz60 human herpe	1370	79	4.8	215	2	Q98TQ9	Q98tq9 gallus gall
1298	79.5	4.8	511	2	Q8UZ61	Q8uz61 human herpe	1371	79	4.8	249	2	Q9SJQ4	Q9sjq4 arabidopsis
1299	79.5	4.8	511	2	Q8UZ64	Q8uz64 human herpe	1372	79	4.8	267	2	Q8R0H4	Q8r0h4 mus musculu
1300	79.5	4.8	511	2	Q8UZ66	Q8uz66 human herpe	1373	79	4.8	308	2	Q74KF4	Q74kf4 lactobacill
1301	79.5	4.8	511	2	Q8UF27	Q8uf27 human herpe	1374	79	4.8	317	2	Q8BEK2	Q8bek2 cowpox viru
1302	79.5	4.8	530	2	Q6F107	Q6f107 mesoplasma	1375	79	4.8	333	2	Q6VAV8	Q6vav8 anopheles g
1303	79.5	4.8	534	2	Q80853	Q80853 arabidopsis	1376	79	4.8	340	2	Q82KQ1	Q82kq1 salmonella
1304	79.5	4.8	540	1	CH60_STRSA	Q8kj16 streptococc	1377	79	4.8	345	2	Q691V5	Q691v5 anolis sagr
1305	79.5	4.8	545	2	Q8BEX1	Q8eex1 shewanella	1378	79	4.8	352	2	Q49782	Q49782 arabidopsis
1306	79.5	4.8	552	2	Q9LJBO	Q9ljbo arabidopsis	1379	79	4.8	353	2	Q8VPM3	Q8vpm3 micrococcu
1307	79.5	4.8	552	1	NFL_BOVIN	P02548 bos taurus	1380	79	4.8	374	2	Q8TAY8	Q8tay8 homo sapien
1308	79.5	4.8	560	2	Q87LX9	Q87lx9 vibrio para	1381	79	4.8	374	2	Q96NF3	Q96nf3 homo sapien
1309	79.5	4.8	572	2	Q9LRW0	Q9lrw0 arabidopsis	1382	79	4.8	382	2	Q6UX15	Q6ux15 homo sapien
1310	79.5	4.8	580	2	Q19315	Q19315 caenorhabdi	1383	79	4.8	392	2	Q82JV1	Q82jv1 streptomyce
1311	79.5	4.8	581	2	Q9VVG9	Q9vv99 drosophila	1384	79	4.8	417	2	Q15828	Q15828 leishmania
1312	79.5	4.8	602	2	Q8SY16	Q8sy16 drosophila	1385	79	4.8	447	2	Q8BIY6	Q8biy6 mus musculu
1313	79.5	4.8	612	2	Q9NVJ6	Q9nvj6 homo sapien	1386	79	4.8	459	2	Q9H915	Q9h915 homo sapien
1314	79.5	4.8	689	2	Q7QN60	Q7qn60 anopheles g	1387	79	4.8	461	2	Q9LH91	Q9lh91 arabidopsis
1315	79.5	4.8	689	2	Q8HYW1	Q8hyw1 bos taurus	1388	79	4.8	482	2	Q76740	Q76740 dictyosteli
1316	79.5	4.8	693	2	Q01600	Q01600 caenorhabdi	1389	79	4.8	492	2	Q94HR9	Q94hr9 arabidopsis
1317	79.5	4.8	721	2	Q86171	Q86171 clostridium	1390	79	4.8	534	2	Q94317	Q94317 schizosacch
1318	79.5	4.8	729	2	Q95RU5	Q95ru5 drosophila	1391	79	4.8	534	2	Q86AL2	Q86al2 dictyosteli
1319	79.5	4.8	752	2	Q640L3	Q640l3 mus musculu	1392	79	4.8	549	2	Q8VBY3	Q8vby3 mus musculu
1320	79.5	4.8	756	2	Q62985	Q62985 rattus norv	1393	79	4.8	554	2	Q8CCJ9	Q8ccj9 mus musculu
1321	79.5	4.8	796	2	Q8MRG9	Q8mr99 drosophila	1394	79	4.8	555	2	Q9VH46	Q9vh46 drosophila
1322	79.5	4.8	796	2	Q9VTR4	Q9vtr4 drosophila	1395	79	4.8	559	1	NUPL_MOUSE	Q8k2k6 mus musculu
1323	79.5	4.8	827	2	Q9SZ08	Q9sz08 arabidopsis	1396	79	4.8	575	2	Q62223	Q62223 caenorhabdi
1324	79.5	4.8	860	1	MUTS_LISMO	Q8y789 listeria mo	1397	79	4.8	594	2	Q6PAN1	Q6pan1 mus musculu
1325	79.5	4.8	867	2	Q6BTV1	Q6bty1 debaryomyce	1398	79	4.8	608	2	Q6F3B7	Q6f3b7 oryza sativ
1326	79.5	4.8	873	2	Q9Y076	Q9y076 leishmania	1399	79	4.8	611	2	Q92EE6	Q92ee6 listeria in
1327	79.5	4.8	887	2	Q6XD56	Q6xd56 gallus gall	1400	79	4.8	626	2	Q8KUUS	Q8kuus synechococc
1328	79.5	4.8	972	2	Q9VFU8	Q9vfus drosophila	1401	79	4.8	644	2	Q817L0	Q817l0 caenorhabdi
1329	79.5	4.8	980	2	Q6NZM5	Q6nzm5 mus musculu	1402	79	4.8	644	2	Q85510	Q85510 xenotrophic
1330	79.5	4.8	985	2	Q67643	Q67643 gallid herp	1403	79	4.8	648	2	Q895B6	Q895b6 clostridium
1331	79.5	4.8	998	1	PPOL_XENLA	P31669 xenopus lae	1404	79	4.8	649	2	Q8JGN6	Q8jgn6 xenopus lae
1332	79.5	4.8	1011	2	Q9XVR0	Q9xvr0 caenorhabdi	1405	79	4.8	692	1	FIS2_ARATH	Q92nt9 arabidopsis
1333	79.5	4.8	1125	2	Q9H2V6	Q9h2v6 homo sapien	1406	79	4.8	702	2	Q6BHB3	Q6bbb3 debaryomyce
1334	79.5	4.8	1137	2	Q6CEC1	Q6cccl1 yarrowia li	1407	79	4.8	710	1	Y026_YEAST	P39744 saccharomyc
1335	79.5	4.8	1212	2	Q42347	Q42347 gallus gall	1408	79	4.8	712	2	Q7Q2L5	Q7q2l5 anopheles g
1336	79.5	4.8	1237	2	Q7WYN2	Q7wyn2 acetivibrio	1409	79	4.8	718	2	Q94HG1	Q94hg1 oryza sativ
1337	79.5	4.8	1258	2	Q8R458	Q8r458 rattus norv	1410	79	4.8	727	2	Q817L1	Q817l1 caenorhabdi
1338	79.5	4.8	1280	2	Q97SQ0	Q97sq7 streptococc	1411	79	4.8	729	2	Q8BW38	Q8bw38 mus musculu
1339	79.5	4.8	1301	2	Q7LTZ7	Q7ltz7 homo sapien	1412	79	4.8	738	2	Q9WT23	Q9wt23 human herpe
1340	79.5	4.8	1306	2	Q7TT18	Q7tt18 mus musculu	1413	79	4.8	748	2	Q9Y6E1	Q9y6e1 homo sapien
1341	79.5	4.8	1306	2	Q90JK31	Q9jk31 mus musculu	1414	79	4.8	780	2	Q7PR05	Q7pr05 anopheles g
1342	79.5	4.8	1329	2	Q9HCE3	Q9hce3 homo sapien	1415	79	4.8	784	2	Q9H5A0	Q9h5a0 homo sapien
1343	79.5	4.8	1346	2	Q7KR62	Q7kr62 drosophila	1416	79	4.8	801	2	Q6P2S1	Q6p2s1 homo sapien
1344	79.5	4.8	1365	1	SUZ2_DROME	P25172 drosophila	1417	79	4.8	822	1	DEXT_STRSL	Q59979 streptococc
1345	79.5	4.8	1368	2	Q9V6J0	Q9v6j0 drosophila	1418	79	4.8	836	1	NOT3_YEAST	P06102 saccharomyc

1419	79	4.8	836	2	Q6B233	Q6b233	saccharomyc		
1420	79	4.8	864	2	Q8ZTU7	Q8ztu7	pyrobaculum		
1421	79	4.8	878	2	Q6W8T0	Q6w8t0	pichia angu		
1422	79	4.8	893	2	Q9LHT1	Q9lht1	arabidopsis		
1423	79	4.8	900	2	Q8C9A0	Q8c9a0	mus musculus		
1424	79	4.8	903	2	Q8BRQ3	Q8brq3	mus musculus		
1425	79	4.8	921	2	Q6CB10	Q6cb10	yarrowia li		
1426	79	4.8	921	2	Q9F496	Q9p496	yarrowia li		
1427	79	4.8	934	2	Q8BRT2	Q8brt2	mus musculus		
1428	79	4.8	949	1	GLK1 RAT	P22756	rattus norv		
1429	79	4.8	951	2	Q9VQ36	Q9vq36	drosophila		
1430	79	4.8	969	2	Q81UJ7	Q81uj7	bacillus an		
1431	79	4.8	1067	2	Q6BUL7	Q6bul7	debaromyce		
1432	79	4.8	1098	1	TCG1 HUMAN	O14776	homo sapien		
1433	79	4.8	1155	2	Q874L2	Q874l2	candida alb		
1434	79	4.8	1238	2	Q9V8B6	Q9v8b6	drosophila		
1435	79	4.8	1260	2	Q9XDB6	Q9xdb6	streptococ		
1436	79	4.8	1287	2	Q9F930	Q9f930	streptococ		
1437	79	4.8	1340	2	Q8B274	Q8b274	sweet potat		
1438	79	4.8	1351	2	Q7YU89	Q7yu89	drosophila		
1439	79	4.8	1378	2	Q8SQ12	Q8sq12	sarcophaga		
1440	79	4.8	1492	2	Q86JC7	Q86jc7	dictyosteli		
1441	79	4.8	1689	2	Q8QZFA	Q8qzf4	crimean-con		
1442	79	4.8	1689	2	Q8QZFS	Q8qzfs	crimean-con		
1443	79	4.8	1689	2	Q991H9	Q991h9	crimean-con		
1444	79	4.8	1736	2	Q81IM6	Q81im6	plasmodium		
1445	79	4.8	1752	2	Q81IK8	Q81ik8	plasmodium		
1446	79	4.8	1752	2	Q9AE52	Q9ae52	ruminococcu		
1447	79	4.8	1849	1	IGA4 HAEIN	P45386	haemophilus		
1448	79	4.8	1904	2	Q38319	Q38319	lactococcus		
1449	79	4.8	2217	2	Q6FNY7	Q6fny7	candida gla		
1450	79	4.8	2880	2	Q65XZ9	Q65xz9	tomato spot		
1451	78.5	4.7	94	2	Q61030	Q61030	trypanosoma		
1452	78.5	4.7	142	2	Q26943	Q26943	trypanosoma		
1453	78.5	4.7	152	2	Q9GVS3	Q9gy83	caenorhabdi		
1454	78.5	4.7	164	2	Q14851	Q14851	homo sapien		
1455	78.5	4.7	216	2	Q8CTD8	Q8ctd8	staphylococ		
1456	78.5	4.7	231	2	Q8EZW6	Q8ezw6	leptospira		
1457	78.5	4.7	232	2	Q27423	Q27423	drosophila		
1458	78.5	4.7	232	2	Q69EV5	Q69ev5	streptococ		
1459	78.5	4.7	232	2	Q69EV7	Q69ev7	streptococ		
1460	78.5	4.7	232	2	Q69EV8	Q69ev8	streptococ		
1461	78.5	4.7	232	2	Q69EX1	Q69ex1	streptococ		
1462	78.5	4.7	251	2	Q8K201	Q8k201	mus musculus		
1463	78.5	4.7	252	2	Q7PND6	Q7pnd6	anopheles g		
1464	78.5	4.7	252	2	Q8OG93	Q8og93	avian pneum		
1465	78.5	4.7	258	2	Q6TV72	Q6tv72	bovine papu		
1466	78.5	4.7	262	2	Q9JMF0	Q9jmf0	mus musculus		
1467	78.5	4.7	270	2	Q9YN72	Q9yn72	vaccinia vi		
1468	78.5	4.7	271	2	Q71DD6	Q71dd6	drosophila		
1469	78.5	4.7	284	2	Q91UD3	Q91ud3	human respi		
1470	78.5	4.7	285	2	Q86H76	Q86h76	dictyosteli		
1471	78.5	4.7	293	2	Q714W8	Q714w8	homo sapien		
1472	78.5	4.7	294	2	Q99322	Q99322	homo sapien		
1473	78.5	4.7	300	2	Q6CCZ0	Q6ccz0	yarrowia li		
1474	78.5	4.7	308	2	Q9IC17	Q9ic17	vaccinia vi		
1475	78.5	4.7	308	2	Q91ZR9	Q91zr9	cantagalo o		
1476	78.5	4.7	314	1	HENA_VACCV	O01218	vaccinia vi		
1477	78.5	4.7	314	2	Q6L4S2	Q6l4s2	oryza sativ		
1478	78.5	4.7	314	2	Q76ZM3	Q76zm3	vaccinia vi		
1479	78.5	4.7	314	2	Q8BE19	Q8bei9	vaccinia vi		
1480	78.5	4.7	320	2	Q741D6	Q741d6	mycobacteri		
1481	78.5	4.7	322	2	Q67RB1	Q67rb1	mycobacteri		
1482	78.5	4.7	322	2	Q62605	Q62605	rattus norv		
1483	78.5	4.7	334	1	MUL15_HUMAN	Q8n387	homo sapien		
1484	78.5	4.7	334	2	Q6VAV5	Q6vav5	anopheles g		
1485	78.5	4.7	334	2	Q6VAV9	Q6vav9	anopheles g		
1486	78.5	4.7	338	2	Q43420	Q43420	homo sapien		
1487	78.5	4.7	338	2	Q95Y19	Q95y19	caenorhabdi		
1488	78.5	4.7	345	2	Q690X9	Q690x9	anolis sagr		
1489	78.5	4.7	345	2	Q691N0	Q691n0	anolis sagr		
1490	78.5	4.7	345	2	Q691T6	Q691t6	anolis sagr		
1491	78.5	4.7	361	2	Q6BWL2	Q6bw12	debaromyce		
1492	78.5	4.7	371	2	O46052	O46052	drosophila		
1493	78.5	4.7	387	1	PAB_PBPMA	Q51911	peptostrept		
1494	78.5	4.7	407	2	Q8REG3	Q8reg3	fusobacteri		
1495	78.5	4.7	420	2	Q8IER5	Q8ier5	plasmodium		
1496	78.5	4.7	422	2	Q69BM2	Q69bm2	homo sapien		
1497	78.5	4.7	423	2	Q04429	Q04429	saccharomyc		
1498	78.5	4.7	430	2	Q9N4F8	Q9n4f8	caenorhabdi		
1499	78.5	4.7	453	2	Q7TOR8	Q7tor8	xenopus lae		
1500	78.5	4.7	456	2	Q84DS8	Q84ds8	listeria mo		
ALIGNMENTS									
RESULT 1									
Q9UNF4									
ID	Q9UNF4	PRELIMINARY;	PRT;	322 AA.					
AC	Q9UNF4;								
DT	01-MAY-2000 (TRENBLrel. 13, Created)								
DT	01-MAR-2001 (TRENBLrel. 16, Last sequence update)								
DT	05-JUL-2004 (TRENBLrel. 27, Last annotation update)								
DE	Hyaluronic acid receptor (XLK01).								
GN	Name=HAR; ORFNames=UNQ230;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]_TaxID=9606;								
RP	SEQUENCE FROM N.A.								
RA	Winkelmann J.C., Basu S., Ozdemir E., Blough R.I.;								
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;								
RA	Clark H.F., Gurney A.L., Abaya E., Bakér K., Baldwin D., Brush J.,								
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,								
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,								
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,								
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,								
RA	Seahagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,								
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,								
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,								
RT	Godowski P.;								
RT	"The secreted protein discovery initiative (SPDI), a large-scale								
RT	effort to identify novel human secreted and transmembrane proteins: a								
RT	bioinformatics assessment."								
RL	Genome Res. 13:2265-2270(2003).								
DR	EMBL; AF127670; AAD49220.2; -.								
DR	EMBL; AY358925; AAQ89284.1; -.								
DR	HSSP; P98066; 107B.								
DR	GO; GO:0005540; F:hyaluronic acid binding; IEA.								
DR	GO; GO:0004872; F:receptor activity; IEA.								
DR	GO; GO:0007155; P:cell adhesion; IEA.								
DR	InterPro; IPR000538; Link.								
DR	PFam; PF00193; Xlink; 1.								
DR	PRINTS; PR01265; LINKMODULE.								
DR	ProDom; PD000918; Link; 1.								
DR	PROSITE; PS50963; LINK_2; 1.								
KW	Receptor.								
SQ	SEQUENCE 322 AA; 35213 MW; 8B4D6D623F52D559 CRC64;								
Query Match									
Best Local Similarity		100.0%;	Score 1657;	DB 2;	Length 322;				
Matches 322;		Conservative	0;	Mismatches	0;	Indels	0;		
QY	1	MARCSFVLLTSTWTTTLLVQSGRLAEELS	IQVSCRIMGITLVSKKANQQLNFTAEKEA	60					
Db	1	MARCSFVLLTSTWTTTLLVQSGRLAEELS	IQVSCRIMGITLVSKKANQQLNFTAEKEA	60					
QY	61	CRLLGLSLAGKDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLVWKVPV	120						
Db	61	CRLLGLSLAGKDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLVWKVPV	120						

```
QY 121 SRQFAAYCYNSSDTWTNSCIPEIITTKOPIFNTQTATQTEFIVSDSYSPYSTIPA 180
Db 121 SRQFAAYCYNSSDTWTNSCIPEIITTKOPIFNTQTATQTEFIVSDSYSPYSTIPA 180
QY 181 PTTTTPAPASTSIIPRKKLICVTEVFMETSTMTSTETEPFVENKAAAFKNEAAGFGVPTAL 240
Db 181 PTTTTPAPASTSIIPRKKLICVTEVFMETSTMTSTETEPFVENKAAAFKNEAAGFGVPTAL 240
QY 241 LVALLFFGAAGLGFVCYVKRVKAFPTNKNQCKEMETKVVKEEKANDSNPNESKKT 300
Db 241 LVALLFFGAAGLGFVCYVKRVKAFPTNKNQCKEMETKVVKEEKANDSNPNESKKT 300
QY 301 DKNPEESKSPSKTTVRCLEAEV 322
Db 301 DKNPEESKSPSKTTVRCLEAEV 322

RESULT 2
Q8TC18 PRELIMINARY; PRT; 322 AA.
AC Q8TC18;
DT 01-JUN-2002 (TrenBLrel. 21, Created)
DT 01-JUN-2002 (TrenBLrel. 21, Last sequence update)
DE 01-OCT-2003 (TrenBLrel. 25, Last annotation update)
DE Extracellular link domain containing 1.
GN Name=XLKDI;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman N., Madan A., Rubin G.M., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026231; AAH26231.1; -.
DR HSSP; P98066; 107B.
DR GO; HGNC:14687; XLKDI.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PSS0963; LINK_2; 1.
SQ SEQUENCE 322 AA; 35183 MW; 0B1EDBD76CE4610A CRC64;

Query Match 99.2%; Score 1643; DB 2; Length 322;
Best Local Similarity 99.1%; Score 1638; DB 2; Length 322;
Matches 319; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Best Local Similarity 99.7%; Pred. No. 1.3e-124;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARCFSLVLLTSTWTTLLVQGSIRABELSIQVSCRIMGITLVSKKANQQLNFTAEKAA 60
Db 1 MARCFSLVLLTSTWTTLLVQGSIRABELSIQVSCRIMGITLVSKKANQQLNFTAEKAA 60
QY 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPV 120
Db 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPV 120
QY 121 SRQFAAYCYNSSDTWTNSCIPEIITTKOPIFNTQTATQTEFIVSDSYSPYSTIPA 180
Db 121 SRQFAAYCYNSSDTWTNSCIPEIITTKOPIFNTQTATQTEFIVSDSYSPYSTIPA 180
QY 181 PTTTTPAPASTSIIPRKKLICVTEVFMETSTMTSTETEPFVENKAAAFKNEAAGFGVPTAL 240
Db 181 PTTTTPAPASTSIIPRKKLICVTEVFMETSTMTSTETEPFVENKAAAFKNEAAGFGVPTAL 240
QY 241 LVALLFFGAAGLGFVCYVKRVKAFPTNKNQCKEMETKVVKEEKANDSNPNESKKT 300
Db 241 LVALLFFGAAGLGFVCYVKRVKAFPTNKNQCKEMETKVVKEEKANDSNPNESKKT 300
QY 301 DKNPEESKSPSKTTVRCLEAEV 322
Db 301 DKNPEESKSPSKTTVRCLEAEV 322

RESULT 3
Q9Y5Y7 PRELIMINARY; PRT; 322 AA.
AC Q9Y5Y7;
DT 01-NOV-1999 (TrenBLrel. 12, Created)
DT 01-NOV-1999 (TrenBLrel. 12, Last sequence update)
DE 01-MAR-2004 (TrenBLrel. 26, Last annotation update)
DE Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA Jackson D.G.;
RA "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
RT receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801 (1999).
DR EMBL; AF118108; AAD42764.1; -.
DR HSSP; P98066; 107B.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR GO; GO:0009653; P:morphogenesis; TAS.
DR GO; GO:0009611; P:response to wounding; TAS.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PSS0963; LINK_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35238 MW; 0EBEA56729CEFF77 CRC64;

Query Match 98.9%; Score 1638; DB 2; Length 322;
Best Local Similarity 99.1%; Pred. No. 3.4e-124;
Matches 319; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 MARCFSLVLLTSTWTTLLVQGSIRABELSIQVSCRIMGITLVSKKANQQLNFTAEKAA 60
Db 1 MARCFSLVLLTSTWTTLLVQGSIRABELSIQVSCRIMGITLVSKKANQQLNFTAEKAA 60

Query Match 99.2%; Score 1643; DB 2; Length 322;
Best Local Similarity 99.1%; Score 1638; DB 2; Length 322;
Matches 319; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 61 CRLGLSLAGKQOVETALKASSETCSYGWGDFVVISRISPNPKCGKNGVGLIWKVPV 120
DB 61 CRLGLSLAGKQOVETALKASSETCSYGWGDFVVISRISPNPKCGKNGVGLIWKVPV 120
QY 121 SRQFAAYCYNSSDWTNSCIPELITTKDPIFNTQTATOTTEFIVSDSYVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDWTNSCIPELITTKDPIFNTQTATOTTEFIVSDSYVASPYSTIPA 180
QY 181 PTTTPPAPASTSIPRKKLICVTEVFEMETSTMSTETEPVENKAAPKNEAAGFGVPTAL 240
DB 181 PTTTPPAPASTSIPRKKLICVTEVFEMETSTMSTETEPVENKAAPKNEAAGFGVPTAL 240
QY 241 LVALLFFGAAGLFCYKRVYKAFPTFNKNQKQKEMIETKVVKBEKANDSNPNESKKT 300
DB 241 LVALLFFGAAGLFCYKRVYKAFPTFNKNQKQKEMIETKVVKBEKANDSNPNESKKT 300
QY 301 DKNPEESKSPSKTTVRCLAEV 322
DB 301 DKNPEESKSPSKTTVRCLAEV 322
RESULT 4
Q6UC88
ID Q6UC88 PRELIMINARY; PRT; 322 AA.
AC Q6UC88;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DE Cell surface retention sequence binding protein-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;
RA Huang S.S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,
Huang J.S.;
RT "Cloning, expression, characterization and role in autocrine cell
growth of cell surface retention sequence binding protein-1.";
RL J. Biol. Chem. 278:43855-43869(2003).
DR EMBL; AY372937; AAQ85130.1; -;
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; Link; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS0963; LINK_2; 1.
SQ SEQUENCE 322 AA; 35561 MW; 4901D1BF92648AE CRC64;
Query Match 70.9%; Score 1174; DB 2; Length 322;
Beat Local Similarity 71.1%; Pred. No. 1.1e-86;
Matches 229; Conservative 34; Mismatches 59; Indels 0; Gaps 0;
QY 1 MARCESLVLILTSIWTTRLLVQGSIRABELSTQVSCRIMGITLVSKKANQINFTEAKBA 60
DB 1 MAKFSGLGLLASIWTTRLLVQGSURSEISILGPCRIMGVTLVTKTQPLNFTAEQEA 60
QY 61 CRLGLSLAGKQOVETALKASSETCSYGWGDFVVISRISPNPKCGKNGVGLIWKVPV 120
DB 61 CRLVGLTLASQOVETAEARKFGETCSYGNVKNQVFIPIRISNPKCGSGVGVVIRSSL 120
QY 121 SRQFAAYCYNSSDWTNSCIPELITTKDPIFNTQTATOTTEFIVSDSYVASPYSTIPA 180
DB 121 SSRHSYCHNSSDIWNSCLPEIITDDPLFNTETATYTTKLWVSDSTHSELSTGPDYV 180
QY 181 PTTTPPAPASTSIPRKKLICVTEVFEMETSTMSTETEPVENKAAPKNEAAGFGVPTAL 240
DB 181 TTTVAPPLASTSTPRKKLICITEAFMDTSAVATERESDIQNRPAFKNEAVGFGVPTAL 240

QY 241 LVALLFFGAAGLFCYKRVYKAFPTFNKNQKQKEMIETKVVKBEKANDSNPNESKKT 300
DB 241 LVALLFFGAAGLFCYKRVYKAFPTFNKNQKQKEMIETKVVKBEKANDSNPNESKKT 300
QY 301 DKNPEESKSPSKTTVRCLAEV 322
DB 301 NKTPEPKSPKTTVRCLAEV 322
RESULT 5
Q8BHC0
ID Q8BHC0 PRELIMINARY; PRT; 318 AA.
AC Q8BHC0;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
DE Extra cellular link domain-containing 1 (Mus musculus adult male lung
cDNA, RIKEN full-length enriched library, clone:1200012G08
DE product:extra cellular link domain-containing 1, full insert
DE sequence).
GN Name=Xlkdl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CZSCH II; TISSUE=Lung, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CZSCH II; TISSUE=Lung, and Mammary gland;
RA Strausberg R.;
RN Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium;


```
QY 94 FVVISRPNPKCKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCIPBI----- 143
Db 92 -VLIPRIKPNCAANYTGITLGNNEISLRVDYVCYNASETEKSLPVLNNEYDFSHN 150
QY 144 -ITTKDPIFNTQTATTTTFIVSDTSYVSASVSTIPATPTTTPAP 188
Db 151 TIDSYPDTLDTIQNSDKSGYQGSV-----TDPAPAMITPDP 188

RESULT 9
CD44_CRIGR STANDARD; PRT; 362 AA.
AC P20944;
DT 01-FEB-1991 (rel. 17, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DE 05-JUL-2004 (rel. 44, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-I) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN Name=CD44;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90304889; PubMed=1694723; DOI=10.1016/0092-8674(90)90694-A;
RA Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;
RT "CD44 is the principal cell surface receptor for hyaluronate.";
RL Cell 61:1303-1313(1990).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- INDUCTION: By EBV.
CC -!- PTM: Extensively modified including N- and O-linked glycosylation,
CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
CC of phosphate to cytoplasmic domain serine residues.
CC -!- SIMILARITY: Contains 1 Link domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M33827; AAA36967.1; -.
CC FIR; A35616; A35616.
CC HSSP; P98066; ITSG.
CC InterPro; IPR001231; CD44 antigen.
CC InterPro; IPR000538; Link.
CC Pfam; PF00193; XLink; 1.
CC PRINTS; PR00659; CD44.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 1.
CC PROSITE; PS01241; Link; 1.
CC PROSITE; PS0963; LINK 2; 1.
CC PROSITE; PS0963; LINK 2; 1.
KW Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;
KW Proteoglycan; Pyrrolidone carboxylic acid; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 362 CD44 antigen.
FT DOMAIN 23 269 Extracellular (Potential).
FT TRANSMEM 270 290 Potential.
FT DOMAIN 291 362 Cytoplasmic (Potential).
FT DOMAIN 34 122 Link.
FT DOMAIN 152 160 Arg/Lys-rich (basic).
FT DOMAIN 226 269 Stem.
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FT MOD_RES 23 23 Pyrrolidone carboxylic acid (By
FT similarity).
FT DISULFID 55 120 By similarity.
FT DISULFID 79 99 By similarity.
FT MOD_RES 292 292 Phosphoserine (by PKC) (By similarity).
FT MOD_RES 326 326 Phosphoserine (By similarity).
FT CARBOHYD 27 27 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 112 112 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 174 174 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 362 AA; 39775 MW; E89EB434B9EC948 CRC64;

Query Match 14.1%; Score 233.5; DB 1; Length 362;
Best Local Similarity 26.3%; Pred. No. 1.6e-10;
Matches 91; Conservative 45; Mismatches 147; Indels 63; Gaps 12;

QY 24 SLRAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEACRLGLSLAGKDVETALKASPE 83
Db 18 SLAHEQIDNITCRVAGVHVEKNGRYSIRTEAADLCOAFNSTLPTWDQVMALSKGFE 77
QY 84 TCSYGMVGDFVVISRISPNPKCKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCIPBI 143
Db 78 TCRYGFI-EGHVIPRIQPNALCAANHTGVILTSNTS-HVDTYCFNASAPLEEDC--- 131
QY 144 ITTKDPIFNTQTATTTTFIVSDST-YVSASVYST-----IPATTTTPAPAS----- 190
Db 132 -TSVTDLPFEGPVITIVNRDGRYKKGERTHQEDIDASNTTDDVDSGSSSEKST 190
QY 191 -----TSIPRRKKLICVTEVFEMETSTMSTE-----TTPFVEN 222
Db 191 SGYVHYTHLPTIHSTADQDPYFGSTWATRDQSSMDPRGNSLTVTDGSKLTHSSGN 250
QY 223 KAAFKNEAAGFGG---VPTALLVLALLFPFGAAGLFCYVKRYKAFPTTKNQOKEMIE 279
Db 251 QDSGLNSTSRPGKPRVPEWLIVLASL-LALAILAVC-----IAVNSRRRCQKKLVI 304
QY 280 TKVVKKEKANDSNPNESKKTDKNPE-----ESKSPSKTTVRCLEAE 321
Db 305 NS--GNGKVEDRKPSSELNGEASKQEMVHLVNKEPSETPDQPMPTAD 348

RESULT 10
ID Q6P8A2 PRELIMINARY; PRT; 437 AA.
AC Q6P8A2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC75816.
GN Name=MGC75816;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
```


298 CQKKLVNSGTVEDRKPSELN-GEASKSQEMVHLVKNKEPTETPDQFMTAD 350

RESULT 12

```
DB CD44 PAFHA STANDARD; PRT; 362 AA.
AC P14745;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN Name=CD44;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciae;
OC Cercopitheciae; Papio.
OX NCBI_TaxID=9557;
RN [1]_
RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-74.
RX MEDLINE=89282830; PubMed=2471974;
RA Idzerda R.B., Carter W.G., Nottenburg C., Wayner E.A., Gallatin W.M.,
RA St John T.;
RT "Isolation and DNA sequence of a cDNA clone encoding a lymphocyte
RT adhesion receptor for high endothelium."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4659-4663(1989).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Extensively modified including N- and O-linked glycosylation,
CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
CC of phosphate to cytoplasmic domain serine residues.
CC -!- SIMILARITY: Contains 1 Link domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M225452; AAA35385.1; -.
DR HSSP; P98066; LTSG.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 1.
DR PROSITE; PS01241; LINK 1; 1.
DR PROSITE; PS00963; LINK 2; 1.
KW Alternative splicing; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; Phosphorylation; Proteoglycan;
KW Pyrrrolidone carboxylic acid; Receptor; Signal; Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 362
FT DOMAIN 21 269
FT TRANSMEM 270 290
FT DOMAIN 291 362
FT DOMAIN 150 158
FT DOMAIN 225 269
FT MOD_RES 21 21
FT DISULFID 53 118
FT DISULFID 77 97
FT MOD_RES 292 292
FT MOD_RES 326 326
FT CARBOHYD 25 25
FT CARBOHYD 57 57
```

```
FT CARBOHYD 100 100 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
FT CONFLICT 67 E -> V (in Ref. 1; AA sequence).
SQ SEQUENCE 362 AA; 39378 MW; 578BFCE7C3D52FFF CRC64;

Query Match 13.4%; Score 222.5; DB 1; Length 362;
Best Local Similarity 25.5%; Pred. No. 1.2e-09;
Matches 92; Conservative 43; Mismatches 127; Indels 99; Gaps 16;

QY 20 LVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAEKACRLGLSLAGKQDVETALK 79
DB 14 LVQLSL--AQIDLNITCFEGYHVEKNGRYSISRTAADLCKAFNSTLPTMAQMEKALS 71
QY 80 ASFTCTSGWVGDFVVISRISPNPKCKGKGVGLWIKVPSRQPAAYCYNSSDTWTNSC 139
DB 72 IGFETCRYGFY-EGHVVIPRIHPNSICAANTGVILTNTS-QYDTTCFNASAPPGEDC 129
QY 140 IPEIITTKDPIFNITQTATQTFEIVSDST-YSVASPYSTIP-----APT----- 182
DB 130 -----TSVTDLPNAPDGPITITIVNRDTRVYKGEYRTNEDINPSPFTDDDVSSGSS 184
QY 183 -----TTPPAPASTSIPRRKKLICVTEVFMETSTMSTETETEPFVNKAAP 226
DB 185 ERSSTLGGYIFVNHFTSPPIPDG-----PWITDSTDRTPATRDQAF 229
QY 227 K-----NEAAGF-----GG-----VPTALLVLALLFPGAAGLGFCY 258
DB 230 DPSGSHHTHGSSESHSGHSGREGGANTSGPLRTPQIPPEWLIILASL-LALALLAVC- 287
QY 259 VKRYVKAPFFINKQOKEMIEIK---VYKEKANDSNPESKKTDK---NPESKSPS 311
DB 288 ----IAVNSRRRCQKKLVNNGNGAVEDRRKSSGLN-GEASKSQEMVHLVKNKESPTD 342
QY 312 K 312
DB 343 Q 343

RESULT 13
CD44 RAT
ID CD44 RAT STANDARD; PRT; 503 AA.
AC P26051; Q99021;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-
DE 24).
GN Name=CD44;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BDIX; TISSUE=Pancreas;
RX MEDLINE=91191552; PubMed=1707342; DOI=10.1016/0092-8674(91)90403-L;
RA Guenther U., Hofmann M., Rudy W., Rebet S., Zoeller M., Haussmann I.,
RA Matzku S., Wenzel A., Ponta H., Herrlich P.;
RT "A new variant of glycoprotein CD44 confers metastatic potential to
RT rat carcinoma cells."
RL Cell 65:13-24(1991).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RA Stevens J.W., Midura R.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SULFATION OF TYR-288.
RX PubMed=9692903;
RX Sleeman J.P., Rahmsdorf U., Steffen A., Ponta H., Herrlich P.;
```

RT "CD44 variant exon v5 encodes a tyrosine that is sulphated.";

RL Bur. J. Biochem. 255:74-80(1998).

CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to

CC mucosal high endothelial venule and to types I and VI collagen.

CC Probably involved in matrix adhesion, lymphocyte activation and

CC lymph node homing.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=2; Synonyms=Long, Meta-1;

CC IsoId=P26051-1. Sequence=Displayed;

CC Name=1; Synonyms=Short;

CC IsoId=P26051-2; Sequence=VSP_005330;

CC -!- PTM: N-glycosylated (By similarity).

CC -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which

CC can be more or less sulfated (By similarity).

CC -!- PTM: Phosphorylated; activation of PKC results in the

CC dephosphorylation of Ser-467 (constitutive phosphorylation site),

CC and the phosphorylation of Ser-433 (By similarity).

CC -!- SIMILARITY: Contains 1 Link domain.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M61875; AAA53532.1; -;

DR EMBL; M61874; AAA53534.1; -;

DR EMBL; U52179; AAA97915.1; -;

DR EMBL; U46957; AAA92920.1; -;

DR PIR; B38745; B38745.

DR HSSP; P98086; LTSG.

DR InterPro; IPR001231; CD44_antigen.

DR InterPro; IPR000538; Link.

DR Pfam; PF00193; XLink; 1.

DR PRINTS; PR00658; CD44.

DR PRINTS; PR01265; LINKMODULE.

DR ProDom; PD000918; Link; 1.

DR PROSITE; PS01241; LINK 1; 1.

DR PROSITE; PS0963; LINK 2; 1.

DR Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;

KW Proteoglycan; Pyridolone carboxylic acid; receptor; signal;

KW Sulfation; Transmembrane.

FT SIGNAL 1 21

FT CHAIN 22 503

FT DOMAIN 22 410

FT TRANSMEM 411 431

FT DOMAIN 432 503

FT DOMAIN 35 124

FT DOMAIN 154 162

FT DOMAIN 228 410

FT MOD_RES 22 22

FT MOD_RES 56 122

FT DISULFID 80 100

FT MOD_RES 288 288

FT MOD_RES 433 433

FT MOD_RES 467 467

FT CARBOHYD 28 28

FT CARBOHYD 60 60

FT CARBOHYD 103 103

FT CARBOHYD 114 114

FT CARBOHYD 124 124

FT CARBOHYD 266 266

FT CARBOHYD 274 274

FT CARBOHYD 306 306

FT VARSPIC 224 385

FT --> SDGSSMDPRGGFDVTVTHGSELA (in isoform

FT 1).

FT /FTId=VSP_005330.

FT R -> S (in Ref. 2).

FT CONFLICT 74 74

FT SEQUENCE 503 AA; 55945 MW; FB489D009BD4EE22 CRC64;

Query Match 13.4%; Score 222; DB 1; Length 503;

Best Local Similarity 25.7%; Pred. No. 2e-09;

Matches 84; Conservative 40; Mismatches 165; Indels 38; Gaps 11;

QY 15 WTRLLVQSLRAEELSIOVSCRMIGITLVSKANQQLNFTAKEACRLLGLSLACKDQV 74

DB 10 WGLLCQLQLSLAQOQIDLNITCYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPMAQM 69

QY 75 ETALKASFETCSYGMVGDFGVISRPSPKCKGKGVGLIWKVPVSRQFAAYCNSSDT 134

DB 70 ELALRGGETCYGFI-EGHVVIPIHFNALCAANTGVYILLASNTSHDYTCFNASAP 128

QY 135 WTNSCIPEIITKDPINFNTQTATQTEFVSDST-YSVASPYST----IPAPT----- 182

DB 129 LEEDC-----TSVTDLPNSFDGPVITITVNRDGTTRYKKGEYRTHQEDIDASNIDEDVS 183

QY 183 -----TTPPA-PASTSIPRKKLICVTEVPMETSTMST-BTEPFVENKAAPKNEAGF 233

DB 184 SGSTIEKSTPEGYILHDLPTSQPTGDRDDAFFIGSTLATIATTPWSAHTKQNBQRTQM 243

QY 234 GGV---PTALLVLLALFFGAAAGLGFVYKRVK--APPFTNKNQCKEMIEKVVKEEKA 288

DB 244 NPIHNPVLLQTTTTRMTDIDRNSTSANGENWQEPQPPFNHNEYQDER-ETPHATSTTW 302

QY 289 NDSNPNEESKTKDK-----NPESKSP 310

DB 303 ADPNSTTBEAATQKEKWFENWQGNP 329

RESULT 14

Q08779 PRELIMINARY; PRT; 780 AA.

AC Q08779;

DT 01-JUL-1997 (Tremblrel. 04, Created)

DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE CD44 protein.

GN Name=CD44;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BDX; TISSUE=Pancreas;

RA Hofmann M.

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U96138; AAB54002.1; -.

DR HSSP; P98066; 1078.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005540; F:hyaluronic acid binding; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR001231; CD44_antigen.

DR InterPro; IPR000538; Link.

DR Pfam; PF00193; XLink; 1.

DR PRINTS; PR00658; CD44.

DR PRINTS; PR01265; LINKMODULE.

DR ProDom; PD000918; Link; 1.

DR SMART; SM00445; Link; 1.

DR PROSITE; PS01241; LINK 1; 1.

DR PROSITE; PS0963; LINK 2; 1.

SQ SEQUENCE 780 AA; 85917 MW; CC4D35AB1EA7377C CRC64;

Query Match 13.2%; Score 219.5; DB 2; Length 780;

Best Local Similarity 24.9%; Pred. No. 5.4e-09;

Matches 86; Conservative 45; Mismatches 144; Indels 71; Gaps 13;

IAITPWSAHTKQNBQRTQNTOWNPIHNPVLLQTTTTRMTDID

RNSTSANGENWQEPQPPFNHNEYQDEETPHATSTTWADP

NTTEEAATQKEKWFENWQGNPPTPSDSHVTEGTASA

HNNHPSQRMSTTQSDVSWTDFDPDPSHPMGQGHQTESK

QY 15 WTRLLVQGSRAEELSIQVSCRMGITLVSKKANQOLNFTTEAKBACRLGLSLAGKQOV 74
Db 10 WGLLCLQLSLAQOQIDLAITCRYAGFVHEKNGRYSISRTAADLCEAFNTTLPTMAQM 69
QY 75 ETALKASFCTSYGVWGDGFVVISRISPNPKCGKNGVGLIWKPVPVSQFAAYCYNSSDT 134
Db 70 ELALRKGFETCRYGFI-EGHVIPRIHPNAICAANNNTGVILLASNTSHDYTCFNASAP 128
QY 135 WNSCIPELIITTKDPINFQTATQTTEFIVSDST-YSVASPYST-----IPAPT----- 182
Db 129 LEEDC-----TSVTDLPNSFDGPFVITIVNRDGTYSKKGEYRTHQEDIDASNIIDEDVS 183
QY 183 -----TTPPA-PASTSIPRKKKLCVTEVFMETSTMSTETEPFVENKAAAFKNEAAG-- 232
Db 184 SGSTTEKSTPEGVILHTDFTSQPTGDRDDAFPIGSTLAT-----IASTVYSKSHATAOK 238
QY 233 -----FGG-----VPTALLVLALLFGAA-----AGLGFCYVKRYVKAPFFT 269
Db 239 QNNWISWFGNSQSTTQTQDSPTTTATTALMTTPTPPKQEAQNWFSW-----PF 289
QY 270 NKNOQKEMETKVVKEEKANDSN-----PNEESK-KTDKNPEESKS 309
Db 290 QPSEKSHLHTTKMPGTESNTNPTGKPKNEENEDETDKYPNFGS 335

RESULT 15

Q98SR5 PRELIMINARY; PRT; 265 AA.
AC Q98SR5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE T cell antigen CD44 isoform b.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Pekin.
RL Chan S.W.S., Warr G.W., Middleton D.L., Higgins D.A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332869; AAK18277.1; -
DR HSSP; P98066; 107B.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF01193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK 1; UNKNOWN_1.
DR PROSITE; PS0963; LINK 2; 1.
SQ SEQUENCE 265 AA; 29215 MW; 77C176E0A998D081 CRC64;

Query Match 13.2%; Score 219; DB 2; Length 265;
Best Local Similarity 28.3%; Pred. No. 1.6e-09;
Matches 66; Conservative 32; Mismatches 103; Indels 32; Gaps 5;

QY 14 IWTRLLVQGSRAEELSIQVSCRMGITLVSKKANQOLNFTTEAKBACRLGLSLAGKQOV 73
Db 6 VVATFGLCLLKLCTETQFNSCRVGVFVHEKNGRYSLTRTEAADLCLALNSTLSTLEQ 65
QY 74 VETALKASFCTSYGVWGDGFVVISRISPNPKCGKNGVGLIWKPVPVSQFAAYCYNSSD 133
Db 66 LEXAHELGETCRYGVF-VGYIVIPRINPYHLCAANHGTGIYKLSANTTGRYDAYCYNATE 124
QY 134 TWNSCIP-----EITTKDP-----IPNTQTATQTTEFIVSDSTYSVASPY 175
Db 125 TRDKACEPIERIDTSLFSLNQGEIVDNEGSRYNADGTRHSGDSSTSGVDENVGSGSH 184

QY 176 STIPAPTTTPPAPAS-----TSIPR-----RKKLICVTEVFMETSTMSTE 215
Db 185 DTTTPVDTSIKRSRSPSYGSVTPVPHLSHSGGGGKKEFPVTNSDDDEISPTSTD 237

Search completed: October 5, 2005, 17:31:31
Job time : 183.744 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2005, 17:16:37 ; Search time 30.4111 Seconds
(without alignments)
1018.766 Million cell updates/sec

Title: US-10-063-510-6
Perfect score: 1657
Sequence: 1 MARCFSVLLTSLTWTRLL.....NPESKSPSKTTVRCLEAEV 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	229.5	13.9	363	2	A37009 CD44 homolog membr
2	222.5	13.4	362	2	A30901 lymphocyte adhesio
3	222.5	13.4	365	2	A34424 CD44 membrane glyco
4	222.5	13.4	365	2	A34424 cell adhesion mole
5	217.5	13.1	362	2	A35616 T-cell surface gly
6	208.5	12.6	366	2	A53286 cell-surface glyco
7	205	12.4	361	2	JH0417 cell adhesion mole
8	202.5	12.2	351	2	S45305 CD44 antigen precu
9	202	12.2	742	2	A47195 lymphocyte homing
10	199.5	12.0	426	2	JH0518 lymphocyte homing
11	199.5	12.0	493	2	S13530 CD44E protein, epi
12	198	11.9	395	2	I77371 CD44R5 - human
13	196.5	11.9	699	2	I37369 epican - human
14	186	11.2	359	2	S24240 lymphocyte surface
15	148.5	9.0	2109	1	I50421 aggrecan precursor
16	145.5	8.8	3562	2	A47171 chondroitin sulfat
17	145	8.8	277	2	A41735 hyaluronate-bindin
18	145	8.8	1069	2	J42681 hypothetical prote
19	144	8.7	275	2	JC6506 tumor necrosis fac
20	143	8.6	2327	2	T42630 aggrecan - bovine
21	137	8.3	276	2	A47290 TSG-6 homolog PS4
22	131.5	7.9	2124	2	A28452 proteoglycan core
23	131	7.9	2132	1	A55182 aggrecan precursor
24	130.5	7.9	883	2	S57653 aggrecan precursor
25	130.5	7.9	883	2	S49126 aggrecan precursor
26	130.5	7.9	2415	1	A35086 aggrecan precursor
27	128.5	7.8	912	2	A54423 aggrecan precursor
28	121	7.3	1340	2	A39808 proteoglycan core
29	117	7.1	340	2	JC7505 brain link protein

30	116	7.0	2397	1	A55535 versican precursor
31	115	6.9	370	2	S29139 aggrecan - pig (fr
32	115	6.9	1643	2	T14274 versican precursor
33	115	6.9	3381	2	T42389 versican precursor
34	114.5	6.9	1257	2	S28764 versican precursor
35	112	6.8	390	1	Q0BE77 glycoprotein 1 pre
36	111.5	6.7	402	2	S73773 dihydrolipoamide a
37	111.5	6.7	909	1	QRXL2 LDL receptor 2 pre
38	111	6.7	2409	1	A60979 versican precursor
39	108	6.5	354	1	LKHU proteoglycan link
40	108	6.5	645	2	T29818 hypothetical prote
41	107.5	6.5	739	2	T21769 hypothetical prote
42	107	6.5	355	1	LKCH proteoglycan link
43	107	6.5	371	2	A53908 brevican precursor
44	107	6.5	408	1	LKRT2 proteoglycan link
45	107	6.5	1268	2	S52781 neurocan - mouse
46	105.5	6.4	113	2	A55885 chondroitin sulfat
47	104.5	6.3	862	2	S43922 versican - pig-tal
48	104	6.3	354	1	S04243 proteoglycan link
49	104	6.3	354	1	S42938 proteoglycan link
50	103.5	6.2	1229	2	T25697 hypothetical prote
51	101.5	6.1	380	2	T28081 hypothetical prote
52	101.5	6.1	768	2	TU0073 hypothetical prote
53	101	6.1	708	2	T19474 hypothetical prote
54	100	6.0	378	2	I46268 brevican precursor
55	100	6.0	1251	2	T21389 hypothetical prote
56	99.5	6.0	1092	1	JN0635 neural cell adhesi
57	99	6.0	896	2	T22061 hypothetical prote
58	99	6.0	5376	2	T42215 zonadhesin - mouse
59	98.5	5.9	796	2	T21460 hypothetical prote
60	98	5.9	771	2	T34376 hypothetical prote
61	97.5	5.9	909	1	QRXL1 LDL receptor 1 pre
62	96.5	5.8	465	2	S46759 hypothetical prote
63	96.5	5.8	660	2	JH0067 chitinase (EC 3.2.
64	96	5.8	449	2	T33257 hypothetical prote
65	96	5.8	1088	1	IUXLNL neural cell adhesi
66	95.5	5.8	376	2	S52137 MID2 protein - yea
67	95.5	5.8	1471	2	B48218 neuroxin III-alpha
68	94.5	5.7	1272	2	S26180 neurofascin - chic
69	94.5	5.7	1390	2	T18883 hypothetical prote
70	94	5.7	1241	2	S01827 period clock prote
71	93	5.6	930	2	B72537 hypothetical prote
72	92.5	5.6	477	2	S53362 mucin 5AC (clone J
73	92.5	5.6	569	2	A11347 hypothetical prote
74	92.5	5.6	851	2	T22696 hypothetical prote
75	92.5	5.6	927	2	T24031 hypothetical prote
76	92.5	5.6	1367	2	S74285 BUD3 protein - yea
77	92	5.6	429	1	JC5861 endo-1,4-beta-xyla
78	92	5.6	846	2	T21700 hypothetical prote
79	92	5.6	966	2	S25365 CYC8 protein - yea
80	91.5	5.5	411	2	A33664 96K lysosomal memb
81	91.5	5.5	639	2	S20887 acta protein precu
82	91.5	5.5	639	2	A51100 actin-assembly ind
83	91.5	5.5	672	2	T32557 hypothetical prote
84	91.5	5.5	681	2	S33316 structural protein
85	91	5.5	246	2	T33965 hypothetical prote
86	91	5.5	747	2	T34329 hypothetical prote
87	91	5.5	2172	2	T20145 hypothetical prote
88	90.5	5.5	575	2	S29315 chaperonin 60 - cu
89	90.5	5.5	662	2	A45155 mucin FIM-C.1 - Af
90	90	5.4	388	2	S36500 E2 protein - human
91	90	5.4	1007	1	T24643 glucan 1,4-alpha-g
92	90	5.4	1367	1	S48478 hypothetical prote
93	89.5	5.4	518	2	T49778 hypothetical prote
94	89.5	5.4	1369	2	S70713 protein-tyrosine k
95	89	5.4	307	1	GSFF3 salivary glue prot
96	89	5.4	416	1	A31959 lysosome-associate
97	89	5.4	517	2	T20658 probable zinc meta
98	89	5.4	5170	2	T15348 hypothetical prote
99	88.5	5.3	193	2	A71415 hypothetical prote
100	88.5	5.3	721	2	B90487 hypothetical prote
101	88.5	5.3	770	2	T22808 hypothetical prote
102	88.5	5.3	1101	2	S15271 endoglucanase C (E

103	88	5.3	456	2	T31483	hypothetical prote
104	88	5.3	564	2	T25945	hypothetical prote
105	88	5.3	602	2	AD2067	hypothetical prote
106	88	5.3	761	2	T00940	hypothetical prote
107	88	5.3	1631	1	SAZOK1	major merozoite su
108	88	5.3	3507	2	T34513	hypothetical prote
109	88	5.3	3570	2	T45025	mucin MUC5B, trach
110	87.5	5.3	825	2	T48431	hypothetical prote
111	87.5	5.3	1085	2	SJ40476	Ca(2+) - sensing rec
112	87.5	5.3	1091	1	IJCHNL	neural cell adhesi
113	87.5	5.3	1802	2	S69703	HKR1 protein precu
114	87.5	5.3	2817	2	B97033	uncharacterized pr
115	87	5.3	235	2	PC2022	mucin like protein
116	87	5.3	752	2	E72616	hypothetical prote
117	87	5.3	1016	2	H71460	probable outer mem
118	87	5.3	1506	2	T30886	integumentary muc
119	87	5.3	1537	2	S53465	flocculation prote
120	86.5	5.2	400	1	A28172	spasmolysin precu
121	86.5	5.2	461	2	T22946	hypothetical prote
122	86.5	5.2	503	2	S63257	probable membrane
123	86.5	5.2	550	2	T29919	hypothetical prote
124	86.5	5.2	740	1	FOLJHD	gag polypeptid -
125	86.5	5.2	1777	2	T34369	hypothetical prote
126	86.5	5.2	2816	2	A57096	nudel protein prec
127	86	5.2	333	2	T27883	hypothetical prote
128	86	5.2	1785	2	A45546	major merozoite su
129	85.5	5.2	575	2	S29316	chaperonin 60 - cu
130	85.5	5.2	649	2	T04606	protein kinase hom
131	85.5	5.2	786	2	T16509	hypothetical prote
132	85.5	5.2	895	2	T02597	Mutator-like trans
133	85	5.1	265	2	T33695	hypothetical prote
134	85	5.1	576	2	S59829	hypothetical prote
135	85	5.1	627	2	G86860	serine/threonine p
136	85	5.1	989	2	T47503	hypothetical prote
137	85	5.1	990	2	I51618	nucleolar phosphop
138	85	5.1	1162	2	T21557	hypothetical prote
139	85	5.1	1779	2	T31085	xylanase - Caldice
140	84.5	5.1	463	2	B82001	probable amino-ac
141	84.5	5.1	493	2	JC5486	membrane glycopro
142	84.5	5.1	562	2	A57088	nucleoporin-like p
143	84.5	5.1	658	2	T39500	serine/threonine-s
144	84.5	5.1	658	2	S60170	protein kinase Pak
145	84.5	5.1	709	2	T28712	hypothetical prote
146	84.5	5.1	1102	2	S65235	probable membrane
147	84.5	5.1	1161	2	S97180	probable membrane
148	84.5	5.1	2481	2	D90011	FmtB protein limpo
149	84.5	5.1	2761	2	T21064	hypothetical prote
150	84	5.1	262	2	S76772	hypothetical prote
151	84	5.1	335	2	H96667	AP2-containing DNA
152	84	5.1	420	2	AB2426	hypothetical prote
153	84	5.1	426	2	B53580	neurexin III beta
154	84	5.1	543	2	S35047	mucin JUL7 - human
155	84	5.1	636	1	VCWVFS	env polypeptid -
156	84	5.1	793	2	AH1094	probable peptidogl
157	84	5.1	996	2	JE0237	apolipoprotein E r
158	84	5.1	1075	2	S48992	flocculation prote
159	84	5.1	1331	2	A48954	mammalian endo-1,4-be
160	84	5.1	1362	2	A75207	amylopullulanase P
161	84	5.1	1832	2	T31113	mucin-like glycopr
162	84	5.1	3020	2	A43932	mucin 2 precursor,
163	83.5	5.0	216	2	I51920	mucin - rhesus mac
164	83.5	5.0	279	2	S53363	mucin 5AC (clone J
165	83.5	5.0	446	2	T45525	hypothetical prote
166	83.5	5.0	967	2	S68852	hypothetical prote
167	83.5	5.0	976	2	A87576	peptidase, M16 fam
168	83.5	5.0	1043	2	E97302	hypothetical prote

249	81	4.9	1169	2	S38181	flocculation prote	322	78.5	4.7	423	2	S69583	hypothetical prote
250	81	4.9	1367	2	S51959	hypothetical prote	323	78.5	4.7	542	1	S64030	probable membrane
251	81	4.9	1609	2	S25345	probable membrane	324	78.5	4.7	591	1	WMBPQ2	gene P2 protein -
252	81	4.9	1726	2	A39401	merozoite surface	325	78.5	4.7	599	2	S46630	hypothetical prote
253	81	4.9	6642	2	T29757	protein UNC-89 - C	326	78.5	4.7	688	2	B42161	cGMP-gated cation
254	80.5	4.9	148	1	S07723	immediate-early se	327	78.5	4.7	815	2	JG0197	myosin-light-chain
255	80.5	4.9	391	1	S15617	E2 protein - human	328	78.5	4.7	825	2	T29634	hypothetical prote
256	80.5	4.9	441	2	T31482	hypothetical prote	329	78.5	4.7	919	1	PX2P1P	H+-exporting ATPase
257	80.5	4.9	543	2	T22585	hypothetical prote	330	78.5	4.7	1011	1	JH0581	NAD ADP-ribosyltra
258	80.5	4.9	592	2	T34446	hypothetical prote	331	78.5	4.7	1356	2	T16754	hypothetical prote
259	80.5	4.9	595	2	A42086	CD30 antigen precu	332	78.5	4.7	1420	2	T17158	CL2AB protein - ra
260	80.5	4.9	742	2	T33514	hypothetical prote	333	78.5	4.7	1435	2	T46611	CL2BA protein - ra
261	80.5	4.9	798	2	T34248	hypothetical prote	334	78.5	4.7	1452	2	T17157	CL2AA protein - ra
262	80.5	4.9	918	2	S58178	glutamate receptor	335	78.5	4.7	1463	2	T17159	CL2BA protein - ra
263	80.5	4.9	1124	2	F71719	inner layer protei	336	78.5	4.7	1467	2	T17160	CL2BC protein - ra
264	80.5	4.9	1159	1	A44280	hypothetical prote	337	78.5	4.7	1478	2	T17185	alpha-latrotoxin r
265	80.5	4.9	2225	2	T26063	hypothetical prote	338	78.5	4.7	1487	2	T14324	zinc metalloprotei
266	80	4.8	153	2	S67294	hypothetical prote	339	78.5	4.7	1876	2	E97944	Ran-binding protei
267	80	4.8	177	1	RGBXGI	regulatory protein	340	78.5	4.7	3224	1	S58884	hypothetical prote
268	80	4.8	345	2	T21776	hypothetical prote	341	78	4.7	253	2	S76719	hypothetical prote
269	80	4.8	359	2	T13478	hypothetical prote	342	78	4.7	260	2	AG2238	hypothetical prote
270	80	4.8	415	2	AE2237	hypothetical prote	343	78	4.7	266	2	T30919	hypothetical prote
271	80	4.8	451	2	S71754	cellular hepatitis	344	78	4.7	287	2	T12471	hypothetical prote
272	80	4.8	468	2	A55116	vacuolar ATPase (E	345	78	4.7	293	2	G87018	probable membrane
273	80	4.8	521	2	S69556	hypothetical prote	346	78	4.7	321	2	T26152	hypothetical prote
274	80	4.8	650	2	T41681	probable serine/th	347	78	4.7	340	2	AH0940	probable ABC trans
275	80	4.8	667	2	A40713	cyclicin I - bovine	348	78	4.7	372	2	T48660	heat shock protein
276	80	4.8	688	2	T18263	S-layer protein -	349	78	4.7	373	2	F81333	Chaperone DnaJ Cj1
277	80	4.8	702	2	T34313	hypothetical prote	350	78	4.7	384	2	T21929	hypothetical prote
278	80	4.8	725	2	A41258	a-agglutinin core	351	78	4.7	425	2	T48724	hypothetical prote
279	80	4.8	881	2	S56032	probable membrane	352	78	4.7	434	2	B84684	hypothetical prote
280	80	4.8	1013	1	S04200	NAD ADP-ribosyltra	353	78	4.7	530	2	A45690	transactivator EBN
281	80	4.8	1348	2	S27812	probable epidermal	354	78	4.7	627	1	VCVM2	env polyprotein -
282	79.5	4.8	152	2	T15170	hypothetical prote	355	78	4.7	655	2	T30044	hypothetical prote
283	79.5	4.8	165	2	A27195	histone H1 - Tetra	356	78	4.7	786	1	A47547	serine proteinase
284	79.5	4.8	184	2	F72525	hypothetical prote	357	78	4.7	1050	2	T31853	hypothetical prote
285	79.5	4.8	354	2	T46740	microfilarial shea	358	78	4.7	1337	2	T30291	dextranase - Strept
286	79.5	4.8	461	1	A35356	tumor necrosis fac	359	78	4.7	1360	2	T33922	hypothetical prote
287	79.5	4.8	510	2	B72007	conserved hypotet	360	78	4.7	1442	1	B48148	protein-tyrosine-p
288	79.5	4.8	510	2	A86618	CT861 hypothetical	361	78	4.7	1634	2	T28517	hypothetical prote
289	79.5	4.8	534	2	G84713	hypothetical prote	362	78	4.7	1723	2	H85657	polymorphic membra
290	79.5	4.8	554	2	JW0094	neurofilament prot	363	78	4.7	1732	2	E72067	polymorphic membra
291	79.5	4.8	580	2	T20716	hypothetical prote	364	78	4.7	1955	1	AGCH	agrin precursor -
292	79.5	4.8	693	2	T25878	hypothetical prote	365	78	4.7	1995	2	T08166	probable membrane
293	79.5	4.8	827	2	T04789	DNA mismatch repai	366	78	4.7	5327	2	T13564	microtubule-associ
294	79.5	4.8	860	2	AC1250	NAD ADP-ribosyltra	367	78	4.7	5275	2	T21933	hypothetical prote
295	79.5	4.8	998	2	S31735	hypothetical prote	368	77.5	4.7	396	2	F83130	probable MFS trans
296	79.5	4.8	1011	2	T20785	hypothetical prote	369	77.5	4.7	401	2	AG3552	branched-chain ami
297	79.5	4.8	1280	2	E95031	alkaline amylopull	370	77.5	4.7	474	1	BMFFSY	synaptotagmin - fr
298	79.5	4.8	1365	2	S14871	suppressor two of	371	77.5	4.7	476	2	T32032	hypothetical prote
299	79	4.8	215	2	S26363	histone H1.1 - hum	372	77.5	4.7	496	2	B41322	N-acetyluramoyl-L
300	79	4.8	249	2	G84781	hypothetical prote	373	77.5	4.7	514	2	JQ1317	activin receptor p
301	79	4.8	352	2	T51659	myb-related transc	374	77.5	4.7	519	2	T45764	hypothetical prote
302	79	4.8	534	2	T39903	serine-rich protei	375	77.5	4.7	526	2	A56573	nuclear pore compl
303	79	4.8	575	2	T21775	hypothetical prote	376	77.5	4.7	607	2	S01939	hypothetical prote
304	79	4.8	611	2	AB1497	internalin protein	377	77.5	4.7	623	2	T18892	hypothetical prote
305	79	4.8	710	2	S67098	probable membrane	378	77.5	4.7	816	2	S64439	hypothetical prote
306	79	4.8	738	2	T44007	hypothetical prote	379	77.5	4.7	860	2	JC4566	chitinase (EC 3.2.
307	79	4.8	739	2	T49456	hypothetical prote	380	77.5	4.7	906	2	G90281	conserved hypotet
308	79	4.8	822	2	JC4076	dextranase (EC 3.2	381	77.5	4.7	938	2	A56731	chromatin assembly
309	79	4.8	836	2	S49940	cell division cont	382	77.5	4.7	975	2	T08606	protein phosphatas
310	79	4.8	949	2	S19808	glutamate receptor	383	77.5	4.7	993	1	P1VXTA	RNA 1 protein - to
311	79	4.8	1098	2	T08599	probable transcrip	384	77.5	4.7	1127	2	E86386	probable mutator-1
312	79	4.8	1849	2	C41859	IGA-specific metal	385	77.5	4.7	1156	2	T23748	hypothetical prote
313	79	4.8	1904	2	T13256	tail-host specific	386	77.5	4.7	1312	2	A97879	beta-N-acetylhexos
314	78.5	4.7	152	2	T28759	hypothetical prote	387	77.5	4.7	1475	2	S42718	nuclear pore compl
315	78.5	4.7	164	2	I53641	mucin SAC - human	388	77.5	4.7	3968	2	A44265	trichorax homolog
316	78.5	4.7	232	2	A60095	larval glue protei	389	77.5	4.7	257	2	G72690	probable spermidin
317	78.5	4.7	294	2	A37232	mucin, tracheal (A	390	77	4.6	350	2	E75341	peptidyl-prolyl ci
318	78.5	4.7	314	1	HNZVZW	hemagglutinin prec	391	77	4.6	352	2	S22805	env polyprotein -
319	78.5	4.7	314	1	JQ1793	hemagglutinin prec	392	77	4.6	453	2	F75206	maltose-binding pe
320	78.5	4.7	322	2	S33715	apomucin precursor	393	77	4.6	528	2	S69589	hypothetical prote
321	78.5	4.7	387	2	A53586	albumin-binding pr	394	77	4.6				

395	77	4.6	553	2	T19894	hypothetical prote	468	76	4.6	1014	1	A39725	NAD ADP-ribosyltra
396	77	4.6	598	2	T22610	hypothetical prote	469	76	4.6	1041	2	H71617	SERA antigen/papai
397	77	4.6	623	2	A48123	cell cycle regulat	470	76	4.6	1046	2	T29776	hypothetical prote
398	77	4.6	639	2	T33166	hypothetical prote	471	76	4.6	1216	2	B90580	hypothetical prote
399	77	4.6	669	1	VCWVEK	env polyprotein -	472	76	4.6	1263	2	AH2011	heterocyst glycoli
400	77	4.6	734	2	B42680	nucleolus-cytoplas	473	76	4.6	1338	2	S09982	protein-tyrosine k
401	77	4.6	750	2	T42614	probable envelope	474	76	4.6	1348	2	A43917	probable epidermal
402	77	4.6	771	2	JC7388	M83 protein - huma	475	76	4.6	1388	2	A53317	collagen alpha 1(X
403	77	4.6	861	2	T23810	hypothetical prote	476	76	4.6	1401	2	T17452	werner syndrome pr
404	77	4.6	862	2	B36786	hypothetical prote	477	76	4.6	1422	2	T42636	protein-tyrosine-p
405	77	4.6	892	2	T09193	ataxin 7 - human	478	76	4.6	1438	2	B71610	WD40 WEB-1 homolo
406	77	4.6	897	2	S05050	SINI-associated pr	479	76	4.6	1489	2	G71406	probable retroviru
407	77	4.6	967	2	G86229	hypothetical prote	480	76	4.6	1513	2	T44045	hypothetical prote
408	77	4.6	977	2	S49004	tyrosine kinase Mp	481	76	4.6	1890	2	T04556	hypothetical prote
409	77	4.6	1016	2	T41720	hypothetical prote	482	76	4.6	2570	2	T17451	fimbriae-associate
410	77	4.6	1237	2	T14633	hypothetical prote	483	75.5	4.6	261	2	T30170	hypothetical prote
411	77	4.6	1401	2	T30247	werner syndrome pr	484	75.5	4.6	273	2	T44657	protein GP80 [impo
412	77	4.6	1513	2	A54895	mucin 2, intestina	485	75.5	4.6	319	1	A35163	carbonate dehydrat
413	77	4.6	2187	2	T30826	nascent polypeptid	486	75.5	4.6	343	2	T40306	hypothetical prote
414	76.5	4.6	284	2	T42367	a-agglutinin core	487	75.5	4.6	348	1	B46216	transcription fact
415	76.5	4.6	349	2	T43457	hypothetical prote	488	75.5	4.6	364	1	COHUG	opsin, green-sensi
416	76.5	4.6	382	2	S27388	neuropeptide Y rec	489	75.5	4.6	387	2	A86302	hypothetical prote
417	76.5	4.6	391	2	C69673	penicillin-binding	490	75.5	4.6	411	2	T03154	DNA polymerase pro
418	76.5	4.6	421	2	A60058	neural cell adhesi	491	75.5	4.6	412	2	E97279	TPR-repeat-contain
419	76.5	4.6	433	2	H84120	methyl-accepting c	492	75.5	4.6	430	1	A46216	transcription fact
420	76.5	4.6	482	2	AG1147	P60 extracellular	493	75.5	4.6	435	2	S40993	hypothetical prote
421	76.5	4.6	484	2	A41487	protein P60 precur	494	75.5	4.6	443	2	D72383	NADH oxidase - The
422	76.5	4.6	505	2	B46629	mucin 6, gastric (495	75.5	4.6	445	2	I38521	inwardly rectifyin
423	76.5	4.6	518	2	G88961	protein F59A7.8 [i	496	75.5	4.6	448	2	S70297	DNA-binding protei
424	76.5	4.6	542	2	I39540	chitinase (EC 3.2.	497	75.5	4.6	468	2	S70297	SP2 protein homol
425	76.5	4.6	549	2	SC4845	IG heavy chain pre	498	75.5	4.6	511	1	VGBEF4	glycoprotein C - h
426	76.5	4.6	640	1	VCVWML	env polyprotein -	499	75.5	4.6	609	2	G87496	peptidase, M23/M37
427	76.5	4.6	679	2	S64258	hypothetical prote	500	75.5	4.6	639	2	T13151	adapter protein CM
428	76.5	4.6	718	2	T29708	hypothetical prote	501	75.5	4.6	665	2	G97213	probable membrane-
429	76.5	4.6	727	2	A88131	protein F10G7.9 [i	502	75.5	4.6	709	2	T32089	hypothetical prote
430	76.5	4.6	749	2	B86403	probable mutator-1	503	75.5	4.6	778	2	T43223	hypothetical prote
431	76.5	4.6	773	2	T00502	probable receptor-	504	75.5	4.6	780	2	A48143	HF-1 regulatory el
432	76.5	4.6	806	2	E69424	hypothetical prote	505	75.5	4.6	963	2	T40290	hypothetical prote
433	76.5	4.6	990	2	T16554	hypothetical prote	506	75.5	4.6	1131	2	T41144	hypothetical serin
434	76.5	4.6	1154	1	VGJHIB	E2 glycoprotein pr	507	75.5	4.6	1166	2	S37692	probable tumor sup
435	76.5	4.6	1379	2	T45119	FIM protein [impor	508	75.5	4.6	1235	2	T13710	protein-tyrosine k
436	76.5	4.6	1736	2	F86178	hypothetical prote	509	75.5	4.6	1237	2	E86457	probable RNA helic
437	76.5	4.6	1946	2	JC6032	lactocepin (EC 3.4	510	75.5	4.6	1473	2	T31422	C-terminal domain-
438	76.5	4.6	3869	2	A48205	All-1 protein +GPE	511	75.5	4.6	1655	2	T32633	hypothetical prote
439	76.5	4.6	5037	2	B35041	ryanodine receptor	512	75.5	4.6	1737	2	A59235	unconventional myo
440	76	4.6	167	2	A33532	mucin SMUC-40 - hu	513	75.5	4.6	1881	2	H95076	zinc metalloprotei
441	76	4.6	172	2	T21753	hypothetical prote	514	75.5	4.6	2526	2	T20531	hypothetical prote
442	76	4.6	243	2	B41710	promastigote surfa	515	75.5	4.6	3176	2	CGHU3A	collagen alpha 3(V
443	76	4.6	356	2	D89979	protein F37B4.9 [i	516	75	4.5	94	2	S53365	mucin 5AC (clone C
444	76	4.6	368	2	S36564	E2 protein - human	517	75	4.5	128	2	T05035	hypothetical prote
445	76	4.6	378	2	A12180	hypothetical prote	518	75	4.5	205	2	S55670	hypothetical prote
446	76	4.6	382	2	B88561	protein F58A4.7b [519	75	4.5	248	2	AF1914	carbon dioxide con
447	76	4.6	384	2	A41710	promastigote surfa	520	75	4.5	256	2	T09034	hypothetical prote
448	76	4.6	389	2	A47013	butanol dehydrogen	521	75	4.5	295	2	T28078	hypothetical prote
449	76	4.6	389	2	E97305	NADH-dependent but	522	75	4.5	310	1	H71054	hypothetical prote
450	76	4.6	499	2	T47722	probable protein k	523	75	4.5	313	2	AH0734	probable bacteriop
451	76	4.6	515	2	AD1162	flagellar motor sw	524	75	4.5	353	2	S33322	(S)-2-hydroxy-acid
452	76	4.6	532	2	T28784	hypothetical prote	525	75	4.5	388	2	T16861	hypothetical prote
453	76	4.6	536	2	T37544	hypothetical serin	526	75	4.5	390	2	A72108	hypothetical prote
454	76	4.6	539	2	T02512	hypothetical prote	527	75	4.5	390	2	B86514	hypothetical prote
455	76	4.6	549	2	T49298	hypothetical prote	528	75	4.5	418	2	T16713	hypothetical prote
456	76	4.6	592	2	T16725	hypothetical prote	529	75	4.5	425	1	A26431	nerve growth facto
457	76	4.6	615	2	T47395	hypothetical prote	530	75	4.5	453	2	C40511	hypothetical prote
458	76	4.6	687	2	A49636	soluble vascular e	531	75	4.5	475	2	E84745	probable splicing
459	76	4.6	699	2	I38073	nucleolar phosphop	532	75	4.5	477	2	T32938	hypothetical prote
460	76	4.6	700	2	A54641	interspersed seque	533	75	4.5	481	2	T38149	pre-mrna splicing
461	76	4.6	763	2	T08929	hypothetical prote	534	75	4.5	554	2	A56596	chitinase (EC 3.2.
462	76	4.6	766	2	B85440	receptor kinase-i	535	75	4.5	604	2	T37994	probable splicing
463	76	4.6	824	2	T23923	hypothetical prote	536	75	4.5	607	2	S63395	probable membrane
464	76	4.6	929	2	G72677	hypothetical prote	537	75	4.5	651	2	T16450	hypothetical prote
465	76	4.6	940	2	AD1374	internalin protein	538	75	4.5	679	2	T19703	hypothetical prote
466	76	4.6	960	1	JN0677	protein-tyrosine k	539	75	4.5	739	2	I56187	transcription fact
467	76	4.6	994	1	MNWM	nonstructural prot	540	75	4.5	775	1	WNBE19	ribonucleoside-dip

541	75	4.5	778	2	T45221	DNA damage checkpo	614	74	4.5	621	2	T20307	hypothetical prote
542	75	4.5	796	2	E96654	hypothetical prote	615	74	4.5	622	2	AC1236	acyltransferase (c
543	75	4.5	858	1	IJRTNC	neural cell adhesi	616	74	4.5	665	1	VCWVKA	env polyprotein pr
544	75	4.5	904	2	T03806	hypothetical prote	617	74	4.5	672	2	T20310	hypothetical prote
545	75	4.5	916	2	T20909	hypothetical prote	618	74	4.5	681	2	A45705	type I transembra
546	75	4.5	940	2	D89723	protein F39D81b [619	74	4.5	689	2	B43491	env polyprotein -
547	75	4.5	948	2	T21998	hypothetical prote	620	74	4.5	731	2	T04455	hypothetical prote
548	75	4.5	1048	1	S61388	dotA protein - Leg	621	74	4.5	739	1	A34873	transcription fact
549	75	4.5	A48292	2	A48292	mucin, tracheobron	622	74	4.5	775	2	A32494	transposable eleme
550	75	4.5	1253	2	T18528	probable pyruvate	623	74	4.5	823	2	G90848	probable exonuclea
551	75	4.5	1741	2	T13610	parallel sister ch	624	74	4.5	823	2	E85706	hypothetical prote
552	75	4.5	1768	2	T13349	parallel sister ch	625	74	4.5	852	2	T06310	hypothetical prote
553	75	4.5	1838	1	CGHU1V	collagen alpha 1(V	626	74	4.5	862	2	S51493	major nitrogen reg
554	75	4.5	1979	2	T17622	hypothetical prote	627	74	4.5	903	2	T00705	N-chimerin homolog
555	75	4.5	3122	2	T17202	DNA-directed DNA p	628	74	4.5	1016	2	T19006	ankyrin related pr
556	75	4.5	3375	2	T19821	hypothetical prote	629	74	4.5	1018	2	T40253	hypothetical prote
557	74.5	4.5	148	2	S50653	hypothetical prote	630	74	4.5	1099	2	G90546	conserved hypothet
558	74.5	4.5	211	2	S28046	TUB8 protein - pot	631	74	4.5	1104	2	S59310	probable membrane
559	74.5	4.5	254	2	D88560	protein F58A4.1 [i	632	74	4.5	1110	2	IS1116	hypothetical prote
560	74.5	4.5	262	2	T33597	hypothetical prote	633	74	4.5	1115	1	IUNSNL	neural cell adhesi
561	74.5	4.5	276	2	T51685	myb-related transc	634	74	4.5	1159	2	S62562	probable nuclear p
562	74.5	4.5	281	2	T49537	hypothetical prote	635	74	4.5	1164	2	B71429	phytochrome D - Ar
563	74.5	4.5	294	2	AI2016	hypothetical prote	636	74	4.5	1390	2	T14004	trfA protein - sli
564	74.5	4.5	310	1	YAZQ31	300K antigen Ag231	637	74	4.5	1694	2	H64106	IgA-specific metal
565	74.5	4.5	321	2	T50966	hypothetical prote	638	74	4.5	1828	2	A40115	microtubule-associ
566	74.5	4.5	382	2	T25280	hypothetical prote	639	74	4.5	1938	1	MWK1	myosin heavy chain
567	74.5	4.5	396	2	T50229	probable transmem	640	74	4.5	2414	2	A54277	transcription adap
568	74.5	4.5	407	2	T26938	hypothetical prote	641	73.5	4.4	168	2	A31196	prespore-specific
569	74.5	4.5	416	2	T20448	hypothetical prote	642	73.5	4.4	182	2	T30078	hypothetical prote
570	74.5	4.5	429	2	S29044	endoglucanase A pr	643	73.5	4.4	253	2	T32879	hypothetical prote
571	74.5	4.5	432	2	T08771	hypothetical prote	644	73.5	4.4	263	2	T38003	hypothetical prote
572	74.5	4.5	478	2	A32555	major merozoite su	645	73.5	4.4	292	2	S24169	hypothetical ser-t
573	74.5	4.5	482	2	T22754	hypothetical prote	646	73.5	4.4	305	2	A44661	mucin - rat
574	74.5	4.5	520	2	S14598	E2 glycoprotein -	647	73.5	4.4	335	2	AE3000	ZK353.4 protein -
575	74.5	4.5	531	2	S08959	hypothetical prote	648	73.5	4.4	335	2	D98283	cell division prot
576	74.5	4.5	551	2	S52287	urbain - silkworm	649	73.5	4.4	345	2	D91201	hypothetical prote
577	74.5	4.5	636	2	T23232	hypothetical prote	650	73.5	4.4	345	2	H86047	type III secretion
578	74.5	4.5	713	2	JE0230	NADPH-cytochrome p	651	73.5	4.4	358	2	A23378	escu [imported] -
579	74.5	4.5	802	2	T21315	hypothetical prote	652	73.5	4.4	371	2	S20075	promastigote surfa
580	74.5	4.5	808	2	T23129	hypothetical prote	653	73.5	4.4	376	2	T48245	hypothetical prote
581	74.5	4.5	884	2	AE3166	ATP-dependent DNA	654	73.5	4.4	381	2	E69862	hypothetical prote
582	74.5	4.5	998	2	S37627	protein-tyrosine k	655	73.5	4.4	397	2	G95287	hypothetical prote
583	74.5	4.5	1042	2	T48801	hypothetical prote	656	73.5	4.4	405	2	A54852	P2B/LAMP-1 precurs
584	74.5	4.5	1595	2	T31082	endo-1,4-beta-xyla	657	73.5	4.4	445	2	A54852	potassium rectifie
585	74.5	4.5	1630	2	A53577	ascites stialoglyco	658	73.5	4.4	447	2	A39321	mucin - rat (fragm
586	74.5	4.5	1902	2	C97702	cell surface antig	659	73.5	4.4	457	2	T20884	hypothetical prote
587	74.5	4.5	1965	2	T33216	hypothetical prote	660	73.5	4.4	458	2	T31631	hypothetical prote
588	74.5	4.5	2688	2	I49477	alpha-A-crystallin	661	73.5	4.4	459	2	I48854	gene murine tumour
589	74.5	4.5	3828	2	T13857	trithorax protein	662	73.5	4.4	476	2	B44997	merozoite surface
590	74.5	4.5	3944	2	T19997	hypothetical prote	663	73.5	4.4	484	1	A24994	cellulose 1,4-beta
591	74	4.5	147	2	S09762	hypothetical prote	664	73.5	4.4	511	1	VBGE1K	glycoprotein C - h
592	74	4.5	223	2	T21930	hypothetical prote	665	73.5	4.4	540	2	H98086	chaperonin GroEL [
593	74	4.5	257	1	MGNZBR	major surface glyco	666	73.5	4.4	540	2	G95222	chaperonin, 60 kDa
594	74	4.5	264	2	A49149	mesoderm developme	667	73.5	4.4	542	2	T19952	hypothetical prote
595	74	4.5	286	2	S44835	F54H12.3 protein -	668	73.5	4.4	550	1	VG1HD6	E2 glycoprotein pr
596	74	4.5	305	2	AB2149	hypothetical prote	669	73.5	4.4	550	2	T26413	hypothetical prote
597	74	4.5	317	2	C85432	hypothetical prote	670	73.5	4.4	556	2	C87609	sensor histidine k
598	74	4.5	332	2	T31928	hypothetical prote	671	73.5	4.4	569	2	A46462	T cell activation
599	74	4.5	339	1	JT0756	group-V allergen 1	672	73.5	4.4	601	2	H90270	hypothetical prote
600	74	4.5	339	2	A56274	sulfur-regulated 3	673	73.5	4.4	602	2	T39866	hypothetical prote
601	74	4.5	344	2	T13975	NADH2 dehydrogenas	674	73.5	4.4	626	2	AB1328	probable peptidogl
602	74	4.5	346	2	H84512	hypothetical prote	675	73.5	4.4	654	2	T33044	hypothetical prote
603	74	4.5	390	2	C97889	UDPglucose 6-dehyd	676	73.5	4.4	696	2	G81262	probable integral
604	74	4.5	397	2	E97176	N-terminal domain	677	73.5	4.4	708	2	F87245	penicillin-binding
605	74	4.5	412	1	AJBORS	argininosuccinate	678	73.5	4.4	713	2	T44447	neuregulin-3 (limp
606	74	4.5	413	2	S28066	sexual differentia	679	73.5	4.4	756	2	JCS886	signaling mediator
607	74	4.5	435	2	T20327	hypothetical prote	680	73.5	4.4	799	2	B71255	probable cell divi
608	74	4.5	437	2	AG1028	prepinin (imported	681	73.5	4.4	819	2	B95136	conserved domain p
609	74	4.5	454	2	T02100	hypothetical prote	682	73.5	4.4	901	2	A44825	phosphoprotein, sy
610	74	4.5	540	1	FOVWHL	gag polyprotein -	683	73.5	4.4	905	2	T02205	Lu-SCAM-1 protei
611	74	4.5	575	2	S39484	DNA-binding protei	684	73.5	4.4	990	2	H88733	protein F32E10.3 [
612	74	4.5	586	2	S66697	probable membrane	685	73.5	4.4	1004	2	T38074	hypothetical prote
613	74	4.5	600	2	T06292	hypothetical prote	686	73.5	4.4	1139	1	E64234	cytadherence-acces

687	73.5	4.4	1291	2	T22382	hypothetical prote	760	72.5	4.4	642	2	T39607	fork head protein
688	73.5	4.4	2332	2	T34434	hypothetical prote	761	72.5	4.4	648	2	PC4395	mucin 3 - human [f
689	73.5	4.4	4385	2	T25042	hypothetical prote	762	72.5	4.4	657	2	AB2415	conserved hypothet
690	73	4.4	188	2	C96593	unknown protein, 9	763	72.5	4.4	663	2	T18631	hypothetical prote
691	73	4.4	198	2	E71837	histone H1 - mouse	764	72.5	4.4	710	2	A99486	ABC transporter, b
692	73	4.4	213	2	S43949	protein-export mem	765	72.5	4.4	728	2	F72693	probable phosphoes
693	73	4.4	260	2	I50109	gastrulation prote	766	72.5	4.4	729	2	G96559	hypothetical prote
694	73	4.4	288	2	JQ2365	polyprotein - Bean	767	72.5	4.4	743	2	D86888	penicillin-binding
695	73	4.4	315	1	HNZVW	hemagglutinin prec	768	72.5	4.4	746	2	T44946	transducer protein
696	73	4.4	326	2	G86333	hypothetical prote	769	72.5	4.4	765	1	S36326	membrane antigen g
697	73	4.4	327	2	S20074	promastigote surfa	770	72.5	4.4	896	1	QQBE21	clathrin assembly
698	73	4.4	359	2	S42787	serine/threonine-r	771	72.5	4.4	907	2	S36327	clathrin assembly
699	73	4.4	369	2	E84291	iron (III) ABC tra	772	72.5	4.4	915	2	C70839	probable mmp13 pro
700	73	4.4	422	1	A55417	synaptotagmin II -	773	72.5	4.4	944	2	C30839	microtubule-associ
701	73	4.4	428	1	Q4ECAD	damX protein (aroS	774	72.5	4.4	982	2	AS3253	NAD ADP-ribosyltra
702	73	4.4	441	2	A43555	GAP-43-related pro	775	72.5	4.4	1016	1	JS0428	protein P200 - Myc
703	73	4.4	448	2	G88639	protein C34H4.2 [i	776	72.5	4.4	1036	2	S73601	DNA-directed DNA p
704	73	4.4	461	2	T51044	related to spore c	777	72.5	4.4	1116	2	S77213	splicing factor Si
705	73	4.4	469	2	E64456	hypothetical prote	778	72.5	4.4	1148	2	T09073	microtubule-associ
706	73	4.4	482	2	A44997	merozoite surface	779	72.5	4.4	1152	2	A33183	hypothetical prote
707	73	4.4	486	2	S66097	cell-cycle protein	780	72.5	4.4	1180	2	E86719	nuclear envelope p
708	73	4.4	486	2	A89927	elastin binding pr	781	72.5	4.4	1199	2	A40670	nucleoporin Nup153
709	73	4.4	492	1	CHBOA3	gamma-aminobutyric	782	72.5	4.4	1219	2	T14578	hypothetical prote
710	73	4.4	496	2	E90181	hypothetical prote	783	72.5	4.4	1222	2	T22490	hypothetical prote
711	73	4.4	509	1	A37259	membrane glycoprot	784	72.5	4.4	1309	1	BVBYD9	RAD9 protein - yea
712	73	4.4	550	2	C75557	hypothetical prote	785	72.5	4.4	1312	2	E95006	beta-N-acetylhexos
713	73	4.4	558	2	A98199	translocated intim	786	72.5	4.4	1555	2	T18688	hypothetical prote
714	73	4.4	558	2	E86045	probable transloca	787	72.5	4.4	1635	2	T14075	chitinase (EC 3.2.
715	73	4.4	600	2	E72027	phosphoenolpyruvat	788	72.5	4.4	1847	2	T18308	probable vitellog
716	73	4.4	600	2	E86597	phosphoenolpyruvat	789	72.5	4.4	1973	2	T18686	hypothetical prote
717	73	4.4	669	2	A46511	envelope protein -	790	72.5	4.4	1973	2	T18686	hypothetical prote
718	73	4.4	688	2	A43491	env polyprotein -	791	72.5	4.4	2305	2	B96608	protein C23Fu2.1 [
719	73	4.4	720	2	T51007	hypothetical prote	792	72.5	4.4	2305	2	T15571	hypothetical prote
720	73	4.4	728	2	T20561	hypothetical prote	793	72.5	4.4	2314	1	A46151	protein-tyrosine-p
721	73	4.4	781	2	T49472	hormone-sensitive	794	72.5	4.4	2897	2	B48666	cell proliferation
722	73	4.4	814	2	T33140	hypothetical prote	795	72.5	4.4	3069	2	H70656	fatty-acid synthas
723	73	4.4	880	2	S44833	F54H12.5 protein -	796	72	4.3	3256	2	A48666	cell proliferation
724	73	4.4	918	2	A36337	membrane glycoprot	797	72	4.3	139	2	G98226	hypothetical prote
725	73	4.4	932	1	VGEBEC	glycoprotein gi pr	798	72	4.3	139	2	A13059	hypothetical prote
726	73	4.4	958	2	T10679	hypothetical prote	799	72	4.3	159	2	F72758	hypothetical prote
727	73	4.4	1055	2	H90023	hypothetical prote	800	72	4.3	199	2	T33525	hypothetical prote
728	73	4.4	1071	2	T22327	hypothetical prote	801	72	4.3	330	2	JE0351	OX40 ligand protei
729	73	4.4	1256	1	A43829	mutamidase-release	802	72	4.3	236	2	T03041	hypothetical prote
730	73	4.4	1320	2	JCS630	TCOF1 protein - mo	803	72	4.3	246	2	PC4397	mucin 3 T10 - huma
731	73	4.4	1345	2	S46817	hypothetical prote	804	72	4.3	282	2	B37994	RF2 protein - saim
732	73	4.4	1702	2	A18859	IgA-specific metal	805	72	4.3	317	1	GERUS	bone sialoprotein
733	73	4.4	1993	2	AF1450	probable peptidogl	806	72	4.3	322	2	G69946	phage-related prot
734	73	4.4	2179	1	GNNYH4	genome polyprotein	807	72	4.3	324	2	S36646	integrin-associate
735	73	4.4	2285	2	T12796	probable transglyc	808	72	4.3	330	2	T49644	hypothetical prote
736	73	4.4	2416	2	T13825	adenomatous polypo	809	72	4.3	334	2	T19637	hypothetical prote
737	73	4.4	2468	2	A83412	hypothetical prote	810	72	4.3	425	1	FOVGC	gag polyprotein -
738	73	4.4	2722	2	T20532	hypothetical prote	811	72	4.3	428	2	D86003	hypothetical prote
739	72.5	4.4	263	2	I51225	snail1 protein - z	812	72	4.3	428	2	F91157	probable membrane
740	72.5	4.4	303	2	S40973	hypothetical prote	813	72	4.3	460	2	A84154	amino acid transpo
741	72.5	4.4	321	2	B95034	dihydropteroate sy	814	72	4.3	508	2	A33378	fasciclin III prec
742	72.5	4.4	321	2	T26153	hypothetical prote	815	72	4.3	509	2	A96563	probable protein k
743	72.5	4.4	328	2	S35336	transcription fact	816	72	4.3	544	2	S07144	neurofilament trip
744	72.5	4.4	340	2	C90894	probable LAC1-type	817	72	4.3	548	1	QRFGL	neurofilament trip
745	72.5	4.4	340	2	F85723	probable LAC1-type	818	72	4.3	576	2	T38293	hypothetical serin
746	72.5	4.4	340	2	G64905	sugar-binding prot	819	72	4.3	587	2	S38634	chaperonin, mitoch
747	72.5	4.4	382	2	T27058	hypothetical prote	820	72	4.3	592	2	D70863	hypothetical prote
748	72.5	4.4	391	2	T35470	probable integral	821	72	4.3	622	2	A90570	lipoprotein (impor
749	72.5	4.4	406	2	T23934	hypothetical prote	822	72	4.3	674	2	S74506	ribonuclease E - S
750	72.5	4.4	415	2	T32490	hypothetical prote	823	72	4.3	677	2	T00369	hypothetical prote
751	72.5	4.4	463	1	A36479	milk fat globule m	824	72	4.3	736	2	T41259	hypothetical prote
752	72.5	4.4	487	2	S40820	probable permease	825	72	4.3	770	1	S30293	transcription fact
753	72.5	4.4	498	1	VGXPLM	surface glycoprote	826	72	4.3	817	2	T21336	hypothetical prote
754	72.5	4.4	499	2	A12449	hypothetical prote	827	72	4.3	855	2	D98004	histidine Motif-Co
755	72.5	4.4	507	2	S05542	hypothetical prote	828	72	4.3	876	2	T98001	hypothetical prote
756	72.5	4.4	511	2	T35194	transcription init	829	72	4.3	884	2	T20405	hypothetical prote
757	72.5	4.4	560	2	T32661	hypothetical prote	830	72	4.3	958	2	T26258	SM74 protein - yea
758	72.5	4.4	580	2	B38418	jockey protein 1 -	831	72	4.3	1034	2	S49947	hypothetical prote
759	72.5	4.4	610	2	S35049	mucin JER57 - huma	832	72	4.3	1038	2	AG2187	hypothetical prote
										1146	2	S46837	hypothetical prote

833	72	4.3	1176	2	T49482	hypothetical prote	906	71	4.3	370	2	S49008	fork head protein
834	72	4.3	1196	2	H85061	hypothetical prote	907	71	4.3	378	2	S00842	leukostatin precu
835	72	4.3	1203	2	T17415	mycelial surface a	908	71	4.3	379	1	S71571	alcohol dehydroge
836	72	4.3	1388	2	A57655	tim (timeless) pro	909	71	4.3	394	2	T21752	hypothetical prote
837	72	4.3	1489	2	T31108	cyst germination s	910	71	4.3	410	1	S68153	cellulase (EC 3.2.
838	72	4.3	1547	2	T28657	blackjack protein,	911	71	4.3	415	2	A35560	lysosomal membrane
839	72	4.3	1570	2	T28272	1-phosphatidylinos	912	71	4.3	433	2	S19996	hypothetical prote
840	72	4.3	1778	2	T50074	probable nucleopor	913	71	4.3	435	2	A87913	protein B0205.10 [
841	72	4.3	1829	2	T24583	hypothetical prote	914	71	4.3	462	2	T32751	hypothetical prote
842	72	4.3	2441	2	S39161	CREB-binding prote	915	71	4.3	474	1	TVPTCA	Ca2+/calmodulin-de
843	72	4.3	2578	2	A56922	transcription fact	916	71	4.3	496	2	T30976	hypothetical prote
844	72	4.3	2971	2	T08026	hypothetical prote	917	71	4.3	500	1	S60929	probable aldehyde
845	71.5	4.3	141	2	A38196	non-structural hyp	918	71	4.3	502	1	I52637	Ca2+/calmodulin-de
846	71.5	4.3	146	2	S52800	hypothetical prote	919	71	4.3	530	2	S62439	hypothetical serin
847	71.5	4.3	162	2	C84948	NADH2 dehydrogenas	920	71	4.3	534	2	G97703	hypothetical prote
848	71.5	4.3	164	2	A26490	histone H1. macron	921	71	4.3	622	2	T15467	hypothetical prote
849	71.5	4.3	178	2	QJ1547	stripe disease-spe	922	71	4.3	626	2	NHRUIA	platelet glycoprot
850	71.5	4.3	231	2	F84311	hypothetical prote	923	71	4.3	665	1	VCWVVR	env polyprotein pr
851	71.5	4.3	263	2	S01360	salivary glue prot	924	71	4.3	669	2	T08827	hypothetical prote
852	71.5	4.3	313	2	QJ1862	31R protein - vari	925	71	4.3	670	2	T13739	probable hormone r
853	71.5	4.3	313	2	T28598	hypothetical prote	926	71	4.3	711	2	T48335	receptor like prot
854	71.5	4.3	313	2	A34677	secretory pathway	927	71	4.3	719	2	T27977	lin-15A protein -
855	71.5	4.3	363	2	T25278	hypothetical prote	928	71	4.3	738	2	I40719	isocitrate dehydro
856	71.5	4.3	372	2	F43674	US7 protein - huma	929	71	4.3	751	2	T21967	hypothetical prote
857	71.5	4.3	373	2	S43455	hypothetical prote	930	71	4.3	767	1	JU0474	glucan 1,4-alpha-g
858	71.5	4.3	381	2	S65212	hypothetical prote	931	71	4.3	778	1	ALBYG	glucan 1,4-alpha-g
859	71.5	4.3	385	2	T38113	hypothetical serin	932	71	4.3	784	2	AH2560	hypothetical prote
860	71.5	4.3	392	2	T49471	mucin (muc3) relat	933	71	4.3	785	2	S54016	SOK2 protein - yea
861	71.5	4.3	393	2	T49578	hypothetical prote	934	71	4.3	791	2	T39924	hypothetical prote
862	71.5	4.3	395	2	I53842	CD43 lp-3 antigen	935	71	4.3	814	1	KXBY	hypothetical prote
863	71.5	4.3	395	2	A43545	leukostatin CD43 p	936	71	4.3	880	2	D89756	protein T23E7.2b [
864	71.5	4.3	408	2	A46712	glycoprotein Iia -	937	71	4.3	968	2	T00353	hypothetical prote
865	71.5	4.3	414	2	B84600	hypothetical prote	938	71	4.3	977	2	H84469	hypothetical prote
866	71.5	4.3	423	2	T22865	hypothetical prote	939	71	4.3	982	2	T19171	hypothetical prote
867	71.5	4.3	442	1	S11712	transcription init	940	71	4.3	1032	2	T18293	guanylate kinase-1
868	71.5	4.3	443	1	D64584	heat shock protein	941	71	4.3	1200	1	SNPSO	ice nucleation pro
869	71.5	4.3	466	2	A10957	chromosomal replic	942	71	4.3	1204	2	C75015	probable pyrolysin
870	71.5	4.3	482	2	T48397	S-receptor kinase-	943	71	4.3	1244	2	T19615	hypothetical prote
871	71.5	4.3	503	2	G75262	hypothetical prote	944	71	4.3	1256	2	G97902	alpha-amylase (EC
872	71.5	4.3	507	2	T50398	hypothetical serin	945	71	4.3	1302	2	T23236	hypothetical prote
873	71.5	4.3	540	1	A55145	thiamine-phosphate	946	71	4.3	1326	2	H89134	protein F25G6.9 [l
874	71.5	4.3	584	2	T19565	hypothetical prote	947	71	4.3	1367	2	T33819	hypothetical prote
875	71.5	4.3	631	2	I52257	episialin - mouse	948	71	4.3	1533	2	T00344	sister chromatid c
876	71.5	4.3	661	1	VCWVCB	env polyprotein -	949	71	4.3	1583	2	S59644	major blood-stage
877	71.5	4.3	665	2	E81444	probable methyl-ac	950	71	4.3	1751	2	A45604	hypothetical prote
878	71.5	4.3	675	2	T47378	probable transposa	951	71	4.3	1819	2	T32008	probable fatty-aci
879	71.5	4.3	755	2	T20950	hypothetical prote	952	71	4.3	1842	2	T43409	fatty acid synthas
880	71.5	4.3	760	1	S07896	transcription fact	953	71	4.3	1842	2	T38781	host cell factor C
881	71.5	4.3	882	2	T01168	hypothetical prote	954	71	4.3	2035	2	A40718	probable transform
882	71.5	4.3	1043	2	T23875	hypothetical prote	955	71	4.3	2090	2	S26058	hypothetical prote
883	71.5	4.3	1121	2	T02764	myosin-I binding p	956	71	4.3	2848	2	T32550	hypothetical prote
884	71.5	4.3	1156	2	T43326	germline RNA helic	957	71	4.3	2957	2	T33152	ryanodine receptor
885	71.5	4.3	1172	2	T32759	hypothetical prote	958	71	4.3	3035	1	I46646	cryptogein - Phyto
886	71.5	4.3	1234	2	T31623	hypothetical prote	959	70.5	4.3	118	2	S49913	mucin 3 (clone S1B
887	71.5	4.3	1260	2	A87046	proteolisin - se	960	70.5	4.3	128	2	A35690	early E3 16k glyco
888	71.5	4.3	1297	2	T30274	hypothetical prote	961	70.5	4.3	146	1	ERAD32	merozoite surface
889	71.5	4.3	1459	2	T32271	protein-tyrosine-p	962	70.5	4.3	172	2	F49247	merozoite surface
890	71.5	4.3	1557	2	D41214	hypothetical prote	963	70.5	4.3	174	2	E49247	hypothetical prote
891	71.5	4.3	1566	2	T20058	hypothetical prote	964	70.5	4.3	193	2	G90125	hypothetical prote
892	71.5	4.3	1630	2	C41214	protein-tyrosine-p	965	70.5	4.3	204	2	S67295	probable membrane
893	71	4.3	98	2	S53367	mucin SAC (clone M	966	70.5	4.3	209	2	C89850	conserved hypothet
894	71	4.3	135	2	T49996	AtAGP4 - Arabidops	967	70.5	4.3	211	2	C71482	probable endonucle
895	71	4.3	168	2	JN0073	glycophorin A - mo	968	70.5	4.3	212	2	F86545	hypothetical prote
896	71	4.3	177	2	G75285	hypothetical prote	969	70.5	4.3	212	2	F20777	hypothetical prote
897	71	4.3	213	2	A86228	hypothetical prote	970	70.5	4.3	236	2	PC4396	mucin 3 T9 - human
898	71	4.3	240	2	T33698	hypothetical prote	971	70.5	4.3	255	2	I46606	MHC SLA-DQ alpha c
899	71	4.3	242	2	T27226	hypothetical prote	972	70.5	4.3	264	2	T09377	hypothetical prote
900	71	4.3	304	2	T15922	hypothetical prote	973	70.5	4.3	284	2	T28018	hypothetical prote
901	71	4.3	310	2	T20535	hypothetical prote	974	70.5	4.3	288	2	T41112	hypothetical prote
902	71	4.3	329	2	T43012	conserved hypothet	975	70.5	4.3	308	2	T29756	hypothetical prote
903	71	4.3	343	2	S75435	hypothetical prote	976	70.5	4.3	312	2	T25994	hypothetical prote
904	71	4.3	349	2	T05857	hypothetical prote	977	70.5	4.3	314	2	B97905	dihydropteroate sy
905	71	4.3	360	2	T33835	hypothetical prote	978	70.5	4.3	316	1	A43661	dihydropteroate sy

979	70.5	4.3	321	2	T19259	hypothetical prote	1052	70	4.2	350	2	S22456	hydroxyproline-ric
980	70.5	4.3	330	2	S28102	rlx protein - Stap	1053	70	4.2	350	2	AH3043	dehydrogenase Atu3
981	70.5	4.3	350	2	A10139	UTP-hexose-1-phosp	1054	70	4.2	350	2	D98242	lipopolysaccharide
982	70.5	4.3	380	1	D34285	ubiquinol-cytochro	1055	70	4.2	355	2	B26883	neural cell adhesi
983	70.5	4.3	382	2	A28067	lysosomal membrane	1056	70	4.2	357	2	E72245	hydrolase, ana/hip
984	70.5	4.3	385	2	F70591	probable kefB prot	1057	70	4.2	358	2	A88082	protein T05A8.7 li
985	70.5	4.3	393	2	S62335	I71-7 protein - fr	1058	70	4.2	360	2	T08673	hypothetical prote
986	70.5	4.3	402	2	E86185	hypothetical prote	1059	70	4.2	409	2	T18726	hypothetical prote
987	70.5	4.3	403	1	S35541	transcription fact	1060	70	4.2	424	2	I51210	synaptotagmin p65
988	70.5	4.3	427	2	C88883	protein JC8.10 lim	1061	70	4.2	424	2	T18723	hypothetical prote
989	70.5	4.3	431	1	JC2002	transcription fact	1062	70	4.2	426	2	T04985	probable transamin
990	70.5	4.3	431	2	T11911	NADH2 dehydrogenas	1063	70	4.2	445	2	S45713	potassium channel
991	70.5	4.3	433	2	S37790	probable serine/th	1064	70	4.2	446	2	S66268	inward rectifier p
992	70.5	4.3	445	2	T23199	hypothetical prote	1065	70	4.2	455	2	A80181	hypothetical prote
993	70.5	4.3	462	2	A48933	gamma-aminobutyric	1066	70	4.2	456	2	T38221	hypothetical serin
994	70.5	4.3	465	2	H82345	mannose-1-phosphat	1067	70	4.2	458	2	T26630	hypothetical prote
995	70.5	4.3	491	2	T52398	hypothetical prote	1068	70	4.2	461	2	T38698	noc1 protein - fis
996	70.5	4.3	522	2	S41819	nucleoporin p62 -	1069	70	4.2	462	2	T19830	hypothetical prote
997	70.5	4.3	526	2	A34896	adenylate cyclase-	1070	70	4.2	487	2	A11505	hypothetical cell
998	70.5	4.3	526	2	C84552	hypothetical prote	1071	70	4.2	497	2	T51195	hypothetical prote
999	70.5	4.3	562	2	A85042	hypothetical prote	1072	70	4.2	529	2	S18453	variant surface gl
1000	70.5	4.3	608	2	A46312	gag polyprotein -	1073	70	4.2	542	2	B47022	chitinase (EC 3.2.
1001	70.5	4.3	616	2	T29234	hypothetical prote	1074	70	4.2	584	2	JC7809	sulfakinin recepto
1002	70.5	4.3	629	2	AE1525	probable peptidogl	1075	70	4.2	589	2	A10684	hypothetical prote
1003	70.5	4.3	649	2	T24505	hypothetical prote	1076	70	4.2	599	2	G71481	probable phosphoen
1004	70.5	4.3	675	2	D85065	receptor protein k	1077	70	4.2	609	2	S62518	hypothetical prote
1005	70.5	4.3	716	2	T28998	hypothetical prote	1078	70	4.2	611	2	T22456	hypothetical prote
1006	70.5	4.3	809	2	T18970	hypothetical prote	1079	70	4.2	613	2	B90294	hypothetical prote
1007	70.5	4.3	814	2	F59430	GTPase regulator a	1080	70	4.2	617	2	T15408	hypothetical prote
1008	70.5	4.3	839	2	I50590	class I INCENP pr	1081	70	4.2	625	2	S34035	hypothetical prote
1009	70.5	4.3	846	2	T38840	hypothetical trp-a	1082	70	4.2	651	2	S18874	nucleolin - Africa
1010	70.5	4.3	874	2	B86322	FGA14.8 protein -	1083	70	4.2	653	2	E86787	hypothetical prote
1011	70.5	4.3	877	2	I50591	class II INCENP pr	1084	70	4.2	662	2	T50464	glucose-regulated
1012	70.5	4.3	893	2	T18271	hypothetical prote	1085	70	4.2	697	2	E96752	hypothetical prote
1013	70.5	4.3	899	2	C84765	hypothetical prote	1086	70	4.2	706	2	S33761	transferrin precu
1014	70.5	4.3	910	1	S73361	dna1 homolog prote	1087	70	4.2	714	2	T22454	hypothetical prote
1015	70.5	4.3	942	2	S53963	MCS1 protein - yea	1088	70	4.2	753	2	T24869	hypothetical prote
1016	70.5	4.3	979	1	A35913	regulatory factor	1089	70	4.2	768	2	E86417	unknown protein, 5
1017	70.5	4.3	999	1	IUHUG3	desmoglein 3 precu	1090	70	4.2	770	2	T51024	related to CH2 zi
1018	70.5	4.3	1015	2	JC6552	DNA topoisomerase	1091	70	4.2	822	2	T51049	related to nucleol
1019	70.5	4.3	1028	2	E85089	probable transposo	1092	70	4.2	823	2	F90914	hypothetical prote
1020	70.5	4.3	1032	2	E89427	protein T08D2.3 li	1093	70	4.2	835	2	JC6140	cell surface-assoc
1021	70.5	4.3	1052	2	C64221	hypothetical 114K	1094	70	4.2	937	2	A56517	nucleoporin Nup98
1022	70.5	4.3	1106	2	T31742	hypothetical prote	1095	70	4.2	971	2	T19431	hypothetical prote
1023	70.5	4.3	1115	2	A47541	protein kinase iRE	1096	70	4.2	971	2	F88448	protein C45G9.10 l
1024	70.5	4.3	1123	2	T18270	hypothetical prote	1097	70	4.2	1004	2	A55142	myosin-light-chain
1025	70.5	4.3	1131	2	T15787	hypothetical prote	1098	70	4.2	1186	2	T19050	hypothetical prote
1026	70.5	4.3	1221	2	A10193	ribonuclease E (BC	1099	70	4.2	1213	2	A41724	limb deformity (ld
1027	70.5	4.3	1320	2	T44231	hypothetical prote	1100	70	4.2	1274	2	JN0015	trp protein - frui
1028	70.5	4.3	1603	2	S17983	gene posterior sex	1101	70	4.2	1275	2	JU0092	trp protein - frui
1029	70.5	4.3	1742	2	T17120	cellulase (EC 3.2.	1102	70	4.2	1415	2	T08945	hypothetical prote
1030	70.5	4.3	1872	2	T00339	hypothetical prote	1103	70	4.2	1420	1	A44361	amiloride-sensitiv
1031	70.5	4.3	2271	2	F90073	hypothetical prote	1104	70	4.2	1589	2	C44766	defective chorion-
1032	70.5	4.3	2717	2	A34203	DNA-binding protei	1105	70	4.2	1784	2	T10532	gag-pol polypotei
1033	70.5	4.3	3054	1	GNBEVE	genome polypotein	1106	70	4.2	1868	2	S48938	hypothetical prote
1034	70	4.2	147	2	JC7938	type II antifreeze	1107	70	4.2	2440	2	S39162	transcription coac
1035	70	4.2	148	2	T32622	hypothetical prote	1108	70	4.2	3163	1	JQ1895	genome polypotein
1036	70	4.2	150	2	T52587	probable arabinoga	1109	69.5	4.2	120	1	W4WL42	E4 protein - human
1037	70	4.2	150	2	T48611	agp6 protein - Ara	1110	69.5	4.2	124	2	E84613	hypothetical prote
1038	70	4.2	209	2	AB2218	hypothetical prote	1111	69.5	4.2	146	2	S52810	hypothetical prote
1039	70	4.2	210	2	JC7830	cytokine-inducible	1112	69.5	4.2	171	2	H86413	hypothetical prote
1040	70	4.2	214	2	A46629	mucin 6, gastric (1113	69.5	4.2	202	2	A82378	hypothetical prote
1041	70	4.2	221	2	T47592	hypothetical prote	1114	69.5	4.2	217	2	S01358	salivary glue prot
1042	70	4.2	234	2	G64858	probable membrane	1115	69.5	4.2	219	2	B72291	hypothetical prote
1043	70	4.2	239	2	B83709	hypothetical prote	1116	69.5	4.2	266	2	H55590	hypothetical prote
1044	70	4.2	256	2	AC2283	hypothetical prote	1117	69.5	4.2	271	2	B96773	hypothetical prote
1045	70	4.2	298	2	C55223	minor tail protein	1118	69.5	4.2	299	2	G70784	probable mmp3 pro
1046	70	4.2	310	2	T26267	hypothetical prote	1119	69.5	4.2	313	2	H36854	hemagglutinin - va
1047	70	4.2	311	2	H96002	probable sugar kin	1120	69.5	4.2	316	2	S58719	probable membrane
1048	70	4.2	321	2	T42750	hypothetical prote	1121	69.5	4.2	326	2	I48351	fos-related antige
1049	70	4.2	329	2	S38082	pathogenesis-relat	1122	69.5	4.2	332	2	F69437	hypothetical prote
1050	70	4.2	333	2	G98297	ribose ABC transpo	1123	69.5	4.2	338	2	S28004	probable cell surf
1051	70	4.2	333	2	AH2985	ABC transporter, m	1124	69.5	4.2	364	2	T32589	hypothetical prote

1125	69.5	4.2	372	1	Q0B588	glycoprotein I pre	1198	69	4.2	416	2	T34279	hypothetical prote
1126	69.5	4.2	372	2	T06745	hypothetical prote	1199	69	4.2	423	2	T44258	transducer protein
1127	69.5	4.2	400	2	T32705	hypothetical prote	1200	69	4.2	424	1	VGBEE9	glycoprotein gp63
1128	69.5	4.2	417	2	AD0200	isocitrate dehydro	1201	69	4.2	427	2	E83711	hypothetical prote
1129	69.5	4.2	423	2	T24383	hypothetical prote	1202	69	4.2	431	2	G86277	Fl41l7.11 protein
1130	69.5	4.2	425	2	T24111	hypothetical prote	1203	69	4.2	443	2	T14916	mitosis-specific c
1131	69.5	4.2	427	2	T38526	ubiquitin regulato	1204	69	4.2	467	2	T26195	hypothetical prote
1132	69.5	4.2	441	2	C75076	heme biosynthesis	1205	69	4.2	483	2	G86902	dextranucrase (EC
1133	69.5	4.2	450	2	C90608	hypothetical prote	1206	69	4.2	486	2	D64474	hypothetical prote
1134	69.5	4.2	458	2	F86433	protein T17H7.5 (f	1207	69	4.2	490	1	C57150	NADP-reducing hydr
1135	69.5	4.2	503	1	VMUT1B	variant surface gl	1208	69	4.2	495	2	T38959	hypothetical prote
1136	69.5	4.2	514	2	A44100	cell adhesion mole	1209	69	4.2	511	2	I50114	early growth respo
1137	69.5	4.2	514	2	A31643	cell adhesion 80K	1210	69	4.2	513	2	S50915	SIN3 protein-bindi
1138	69.5	4.2	519	2	S69989	unspecific monooxy	1211	69	4.2	525	2	A35596	nuclear pore glyco
1139	69.5	4.2	520	2	S14600	E2 glycoprotein pr	1212	69	4.2	538	2	S60645	NADH2 dehydrogenas
1140	69.5	4.2	532	2	G70906	probable coA ligas	1213	69	4.2	555	2	B41492	58K antigen - Rick
1141	69.5	4.2	537	2	B97013	and cellulose-bind	1214	69	4.2	556	2	S06838	gamma-aminobutyric
1142	69.5	4.2	538	2	AG2902	conserved hypothet	1215	69	4.2	556	2	S51892	probable membrane
1143	69.5	4.2	550	2	H97677	hypothetical prote	1216	69	4.2	583	2	T18999	hypothetical prote
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1145	69.5	4.2	552	2	T25593	hypothetical prote	1218	69	4.2	611	2	A53418	calmegin precursor
1146	69.5	4.2	568	2	A34891	Ig heavy chain pre	1219	69	4.2	647	2	B34457	204 protein - mous
1147	69.5	4.2	574	2	A86365	probable auxin tra	1220	69	4.2	650	2	S22835	alpha-egglutinin -
1148	69.5	4.2	593	2	S55189	hypothetical prote	1221	69	4.2	651	2	T21175	hypothetical prote
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1150	69.5	4.2	610	2	S59394	protein kinase RCK	1223	69	4.2	658	2	T41309	hypothetical threo
1151	69.5	4.2	611	2	A54086	calnexin-t - mouse	1224	69	4.2	670	2	F84540	hypothetical prote
1152	69.5	4.2	629	2	S20516	dnak-type molecula	1225	69	4.2	677	2	S54561	RNA14 protein - ye
1153	69.5	4.2	640	2	T25367	hypothetical prote	1226	69	4.2	725	2	E96592	hypothetical prote
1154	69.5	4.2	645	2	S41372	dnak-type molecula	1227	69	4.2	739	2	H72364	aspartokinase II -
1155	69.5	4.2	646	2	T19206	hypothetical prote	1228	69	4.2	790	2	T34293	hypothetical prote
1156	69.5	4.2	658	2	JC8011	G protein-coupled	1229	69	4.2	793	1	KXRTF	furin (EC 3.4.21.7
1157	69.5	4.2	675	2	T03744	myoD protein inhib	1230	69	4.2	815	2	T49207	receptor kinase-li
1158	69.5	4.2	719	2	T47727	hypothetical prote	1231	69	4.2	824	2	S26706	transcription fact
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1160	69.5	4.2	782	2	A82940	hypothetical prote	1233	69	4.2	854	1	QRHYLD	LDL receptor precu
1161	69.5	4.2	816	2	A49151	fibroblast growth	1234	69	4.2	871	2	T28706	hypothetical prote
1162	69.5	4.2	833	2	AF2089	hypothetical prote	1235	69	4.2	879	1	QRRTLT	LDL receptor precu
1163	69.5	4.2	844	2	B64678	NADH2 dehydrogenas	1236	69	4.2	903	1	VGBEK1	glycoprotein B pre
1164	69.5	4.2	850	1	MMHUE4	erythrocyte membra	1237	69	4.2	988	2	A40628	probable transposa
1165	69.5	4.2	852	2	T46091	hypothetical prote	1238	69	4.2	995	2	T27327	hypothetical prote
1166	69.5	4.2	862	2	T45289	hypothetical prote	1239	69	4.2	1007	2	JC8066	138K protein - Tet
1167	69.5	4.2	871	2	S47518	cadherin - African	1240	69	4.2	1157	2	A55152	PAS1 protein - yea
1168	69.5	4.2	942	2	T19553	hypothetical prote	1241	69	4.2	1203	2	T04294	hypothetical prote
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1172	69.5	4.2	1132	2	T43483	translation initia	1245	69	4.2	1385	2	T13415	hypothetical prote
1173	69.5	4.2	1460	2	S48457	nucleoporin RAT7 -	1246	69	4.2	1455	1	A48925	mannose receptor p
1174	69.5	4.2	1502	2	S45429	probable membrane	1247	69	4.2	1624	2	T25592	hypothetical prote
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1177	69.5	4.2	1875	2	S38173	myosin-like protei	1250	69	4.2	1758	2	S57015	probable purine nu
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1182	69	4.2	234	2	T35448	hypothetical prote	1255	69	4.2	2329	2	S44625	C50C3.6 protein -
1183	69	4.2	255	2	T22429	hypothetical prote	1256	69	4.2	2361	2	T25752	hypothetical prote
1184	69	4.2	258	2	S23106	p1A protein - shi	1257	69	4.2	2464	1	QRMS91	microtubule-associ
1185	69	4.2	284	2	T06241	histone H1 (clone	1258	68.5	4.1	168	2	S52994	arabinogalactan-11
1186	69	4.2	299	2	S44554	citrate transport	1259	68.5	4.1	189	1	ERAD75	early B3 20.6K gly
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1188	69	4.2	339	2	S08981	malate dehydrogena	1261	68.5	4.1	204	2	S51232	gibberellin-respon
1189	69	4.2	339	2	F97121	probable membrans-	1262	68.5	4.1	218	2	AH1837	hypothetical prote
1190	69	4.2	343	2	G86709	hypothetical prote	1263	68.5	4.1	246	2	S47805	hypothetical 27.4K
1191	69	4.2	344	1	RWRTC2	T-cell surface gly	1264	68.5	4.1	246	2	D91186	probable outer mem
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1194	69	4.2	382	2	S71669	finger protein MIG	1267	68.5	4.1	261	2	D84262	hypothetical prote
1195	69	4.2	387	2	T15462	hypothetical prote	1268	68.5	4.1	280	2	AE2031	gamma-tocopherol m
1196	69	4.2	396	2	T26987	hypothetical prote	1269	68.5	4.1	287	2	S45662	histone H1 - tomat
1197	69	4.2	400	1	A39822	leukosialin precur	1270	68.5	4.1	287	2	D95406	hypothetical prote

1271	68.5	4.1	288	2	T22846	hypothetical prote	1344	68	4.1	208	1	HSRT1T	histone H1t - rat
1272	68.5	4.1	318	2	T20063	hypothetical prote	1345	68	4.1	211	2	H72608	hypothetical prote
1273	68.5	4.1	345	2	T12344	NADH2 dehydrogen	1346	68	4.1	228	2	T33579	hypothetical prote
1274	68.5	4.1	349	2	T42965	glycoprotein - ate	1347	68	4.1	245	2	D81977	hypothetical prote
1275	68.5	4.1	359	2	G70814	probable far prote	1348	68	4.1	246	2	H90833	major tail protein
1276	68.5	4.1	378	2	T35403	probable polyprote	1349	68	4.1	256	2	B85691	probable tail comp
1277	68.5	4.1	385	2	JC77239	polyferredoxin [im	1350	68	4.1	268	2	T32740	hypothetical prote
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1279	68.5	4.1	394	2	G84206	hypothetical prote	1352	68	4.1	288	2	T21790	CIN5 protein - yea
1280	68.5	4.1	408	1	QRHUBE	beta-3-adrenergic	1353	68	4.1	295	2	S50316	hypothetical prote
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1284	68.5	4.1	414	1	QRHUB3	cell division prot	1357	68	4.1	360	2	S69063	probable membrane
1285	68.5	4.1	414	2	G84091	protein F59A7.1 [i	1358	68	4.1	372	2	T45628	glycerophosphodis
1286	68.5	4.1	420	2	A89962	synaptotagmin P65	1359	68	4.1	378	2	S61992	SLG1 protein - yea
1287	68.5	4.1	421	2	S09595	5-aminoimidazole r	1360	68	4.1	380	1	S51826	alcohol dehydrogen
1288	68.5	4.1	426	2	A35641	protein F2D10.28 (1361	68	4.1	384	2	H64161	hypothetical prote
1289	68.5	4.1	435	2	C86340	hypothetical prote	1362	68	4.1	387	2	A56275	1,3-propanediol de
1290	68.5	4.1	435	2	T23350	heat shock protein	1363	68	4.1	388	2	T43019	probable DNA-bindi
1291	68.5	4.1	443	2	F71929	probable exported	1364	68	4.1	402	2	T20595	hypothetical prote
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1294	68.5	4.1	502	2	T21935	cytochrome P450-li	1367	68	4.1	422	1	BMHU1Y	synaptotagmin I -
1295	68.5	4.1	509	2	T48459	fumarate hydratase	1368	68	4.1	423	2	T14531	S-locus-specific g
1296	68.5	4.1	514	1	A47692	hypothetical prote	1369	68	4.1	423	2	H84257	Htr13 transducer [
1297	68.5	4.1	527	2	T26732	hypothetical prote	1370	68	4.1	426	2	I48379	gene hb protein -
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1300	68.5	4.1	553	2	A49364	59 protein, brain	1373	68	4.1	461	2	D96647	hypothetical prote
1301	68.5	4.1	573	2	H95744	probable cytosolic	1374	68	4.1	461	2	T39862	hypothetical prote
1302	68.5	4.1	588	2	JC8021	chitinase (EC 3.2.	1375	68	4.1	479	2	A84588	probable tyrosine
1303	68.5	4.1	592	2	T32402	hypothetical prote	1376	68	4.1	487	1	S07061	glutamate receptor
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1305	68.5	4.1	630	2	A39344	tumor-associated m	1378	68	4.1	500	2	A11913	apolipoprotein N-a
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1311	68.5	4.1	696	2	G71829	probable out mem	1384	68	4.1	543	2	A38093	transformation-sen
1312	68.5	4.1	697	2	A86402	protein T22C5.17 (1385	68	4.1	550	2	T06379	SAR DNA-binding pr
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1325	68.5	4.1	865	2	AC1966	hypothetical prote	1398	68	4.1	632	2	T48616	hypothetical prote
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1327	68.5	4.1	915	2	T33030	hypothetical prote	1400	68	4.1	645	2	T16078	hypothetical prote
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C;Comment: This protein was isolated from the herpes papio induced B cell lymphoma.
C;Genetics:
A;Gene: CD44; ECMIII; Hermes-1 antigen
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cytoskeleton; extracellular matrix; glycoprotein; lipoprotein; surface antigen
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Query Match 13.4%; Score 222.5; DB 2; Length 362;
Best Local Similarity 25.5%; Pred. No. 3.1e-10;
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QY 140 IPEIITTKDPIFNTQTATQTFEIVSDST--YSVASPYSTIP-----APT----- 182
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QY 227 K-----NEMAGF-----GG-----VPTALLVLALLFFGAAGLGFCY 258
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C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 01-Dec-2000
C;Accession: A34424; A34907
R;Nottenburg, C.; Rees, G.; St. John, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989
A;Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate
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R;Wolfe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.
J. Biol. Chem. 265, 341-347, 1990
A;Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antigen
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A;Molecule type: mRNA

A;Residues: 8-195,'G',197-365 <WOL>
A;Cross-references: GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:g200335
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

Query Match 13.4%; Score 222.5; DB 2; Length 365;
Best Local Similarity 24.5%; Pred. No. 3.1e-10;
Matches 88; Conservative 56; Mismatches 150; Indels 65; Gaps 14;

QY 15 WTR---LLVQSLR--ABEELSIQVSCRMGITLVSKKANQOLNFTAEKACRLGLSLA 69
DB ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : :
6 WHTAWGLCLQLSLAHPHQDILNITCRYAGVHFVHVEKNGRYSISRTEAADLCAQFNSTLP 65

QY 70 GKQVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVLIWKVPVSRQFAAYCY 129
DB ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : :
66 TMDQMKALSFGFETCRYGFI-EGNVIPRIHPNAICAAHNTGVILTSNTSHDYTYCF 124

QY 130 NSSDWTNNSCIPFIIITTKDPIFNTQTATQTFEIVSDST--YSVASPYST----- 177
DB ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : :
125 NASAPPEEDC-----TSVTDLPNSFDGPVTITIVNRDGRYKKEGYRTHQEDIDASNII 179

QY 178 ----IPAPTTTTPPAPAS-----TSIPRRKKLICVTEVFMTSTMTST-ETEPFVENKAAPK- 227
DB ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : :
180 DDDVSSGSTIEBKSTPESYIHLTYLPTEQPTGDDDFIRSTLATRDRSSKDSRGSSRT 239

QY 228 ---NEAAGFGG-----VPTALLVLALLFFGAAGLGFCYVKRYKVA 265
DB ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : :
240 VTHGSELAGHSANODSGVTTSQPMRPPQIPFWIILIASL-LALALILAVC-----TAV 293

QY 266 PFPTNKNQKEMI---ETKVVEKANDSNPEESKTKDKNPEESKSPSKTTVRCLEAE 321
DB ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : :
294 NSRRCGQKKLVINGNGTVEDRKPSELN-GEASKSQEMVHLVNKESSETPDQCMTAD 351

RESULT 4
B38745
cell adhesion molecule CD44 precursor, long form (meta-1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: B38745; A38745
R;Guenther, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; Haubmann, I.; Matzku, S.
Cell 65, 13-24, 1991
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcinoma
A;Reference number: A38745; MUID:91191552; PMID:1707342
A;Accession: B38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-503 <GUE>
A;Cross-references: UNIPROT:P26051; GB:M61874; NID:G576534; PIDN:AAA53534.1; PID:G576535
C;Keywords: cell adhesion

Query Match 13.4%; Score 222; DB 2; Length 503;
Best Local Similarity 25.7%; Pred. No. 5e-10;
Matches 84; Conservative 40; Mismatches 165; Indels 38; Gaps 11;

QY 15 WTRLLVQSLRAEELSIQVSCRMGITLVSKKANQOLNFTAEKACRLGLSLAGKQV 74
DB ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : :
10 WGLLCLQLSLAQOQIDILNITCRYAGVHFVHVEKNGRYSISRTEAADLCEAFNTLPTMAQM 69

QY 75 ETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVLIWKVPVSRQFAAYCNSST 134
DB ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : :
70 ELALRKFETCRYGFI-EGHVVIPIRIHNSICAANNTGVILLASNTSHDYTYCFNASAP 128

QY 135 WTNSCIPFIIITTKDPIFNTQTATQTFEIVSDST--YSVASPYST---IPAPT----- 182
DB ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : :
129 LEEDC-----TSVTDLPNSFDGPVTITIVNRDGRYKKEGYRTHQEDIDASNIIDEDVS 183

QY 183 -----TTPPA-PASTSIPRRKKLICVTEVFMTSTMTST-ETEPFVENKAAPKQEAAGF 233

Db 184 SGTISKSTPEGVILLHTDPTSOPTGDRDDAFFIGSTGLATATPWPWSAHTKQNBERTQW 243
QY 234 GGV---PTALLVLALLFFGAAGLGCYVVKV--AFPTNKNQOKEMETKVVKEKA 288
Db 244 NPIHSNPEVLQTTTWTIDRNSTGAHGNWTQEPQPFNNHVEYQDEE-ETPHATSTTW 302
QY 289 NDSNPNNEESKTKD-----NPBESKSP 310
Db 303 ADPNSTTEEAATQEKWFENWQGNP 329

RESULT 5
A35616
T-cell surface glycoprotein CD44 - hamster
C:Species: Cricetineae gen. sp. (hamster)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A35616
R:Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed, B.
Cell 61, 1303-1313, 1990
A:Title: CD44 is the principal cell surface receptor for hyaluronate.
A:Reference number: A35616; MUID:90304889; PMID:1694723
A:Accession: A35616
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-362 <ARU>
A:Cross-references: UNIPROT:P20944
C:Superfamily: human cell adhesion protein CD44
C:Keywords: cell adhesion; glycoprotein; transmembrane protein

Query Match 13.1%; Score 217.5; DB 2; Length 362;
Best Local Similarity 25.4%; Pred. No. 7.7e-10;
Matches 88; Conservative 46; Mismatches 149; Indels 63; Gaps 12;

QY 24 SLRAEELSIOVSRIMGITLVSKKANQOLFTEAKEACRLGLSLAGKQDVETALKASPE 83
Db 18 SLAHEQIDLNITCRVAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTWDMQYNALSKGFE 77

QY 84 TCSYGVGDGVFVVISRISPNPKCGKNGVGLWIKVPSRQFAAYCYNNSDWTWNSCIPEI 143
Db 78 TCRYGFI-EGHVVIPRIQPNALCAANHGTGYVILTSNTS-HYDYTCFNASAPLEEDC---- 131

QY 144 ITTKDPIFNQTATOTTEFIVSDST-YSVASPYST-----IPAPTTTPPAPAS----- 190
Db 132 -TSVTDLPNSFEGPVTITVNRDGTYSKKGEYRTHQEDIDASNTDDVSSGSSSEKST 190

QY 191 -----TSIPRRKKLICVTEVFMTSTWSTE-----TTPFVEN 222
Db 191 SGGYVFHTYLTPIHSTADQDDPYFTIGSTWATRDQSSMDPRGNSLTVTDGSKLTGHSSGN 250

QY 223 KAAFKNEAAGFG---GVPTALLVLALLFFGAAGLGCYVVKVKAFFPTNKNQOKEMIE 279
Db 251 QDSGANTTSRGRKGPQIPWLVILASL-LALALILAVC-----IAVNSRRCGQKKLVI 304

QY 280 TKVVKEEKANDSNPNBESKTKDNPE-----ESKSPSKTTVTRCLEARE 321
Db 305 NS--GNGKVEDRKPSLNGEASKSQBMVHLVNKEPSETPDQFMFAD 348

RESULT 6
A53286
cell-surface glycoprotein CD44 precursor - bovine
N:Alternate names: CD44 protein
C:Species: Bos primigenius taurus (cattle)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A53286; S22123
R:Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.
Mol. Immunol. 28, 1131-1135, 1991
A:Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.
A:Reference number: A53286; MUID:92017904; PMID:1922105
A:Accession: A53286
A:Molecule type: mRNA
A:Residues: 1-366 <BOS>

A:Cross-references: UNIPROT:Q29423; EMBL:X67881; NID:g186; PIDN:CAA44675.1; PID:g187
A>Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBIP:63419)
C:Superfamily: human cell adhesion protein CD44
C:Keywords: cell adhesion; glycoprotein; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>
F:274-294/Domain: transmembrane #status predicted <TM>
F:25-57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predicted:

Query Match 12.6%; Score 208.5; DB 2; Length 366;
Best Local Similarity 23.8%; Pred. No. 4.1e-09;
Matches 81; Conservative 44; Mismatches 142; Indels 73; Gaps 11;

QY 20 LVQGSRLRAEELSIOVSRIMGITLVSKKANQOLFTEAKEACRLGLSLAGKQDVETALK 79
Db 14 LVQLSL--AQIDNLNITCRVAGVFHVEKNGRYSISKTEAADLCKAFNSTLPTWQAQMEAAARN 71

QY 80 ASFETCSYGVGDGVFVVISRISPNPKCGKNGVGLWIKVPSRQFAAYCYNNSDWTWNSC 139
Db 72 IGFETCRYGFI-EGHVVIPRIHPNSICAANTGVVILTSNTS-QYDTTCFNASAPPGEDC 129

QY 140 IPEIITTKDPIFNQTATOTTEFIVSDST-YSVASPYSTIP-----APTTPPAPAS 190
Db 130 -----TSVTDLPNAVEGPITITVNRDGTTRYTKGEYRTPNEDINPSVSPSPDDENS 184

QY 191 TSIPRRKKLICVTEVF-----METSTMSTETETEPVENKAAPFK 227
Db 185 SGSPSERSTSGYSIFHTHLPVHPSPRRPMSQRAENTSDTRDYGSSHDPSGRSVYTHA 244

QY 228 NEAAGFGG-----VPTALLVLALLFFGAAGLGCYVVKVKAFFPT 269
Db 245 SESAGHSGSBEHGANTTSGPMRKQIPWLVILASL-LALALILAVC-----IAVNSRR 298

QY 270 NKNQOKEMIEYKVKVEEKANDSNPNBESKTKDNPEESKS 309
Db 299 RCGQKKKLVIN-----NGNGTMEERKPSGLNGEASKS 330

RESULT 7
JH0417
cell adhesion molecule CD44 - human
C:Species: Homo sapiens (man)
C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C:Accession: JH0417; A32376; G02251; A32377
R:Harn, H.J.; Isola, N.; Cooper, D.L.
Biochem. Biophys. Res. Commun. 178, 1127-1134, 1991
A:Title: The multispecific cell adhesion molecule CD44 is represented in reticulocyte c
A:Reference number: JH0417; MUID:91337049; PMID:1840487
A:Accession: JH0417
A:Molecule type: mRNA
A:Residues: 1-361 <HAR>
A:Cross-references: UNIPROT:Q92493; GB:M59040; NID:g180129; PIDN:AAA51950.1; PID:g180130
A:Experimental source: reticulocyte
A>Note: the authors translated the codon ATG for residues 63, 66 and 239 as Trp and GGA
R:Stamenkovic, I.; Amiot, M.; Pesando, J.M.; Seed, B.
Cell 56, 1057-1062, 1989
A:Title: A lymphocyte molecule implicated in lymph node homing is a member of the cartil
A:Reference number: A32376; MUID:89168434; PMID:2466575
A:Accession: A32376
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-238,'E',240-361 <STA>
A:Cross-references: GB:M24915; NID:g180196; PIDN:AAA35674.1; PID:g180197
R:Bosch, P.P.; Stevens, J.W.; Buckwalter, J.A.; Midura, R.J.
Submitted to the EMBL Data Library, November 1995
A:Reference number: H00921
A:Accession: G02251
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-25,'M',27-108,'S',110-361 <BOS>
A:Cross-references: EMBL:U040373; NID:g1101785; PID:g1101786
R:Goldstein, L.A.; Zhou, D.F.H.; Picker, L.J.; Minty, C.N.; Bargatze, R.F.; Ding, J.F.;
Cell 56, 1063-1072, 1989

A;Experimental source: lymphocyte, cell line KG1a
R;Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datta, Biochem. Biophys. Res. Commun. 182, 569-578, 1992
A;Title: The complex CD44 transcriptional unit: alternative splicing of three internal exons
A;Reference number: PH0859; MUID:92134271; PMID:1734871
A;Accession: PH0859
A;Molecule type: DNA
A;Residues: 223-357 <COO>
R;Brown, T.A.; Bouchard, T.; St. John, T.; Wayner, E.; Carter, W.G. J. Cell Biol. 113, 207-221, 1991
A;Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfate proteoglycan
A;Reference number: A39209; MUID:91177958; PMID:2007624
A;Accession: A39209
A;Molecule type: mRNA
A;Residues: 184-376 <BRO>
A;Cross-references: GB:X55938; NID:929802; PIDN:CAA39404.1; PID:9330047
R;Jackson, D.G.; Buckley, J.; Bell, J.I. J. Biol. Chem. 267, 4733-4739, 1992
A;Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by independent alternative splicing of three internal exons
A;Reference number: A42402; MUID:92165834; PMID:1537855
A;Accession: A42402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 217-223, 288-359 <JAC>
A;Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIPI:83965)
A;Note: variant B
A;Accession: C42402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 217-320 <JAC>
A;Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIPI:83969)
R;Shepley, M.P.; Racanietello, V.R. J. Virol. 68, 1301-1308, 1994
A;Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocyte homing receptor CD44
A;Reference number: A53029; MUID:94149816; PMID:7508992
A;Accession: A53029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 67-76, 'X', '78-89 <SHE>
C;Genetics:
A;Gene: GDB:CD44; MDU2; MDU3; MI
A;Cross-references: GDB:120739; OMIM:107269
A;Map position: lipter-1lp13
A;Introns: 35/1; 65/1; 133/1
C;Superfamily: human cell adhesion protein CD44
C;Keywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glycosylation; lymphocyte homing receptor CD44, splice form CD44R1 #status predicted <F>
F;1-223,288-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status predicted <F>
F;299/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;354/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
Query Match 12.0%; Score 199.5; DB 2; Length 426;
Best Local Similarity 22.2%; Pred. No. 2.6e-08;
Matches 83; Conservative 48; Mismatches 138; Indels 105; Gaps 12;
QY 25 LRAEELSIQVSRIMGITLVSKANQQLNFTAKACRLGLSLACKQDVETALKASRET 84
DB 17 LSLAQIDLNITCFAGVFHVEKNRYSISRTEADLCKAFNSTLPTMAOMEKALSIGFET 76
QY 85 CSYGWVGDFVVISRISPNPKCKGKNGVGLIWKVPVSROFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHWIPIRHPNSICAAANTGVILTSNTS-QYDYTCFNASAPPEDECTSVTD 134
QY 141 -----PEIITKDPINFQTATQTE-----FI 163
DB 135 LPNAPDGPITITVNRDGRYVQKGYRTNPEDIYPSNPTDDVSSGSSRSSTSGGYI 194
QY 164 -----VSDST-----YSVASPYSTIPATPTTPAPASTSIPRKKLIC 201
DB 195 FYTFSTVHIPEDSPWITDSDRIPATNMDSHSTTLQPTANPNGLVEDLDRGTGLSM 254
QY 202 VTEFVMTSTMSTETEPFVENK-----AAFKNEAAG 232
DB 255 TTQQ-SNSQSFSTSHGLEEDKHPTTSLTSSNRNDVTG 293
Query Match 12.0%; Score 199.5; DB 2; Length 426;
Best Local Similarity 22.2%; Pred. No. 2.6e-08;
Matches 83; Conservative 48; Mismatches 138; Indels 105; Gaps 12;
QY 25 LRAEELSIQVSRIMGITLVSKANQQLNFTAKACRLGLSLACKQDVETALKASRET 84
DB 17 LSLAQIDLNITCFAGVFHVEKNRYSISRTEADLCKAFNSTLPTMAOMEKALSIGFET 76
QY 85 CSYGWVGDFVVISRISPNPKCKGKNGVGLIWKVPVSROFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHWIPIRHPNSICAAANTGVILTSNTS-QYDYTCFNASAPPEDECTSVTD 134
QY 141 -----PEIITKDPINFQTATQTE-----FI 163
DB 135 LPNAPDGPITITVNRDGRYVQKGYRTNPEDIYPSNPTDDVSSGSSRSSTSGGYI 194
QY 164 -----VSDST-----YSVASPYSTIPATPTTPAPASTSIPRKKLIC 201
DB 195 FYTFSTVHIPEDSPWITDSDRIPATNMDSHSTTLQPTANPNGLVEDLDRGTGLSM 254
QY 202 VTEFVMTSTMSTETEPFVENK-----AAFKNEAAGFGVGP-----TALLVALL 246

DB 255 TTQQ-SNSQSFSTSHGLEEDKHPTTSLTSSNRNDVTGRRDPNHSSEGSTLL----- 308
QY 247 FFGAAAGLFCYVVKVYKAFPTNKQKQEMIEITKV-----VKEEKANDSNPN-EESKKT 300
DB 309 -----EGTSHYPHTKESRTFIPVTSAKTSGFGVTAVTVGDSNVNRSLSG 355
QY 301 DKNPEESKSPSKTT 314
DB 356 DQDTFHPSGSHTT 369
RESULT 11
S13530
CD44E protein, epithelial - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: S13530
R;Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B. EMBO J. 10, 343-348, 1991
A;Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with different extracellular domains
A;Reference number: S13530; MUID:91122041; PMID:1991450
A;Accession: S13530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-493 <STA>
A;Cross-references: EMBL:X55150; NID:929800; PIDN:CAA38951.1; PID:929801
C;Keywords: transmembrane protein
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 3.1e-08;
Matches 66; Conservative 39; Mismatches 100; Indels 75; Gaps 8;
QY 25 LRAEELSIQVSRIMGITLVSKANQQLNFTAKACRLGLSLACKQDVETALKASRET 84
DB 17 LSLAQIDLNITCFAGVFHVEKNRYSISRTEADLCKAFNSTLPTMAOMEKALSIGFET 76
QY 85 CSYGWVGDFVVISRISPNPKCKGKNGVGLIWKVPVSROFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHWIPIRHPNSICAAANTGVILTSNTS-QYDYTCFNASAPPEDECTSVTD 134
QY 141 -----PEIITKDPINFQTATQTE-----FI 163
DB 135 LPNAPDGPITITVNRDGRYVQKGYRTNPEDIYPSNPTDDVSSGSSRSSTSGGYI 194
QY 164 -----VSDST-----YSVASPYSTIPATPTTPAPASTSIPRKKLIC 201
DB 195 FYTFSTVHIPEDSPWITDSDRIPATNMDSHSTTLQPTANPNGLVEDLDRGTGLSM 254
QY 202 VTEFVMTSTMSTETEPFVENK-----AAFKNEAAG 232
DB 255 TTQQ-SNSQSFSTSHGLEEDKHPTTSLTSSNRNDVTG 293
RESULT 12
I77371
CD44R5 - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: I77371
R;Tanabe, K.K.; Nishi, T.; Sava, H. Mol. Carcinog. 7, 212-220, 1993
A;Title: Novel variants of CD44 arising from alternative splicing: changes in the CD44 protein structure
A;Reference number: I57483; MUID:93356912; PMID:8352881
A;Accession: I77371
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-395 <RES>
A;Cross-references: GB:S66400; NID:9435697; PIDN:AAB27919.1; PID:9435700
C;Genetics:
A;Gene: GDB:CD44
A;Map position: 1lp1p13

A;Introns: 257/1
C;Superfamily: human cell adhesion protein CD44

Query Match 11.9%; Score 198; DB 2; Length 395;
Best Local Similarity 23.0%; Pred. No. 3.1e-08;
Matches 85; Conservative 49; Mismatches 145; Indels 90; Gaps 14;

QY 25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTFAKEACRLGLSLAGKQVETALKASPET 84
DB 17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEADLCKAFNSTLPTMAQMEKALSIGPET 76
QY 85 CSYGWVGDFVVISRISPNKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHVVIPIHPNSICAANNVTGYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134
QY 141 -----PEIITKDPINFNTQATOTTEFIVSDSYVASPYST 177
DB 135 LPNAFDGPITITIVNRDGRYVQKGEYRTNPEDIYPSNPTDDVSSGSSRSSTSGGYI 194
QY 168 --TYSVASPY-----STIPATPTTPAPASTSI-PRRKKLICVTEFVEMSTWST 214
DB 195 FYTFSTVHPIDPDESPWITDSDRIPATNMDSHSTTLQPTANPTGLVEDLDRTGPLSM 254
QY 215 ET-----EPFVENKAAAFNEAAGF-----GG-----VPTALLVLALLFFGA 250
DB 255 TTRDQDTHPSSGSHTHGSESDGSHSQEGGANTTSGPIPTPQIPPEWLIIILASL-LAL 313
QY 251 AAGLGFYVYKRVKAPFNTKNQOKEMIETK---VVKEEKANDSNPNBESKTKDK----N 303
DB 314 ALILAVC-----IAVNSRRRCQKKLVINSNGAVEDRKPSGLN-GEASKSQEMVHLVN 367
QY 304 PRESKSPSK 312
DB 368 KESSETPDQ 376

RESULT 13
I37369
epican - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Aug-2001
C;Accession: I37369; S24631
R;Kugelman, L.C.; Ganguly, S.; Haggerty, J.G.; Weisman, S.M.; Milstone, L.M.
J. Invest. Dermatol. 99, 866-891, 1992
A;Title: The core protein of epican, a heparan sulfate proteoglycan on keratinocytes, is
A;Note: corrected and republished from J. Invest. Dermatol. 99, 381-385, 1992
A;Reference number: I37369; PMID:1281868
A;Accession: I37369
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-699 <RES>
A;Cross-references: EMBL:X66733; NID:g31190; PID:g31191

Query Match 11.9%; Score 196.5; DB 2; Length 699;
Best Local Similarity 25.4%; Pred. No. 8.3e-08;
Matches 60; Conservative 34; Mismatches 93; Indels 49; Gaps 7;

QY 25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTFAKEACRLGLSLAGKQVETALKASPET 84
DB 17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEADLCKAFNSTLPTMAQMEKALSIGPET 76
QY 85 CSYGWVGDFVVISRISPNKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHVVIPIHPNSICAANNVTGYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134
QY 141 -----PEIITKDPINFNTQATOTTEFIVSDSYVASPYST 177
DB 135 LPNAFDGPITITIVNRDGRYVQKGEYRTNPEDIYPSNPTDDVSSGSSRSSTSGGY- 193
QY 171 VASPYSTI-PAPTPTTP--APASTSIPIRRKKLICVTEFVEMSTWSTETEPFVENK 223
DB 194 IFYTFSTVHPIDPDESPWITDSDRIPATNS-----TSSNTISAGNEPNEENE 240

RESULT 14
S24240
lymphocyte surface antigen CD44 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: I46245; S24240
R;Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis, W.; Butc
Immunogenetics 37, 474-477, 1993
A;Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.
A;Reference number: I46245; MUID:93170897; PMID:8436424
A;Accession: I46245
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-359 <TA>
A;Cross-references: UNIPROT:Q05078; EMBL:X6862; NID:g1059; PIDN:CAA47331.1; PID:g1060
C;Superfamily: human cell adhesion protein CD44
C;Keywords: surface antigen; transmembrane protein

Query Match 11.2%; Score 186; DB 2; Length 359;
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DB 252 ASTTSGPIRRRPQIPPEWLIIILASL-LALALILAVC-----IAVNSRRRCGKKLVINNGN 305
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DB 306 GAVDDRKASGLN-GEASKSQEMVHLVNKESSETQDQFWTAD 345

RESULT 15
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N;Alternate names: cartilage chondroitin sulfate proteoglycan core protein
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072
R;Li, H.; Schwartz, N.B.; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A;Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
A;Reference number: A48884; MUID:94043149; PMID:8226878
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A;Cross-references: UNIPROT:P07898; GB:L21913; NID:g416133; PIDN:AAB19128.1; PID:g4161334
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 296, 885-887, 1993
A;Reference number: S39796; MUID:94107258; PMID:8280087
A;Contents: annotation; erratum
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OM protein - protein search, using sw model

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974.620 Million cell updates/sec

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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 3909, Ap	322	US-10-723-860-3909	322	98.9	1638	249
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Sequence 1285, Ap	16	US-10-473-127-1285	16	12.6	208.5	259
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Sequence 1308, Ap	436	US-10-473-127-1308	436	12.3	203	280
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359	145	8.8	277	14	US-10-247-671-185	Sequence 185, App	1126	121.5	7.3	360	16	US-10-215-371-213	Sequence 213, App
360	145	8.8	277	15	US-10-295-027-292	Sequence 292, App	1127	121.5	7.3	360	16	US-10-771-187-213	Sequence 213, App
361	145	8.8	277	15	US-10-295-027-1237	Sequence 1237, Ap	1128	121.5	7.3	360	17	US-10-963-467-213	Sequence 213, App
362	145	8.8	277	16	US-10-723-860-4326	Sequence 4326, Ap	1129	121.5	7.3	360	17	US-10-978-255-213	Sequence 213, App
363	145	8.8	1069	15	US-10-028-248A-39	Sequence 39, Appl	1130	121.5	7.3	360	18	US-10-797-366-213	Sequence 213, App
364	145	8.8	1069	15	US-10-107-782-39	Sequence 39, Appl	1134	121	7.3	528	10	US-09-759-130B-341	Sequence 341, App
365	145	8.8	2626	15	US-10-634-574-4	Sequence 4, Appl	1135	121	7.3	528	14	US-10-189-123-71	Sequence 71, Appl
366	143.5	8.7	95	15	US-10-424-599-248857	Sequence 248857, A	1136	121	7.3	528	14	US-10-188-495-71	Sequence 71, Appl
367	134	8.1	897	15	US-10-028-248A-41	Sequence 41, Appl	1137	121	7.3	528	16	US-10-741-790-341	Sequence 341, App
368	134	8.1	897	15	US-10-028-248A-211	Sequence 211, App	1138	121.5	7.3	528	17	US-10-314-942-20	Sequence 20, Appl
369	134	8.1	897	15	US-10-107-782-41	Sequence 41, Appl	1139	118.5	7.2	1642	17	US-10-741-600-1176	Sequence 1176, Ap
370	134	8.1	897	15	US-10-107-782-211	Sequence 211, App	1140	118.5	7.2	1642	17	US-10-741-600-1178	Sequence 1178, Ap
371	134	8.1	2675	15	US-10-028-248A-2	Sequence 2, Appl	1141	118.5	7.2	3396	16	US-10-788-792-170	Sequence 170, App
372	134	8.1	2675	15	US-10-107-782-2	Sequence 2, Appl	1142	118.5	7.2	3396	17	US-10-741-600-1172	Sequence 1172, Ap
373	133	8.0	1192	15	US-10-028-248A-40	Sequence 40, Appl	1143	118.5	7.2	3396	17	US-10-741-600-1173	Sequence 1173, Ap
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1296	90	5.4	364	17	US-10-663-497-27	Sequence 27, Appl	1369	86.5	5.2	1579	18	US-10-263-929-122	Sequence 122, App
1297	90	5.4	629	20	US-11-097-143-5313	Sequence 5313, Ap	1370	86.5	5.2	2781	15	US-10-723-860-1472	Sequence 1472, Ap
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1301	90	5.4	1367	9	US-09-801-368-108	Sequence 108, App	1374	86	5.2	390	17	US-10-732-923-20210	Sequence 20210, A
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1307	89.5	5.4	1368	17	US-10-732-923-13518	Sequence 13518, A	1380	85.5	5.2	346	15	US-10-432-290-11	Sequence 11, Appl
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1311	89	5.4	416	15	US-10-371-089-26	Sequence 26, Appl	1384	85.5	5.2	686	15	US-10-282-122A-43763	Sequence 43763, A
1312	89	5.4	416	15	US-10-371-089-26	Sequence 26, Appl	1385	85.5	5.2	781	15	US-10-074-978A-286	Sequence 286, App
1313	89	5.4	416	15	US-10-371-260-26	Sequence 26, Appl	1386	85.5	5.2	781	15	US-10-664-456-16	Sequence 16, Appl
1314	89	5.4	416	16	US-10-684-422-68	Sequence 68, Appl	1387	85.5	5.2	792	9	US-09-802-207-27	Sequence 27, Appl
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1316	89	5.4	416	18	US-10-287-436A-1224	Sequence 1224, Ap	1389	85.5	5.2	841	16	US-11-097-143-39828	Sequence 39828, A
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1320	89	5.4	2588	16	US-10-437-963-138279	Sequence 138279,	1393	85.5	5.2	1794	10	US-09-965-738-149	Sequence 149, App
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1322	88.5	5.3	358	18	US-10-450-763-45673	Sequence 45673, A	1395	85.5	5.2	2055	14	US-10-193-874-20	Sequence 20, Appl
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1324	88.5	5.3	615	15	US-10-328-818-14	Sequence 14, Appl	1397	85.5	5.2	2586	9	US-09-723-485A-14	Sequence 14, Appl
1325	88	5.3	125	15	US-10-424-599-221671	Sequence 221671,	1398	85.5	5.2	2586	9	US-09-802-318-11	Sequence 11, Appl
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1327	88	5.3	995	10	US-09-836-353A-48	Sequence 48, Appl	1400	85.5	5.2	2586	9	US-09-905-129-11	Sequence 11, Appl
1328	88	5.3	3507	15	US-10-369-493-5784	Sequence 5784, Ap	1401	85.5	5.2	2586	9	US-09-991-630-11	Sequence 11, Appl
1329	87.5	5.3	536	14	US-10-218-743-21	Sequence 21, Appl	1402	85.5	5.2	2586	9	US-09-991-630-14	Sequence 14, Appl
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130	86.5	5.2	807	4	US-09-294-663-4	Sequence 4, Appli	203	82	4.9	553	3	US-08-951-086-2	Sequence 2, Appli
131	86.5	5.2	2781	4	US-09-698-295-10	Sequence 10, Appl	204	82	4.9	553	3	US-09-430-669-2	Sequence 2, Appli
132	86.5	5.2	2907	4	US-09-698-295-1	Sequence 1, Appli	205	82	4.9	715	3	US-09-215-221-25	Sequence 25, Appl
133	86	5.2	750	3	US-09-165-239A-4	Sequence 3, Appli	206	82	4.9	1026	4	US-09-248-796A-16128	Sequence 16128, A
134	86	5.2	786	3	US-09-103-429A-3	Sequence 4, Appli	207	82	4.9	1083	4	US-09-538-092-812	Sequence 812, App
135	86	5.2	805	3	US-09-103-429A-4	Sequence 4, Appli	208	81.5	4.9	522	4	US-09-248-796A-14121	Sequence 14121, A
136	86	5.2	905	3	US-08-666-221B-10	Sequence 10, Appl	209	81.5	4.9	586	2	US-08-630-822A-70	Sequence 70, Appl
137	85.5	5.2	531	4	US-09-270-767-32631	Sequence 32631, A	210	81.5	4.9	586	2	US-09-005-069-70	Sequence 70, Appl
138	85.5	5.2	531	4	US-09-270-767-47848	Sequence 47848, A	211	81.5	4.9	586	3	US-09-171-156A-30	Sequence 30, Appl
139	85.5	5.2	781	4	US-09-949-016-6959	Sequence 6959, Ap	212	81.5	4.9	586	4	US-09-004-730A-30	Sequence 30, Appl
140	85	5.1	318	4	US-09-902-540-10266	Sequence 10266, A	213	81.5	4.9	586	4	US-08-981-799A-30	Sequence 30, Appl
141	84.5	5.1	270	4	US-09-248-796A-14475	Sequence 14475, A	214	81.5	4.9	687	2	US-08-540-804-4	Sequence 4, Appli
142	84.5	5.1	507	4	US-09-949-016-8889	Sequence 8889, Ap	215	81.5	4.9	687	2	US-08-218-265-4	Sequence 4, Appli
143	84.5	5.1	507	4	US-09-949-016-8897	Sequence 8897, Ap	216	81.5	4.9	687	3	US-08-521-872-4	Sequence 4, Appli
144	84.5	5.1	1011	3	US-08-836-325-2	Sequence 2, Appli	217	81.5	4.9	687	3	US-08-590-399-4	Sequence 4, Appli
145	84.5	5.1	1011	3	US-09-457-571-2	Sequence 2, Appli	218	81.5	4.9	1445	1	US-08-015-986A-2	Sequence 2, Appli
146	84.5	5.1	1984	3	US-08-836-325-10	Sequence 10, Appl	219	81.5	4.9	1445	2	US-08-446-363-2	Sequence 2, Appli
147	84.5	5.1	1984	4	US-09-457-571-10	Sequence 10, Appl	220	81	4.9	49	1	US-08-340-428B-23	Sequence 23, Appl
148	84.5	5.1	1989	3	US-08-836-325-12	Sequence 12, Appl	221	81	4.9	49	5	PCT-US93-07306-23	Sequence 23, Appl
149	84.5	5.1	1989	4	US-09-457-571-12	Sequence 12, Appl	222	81	4.9	413	3	US-08-669-408B-10	Sequence 10, Appl
150	84	5.1	216	3	US-08-928-361B-8	Sequence 8, Appli	223	81	4.9	531	4	US-09-248-796A-15560	Sequence 15560, A
151	84	5.1	216	3	US-08-928-361B-27	Sequence 27, Appl	224	81	4.9	855	2	US-08-816-693A-2	Sequence 2, Appli
152	84	5.1	216	4	US-09-588-995A-8	Sequence 8, Appli	225	81	4.9	855	3	US-08-885-291-2	Sequence 2, Appli
153	84	5.1	920	1	US-07-718-575-10	Sequence 10, Appl	226	81	4.9	855	3	US-09-496-672-2	Sequence 2, Appli
154	84	5.1	920	1	US-08-481-206-10	Sequence 10, Appl	227	81	4.9	855	4	US-09-618-425-11	Sequence 11, Appl
155	84	5.1	920	2	US-08-486-269A-10	Sequence 10, Appl	228	81	4.9	883	4	US-09-248-796A-18931	Sequence 18931, A
156	84	5.1	1721	3	US-08-700-651-5	Sequence 5, Appli	229	80.5	4.9	334	4	US-09-197-970B-7	Sequence 7, Appli
157	84	5.1	1721	3	US-08-928-361B-6	Sequence 6, Appli	230	80.5	4.9	478	4	US-09-345-473E-51	Sequence 51, Appl
158	84	5.1	1721	4	US-09-588-995A-6	Sequence 6, Appli	231	80.5	4.9	556	4	US-09-949-016-11052	Sequence 11052, A
159	84	5.1	1837	3	US-08-928-361B-5	Sequence 5, Appli	232	80.5	4.9	595	2	US-08-232-087A-2	Sequence 2, Appli
160	84	5.1	1837	4	US-09-588-995A-5	Sequence 5, Appli	233	80.5	4.9	595	3	US-09-006-353A-9	Sequence 9, Appli
161	83.5	5.0	346	2	US-08-687-702-36	Sequence 36, Appl	234	80.5	4.9	595	4	US-09-573-986-9	Sequence 9, Appli
162	83.5	5.0	393	3	US-09-377-557-14	Sequence 14, Appl	235	80.5	4.9	595	4	US-09-949-016-6048	Sequence 6048, Ap
163	83.5	5.0	562	2	US-08-687-702-1	Sequence 1, Appli	236	80.5	4.9	624	4	US-09-877-730-24	Sequence 24, Appl
164	83.5	5.0	879	1	US-08-220-151-2	Sequence 2, Appli	237	80.5	4.9	642	4	US-09-949-016-8043	Sequence 8043, Ap
165	83.5	5.0	879	1	US-08-220-151-3	Sequence 3, Appli	238	80.5	4.9	673	4	US-09-949-016-7388	Sequence 7388, Ap
166	83.5	5.0	879	1	US-08-413-118-2	Sequence 2, Appli	239	80.5	4.9	712	4	US-09-877-730-22	Sequence 22, Appl
167	83.5	5.0	879	1	US-08-413-118-3	Sequence 3, Appli	240	80.5	4.9	793	4	US-09-877-730-28	Sequence 28, Appl
168	83.5	5.0	879	1	US-08-413-118-106	Sequence 106, App	241	80.5	4.9	991	4	US-09-877-730-12	Sequence 12, Appl
169	83.5	5.0	879	3	US-08-473-446-2	Sequence 2, Appli	242	80.5	4.9	1069	4	US-09-877-730-2	Sequence 2, Appli
170	83.5	5.0	879	3	US-08-473-446-3	Sequence 3, Appli	243	80.5	4.9	1072	4	US-09-877-730-18	Sequence 18, Appl
171	83.5	5.0	879	3	US-08-473-446-106	Sequence 106, App	244	80.5	4.9	1150	4	US-09-877-730-8	Sequence 8, Appli
172	83.5	5.0	1579	4	US-09-538-092-1258	Sequence 1258, Ap	245	80	4.8	52	1	US-08-225-477B-10	Sequence 10, Appl
173	83	5.0	147	3	US-09-230-637-43	Sequence 43, Appl	246	80	4.8	52	5	PCT-US95-04353-10	Sequence 10, Appl
174	83	5.0	175	4	US-09-270-767-33553	Sequence 33553, A	247	80	4.8	95	4	US-09-252-991A-28504	Sequence 28504, A
175	83	5.0	175	4	US-09-270-767-48770	Sequence 48770, A	248	80	4.8	251	4	US-09-248-796A-23216	Sequence 23216, A
176	83	5.0	205	4	US-09-248-796A-21984	Sequence 21984, A	249	80	4.8	257	4	US-09-902-540-15102	Sequence 15102, A
177	83	5.0	351	4	US-09-248-796A-23675	Sequence 23675, A	250	80	4.8	372	4	US-09-248-796A-19896	Sequence 19896, A
178	83	5.0	409	4	US-09-538-092-1214	Sequence 1214, Ap	251	80	4.8	404	4	US-09-270-767-41751	Sequence 41751, A
179	83	5.0	409	4	US-09-949-016-6281	Sequence 6281, Ap	252	80	4.8	423	4	US-09-270-767-44448	Sequence 44448, A
180	83	5.0	454	4	US-09-949-016-11120	Sequence 11120, A	253	80	4.8	451	1	US-08-287-001A-2	Sequence 2, Appli
181	83	5.0	736	3	US-09-457-040B-26	Sequence 26, Appl	254	80	4.8	451	5	PCT-US95-09941-2	Sequence 2, Appli
182	82.5	5.0	203	4	US-09-270-767-35040	Sequence 35040, A	255	80	4.8	468	2	US-08-959-011-3	Sequence 3, Appli
183	82.5	5.0	203	4	US-09-270-767-50257	Sequence 50257, A	256	80	4.8	823	4	US-09-248-796A-16699	Sequence 16699, A
184	82.5	5.0	219	3	US-09-134-001C-5651	Sequence 5651, Ap	257	80	4.8	893	4	US-08-189-738A-18	Sequence 18, Appl
185	82.5	5.0	447	4	US-09-252-991A-28081	Sequence 28081, A	258	79.5	4.8	153	4	US-09-252-991A-17880	Sequence 17880, A
186	82.5	5.0	591	4	US-09-270-767-32687	Sequence 32687, A	259	79.5	4.8	154	4	US-09-270-767-40476	Sequence 40476, A
187	82.5	5.0	591	4	US-09-270-767-47904	Sequence 47904, A	260	79.5	4.8	154	4	US-09-270-767-55692	Sequence 55692, A
188	82.5	5.0	790	4	US-09-949-016-7017	Sequence 7017, Ap	261	79.5	4.8	324	4	US-09-483-039A-8593	Sequence 8593, Ap
189	82.5	5.0	790	4	US-09-949-016-8169	Sequence 8169, Ap	262	79.5	4.8	374	4	US-09-248-796A-17283	Sequence 17283, A
190	82.5	5.0	790	4	US-09-949-016-8170	Sequence 8170, Ap	263	79.5	4.8	461	1	US-08-385-229-2	Sequence 2, Appli
191	82.5	5.0	866	1	US-08-405-392-17	Sequence 17, Appl	264	79.5	4.8	461	2	US-08-650-000-2	Sequence 2, Appli
192	82.5	5.0	866	3	US-08-487-691-17	Sequence 17, Appl	265	79.5	4.8	461	3	US-09-042-785A-7	Sequence 7, Appli

266	79.5	4.8	461	3	US-08-477-347-3	Sequence 3, Appli	357	77	4.6	162	3	US-09-068-140A-2	Sequence 2, Appli
267	79.5	4.8	461	3	US-09-006-353A-4	Sequence 4, Appli	358	77	4.6	173	3	US-09-068-140A-13	Sequence 13, Appli
268	79.5	4.8	461	3	US-08-476-862-2	Sequence 2, Appli	359	77	4.6	249	3	US-08-700-651-15	Sequence 15, Appli
269	79.5	4.8	461	4	US-09-573-986-4	Sequence 4, Appli	360	77	4.6	249	3	US-08-928-361B-20	Sequence 20, Appli
270	79.5	4.8	461	4	US-08-406-824A-2	Sequence 2, Appli	361	77	4.6	249	4	US-09-588-995A-20	Sequence 20, Appli
271	79.5	4.8	461	4	US-09-800-909-2	Sequence 2, Appli	362	77	4.6	714	4	US-09-949-016-7038	Sequence 7038, Ap
272	79.5	4.8	461	4	US-09-758-124-2	Sequence 3, Appli	363	77	4.6	908	4	US-09-949-016-7580	Sequence 7580, Ap
273	79.5	4.8	461	4	US-09-800-908-3	Sequence 3, Appli	364	77	4.6	1140	4	US-09-538-092-6547	Sequence 647, App
274	79.5	4.8	461	4	US-09-896-096A-17	Sequence 17, Appl	365	77	4.6	1401	3	US-09-127-670-6	Sequence 6, Appli
275	79.5	4.8	461	4	US-09-949-016-6019	Sequence 6019, Ap	366	77	4.6	2123	3	US-08-968-685A-10	Sequence 10, Appl
276	79.5	4.8	461	6	5395760-2	Patent No. 5395760	367	76.5	4.6	134	4	US-09-248-796A-27317	Sequence 27317, A
277	79.5	4.8	461	6	5395760-2	Patent No. 5395760	368	76.5	4.6	240	2	US-08-114-555A-8	Sequence 8, Appli
278	79.5	4.8	431	4	US-09-949-016-7840	Sequence 7840, Ap	369	76.5	4.6	240	3	US-08-559-397A-14	Sequence 14, Appl
279	79.5	4.8	515	4	US-09-198-452A-1094	Sequence 1094, Ap	370	76.5	4.6	303	4	US-09-248-796A-14269	Sequence 14269, A
280	79.5	4.8	515	4	US-09-438-185A-1021	Sequence 1021, Ap	371	76.5	4.6	348	3	US-09-216-295-16	Sequence 16, Appl
281	79.5	4.8	559	4	US-09-543-681A-7241	Sequence 7241, Ap	372	76.5	4.6	348	4	US-09-632-570-16	Sequence 16, Appl
282	79.5	4.8	601	4	US-09-270-767-45496	Sequence 45496, A	373	76.5	4.6	348	4	US-09-632-575-46	Sequence 46, Appl
283	79.5	4.8	756	1	US-08-434-730-16	Sequence 16, Appl	374	76.5	4.6	382	1	US-08-415-818-7	Sequence 7, Appli
284	79.5	4.8	985	5	PCT-US96-03916-6	Sequence 6, Appli	375	76.5	4.6	382	2	US-08-894-236-7	Sequence 7, Appli
285	79.5	4.8	985	5	PCT-US96-03916-6	Sequence 6, Appli	376	76.5	4.6	382	2	US-08-894-236-7	Sequence 7, Appli
286	79.5	4.8	1114	4	US-09-262-537-34	Sequence 34, Appl	377	76.5	4.6	382	5	PCT-US96-01444-7	Sequence 7, Appli
287	79.5	4.8	1123	4	US-09-262-537-34	Sequence 34, Appl	378	76.5	4.6	397	4	US-09-198-452A-201	Sequence 201, App
288	79.5	4.8	1177	4	US-09-262-537-2	Sequence 2, Appli	379	76.5	4.6	397	4	US-09-438-185A-188	Sequence 188, App
289	79.5	4.8	1403	4	US-09-262-537-6	Sequence 6, Appli	380	76.5	4.6	452	4	US-08-127-499A-26	Sequence 26, Appl
290	79	4.8	175	3	US-08-700-651-12	Sequence 12, Appl	381	76.5	4.6	484	1	US-08-482-847-26	Sequence 26, Appl
291	79	4.8	175	3	US-08-928-361B-17	Sequence 17, Appl	382	76.5	4.6	484	1	US-08-482-847-26	Sequence 26, Appl
292	79	4.8	175	4	US-09-588-995A-17	Sequence 17, Appl	383	76.5	4.6	901	4	US-09-248-796A-14747	Sequence 14747, A
293	79	4.8	217	4	US-09-949-016-11174	Sequence 11174, A	384	76.5	4.6	1013	3	US-08-860-886-2	Sequence 2, Appli
294	79	4.8	334	4	US-09-107-532A-6336	Sequence 6336, Ap	385	76.5	4.6	5037	4	US-09-424-783-4	Sequence 4, Appli
295	79	4.8	374	4	US-09-489-847-166	Sequence 166, App	386	76	4.6	5037	4	US-09-270-767-61124	Sequence 4, Appli
305	79	4.8	398	4	US-09-248-796A-21599	Sequence 21599, A	387	76	4.6	299	4	US-09-270-767-44350	Sequence 44350, A
306	79	4.8	638	4	US-09-248-796A-18739	Sequence 18739, A	388	76	4.6	321	4	US-09-248-796A-20146	Sequence 20146, A
307	79	4.8	1312	3	US-09-345-882-29	Sequence 29, Appl	389	76	4.6	345	4	US-09-543-681A-6150	Sequence 6150, Ap
308	79	4.8	1848	3	US-08-296-791-6	Sequence 6, Appli	390	76	4.6	380	3	US-09-134-001C-4558	Sequence 4558, Ap
309	79	4.8	1848	4	US-09-839-996-6	Sequence 6, Appli	391	76	4.6	386	4	US-09-328-352-4722	Sequence 4722, Ap
310	79	4.8	1848	4	US-10-080-505-6	Sequence 6, Appli	392	76	4.6	402	4	US-09-270-767-45612	Sequence 45612, A
311	79	4.8	1848	4	US-10-645-605-6	Sequence 6, Appli	402	76	4.6	563	4	US-09-949-016-10405	Sequence 10405, A
312	79	4.8	1848	5	PCT-US95-10661A-6	Sequence 6, Appli	403	76	4.6	687	1	US-08-232-538-6	Sequence 6, Appli
313	79	4.8	3969	3	US-08-061-376-5	Sequence 5, Appli	404	76	4.6	687	1	US-08-786-164-6	Sequence 6, Appli
314	78.5	4.7	130	3	US-08-700-651-9	Sequence 9, Appli	405	76	4.6	687	3	US-09-427-353-2	Sequence 2, Appli
315	78.5	4.7	130	3	US-08-928-361B-14	Sequence 14, Appl	406	76	4.6	758	2	US-08-874-678-1	Sequence 1, Appli
316	78.5	4.7	130	4	US-09-588-995A-14	Sequence 14, Appl	407	76	4.6	758	3	US-08-643-839-1	Sequence 1, Appli
317	78.5	4.7	322	4	US-09-248-796A-23680	Sequence 23680, A	408	76	4.6	758	3	US-09-051-363-24	Sequence 24, Appl
318	78.5	4.7	360	4	US-09-489-039A-9383	Sequence 9383, Ap	409	76	4.6	758	3	US-09-348-886-1	Sequence 1, Appli
319	78.5	4.7	431	4	US-09-949-016-8402	Sequence 8402, Ap	410	76	4.6	780	2	US-08-232-538-14	Sequence 14, Appl
320	78.5	4.7	542	4	US-09-538-092-289	Sequence 289, App	411	76	4.6	780	2	US-08-786-164-14	Sequence 14, Appl
321	78.5	4.7	595	1	US-08-225-989-2	Sequence 2, Appli	412	76	4.6	985	4	US-09-248-796A-16090	Sequence 16090, A
322	78.5	4.7	595	1	US-08-570-923-2	Sequence 2, Appli	413	76	4.6	1014	3	US-09-078-347A-3	Sequence 3, Appli
323	78.5	4.7	595	1	US-08-580-014-2	Sequence 2, Appli	414	76	4.6	1014	4	US-09-596-248D-25	Sequence 25, Appl
324	78.5	4.7	595	3	US-09-079-785-2	Sequence 2, Appli	415	76	4.6	1063	4	US-09-596-248D-47	Sequence 47, Appl
325	78.5	4.7	595	4	US-09-921-667-6	Sequence 6, Appli	416	76	4.6	1338	3	US-08-750-141A-3	Sequence 3, Appli
326	78.5	4.7	595	4	US-09-628-126-2	Sequence 2, Appli	417	76	4.6	1338	4	US-09-119-014D-6	Sequence 6, Appli
327	78.5	4.7	653	4	US-09-520-781-10	Sequence 10, Appl	418	76	4.6	1401	3	US-08-781-891-206	Sequence 206, App
328	78.5	4.7	3254	2	US-08-705-660-34	Sequence 34, Appl	419	76	4.6	1401	4	US-09-618-166-206	Sequence 206, App
329	78.5	4.7	3224	3	US-08-989-045-34	Sequence 34, Appl	420	76	4.6	1426	3	US-09-136-574A-43	Sequence 43, Appl
330	78.5	4.7	3224	4	US-09-538-092-1161	Sequence 1161, Ap	421	76	4.6	1645	4	US-09-976-594-769	Sequence 769, App
331	78.5	4.7	3224	4	US-09-315-355A-34	Sequence 34, Appl	422	75.5	4.6	258	3	US-08-961-083-90	Sequence 90, Appl
332	78.5	4.7	280	4	US-09-806-536A-1	Sequence 1, Appli	423	75.5	4.6	258	4	US-09-536-784-90	Sequence 90, Appl
333	78	4.7	300	4	US-09-248-796A-16245	Sequence 16245, A	424	75.5	4.6	348	1	US-08-035-392-2	Sequence 2, Appli
334	78	4.7	398	4	US-09-248-796A-14978	Sequence 14978, A	425	75.5	4.6	430	1	US-08-504-511A-2	Sequence 2, Appli
335	78	4.7	494	4	US-09-248-796A-16546	Sequence 16546, A	426	75.5	4.6	430	1	US-08-035-392-4	Sequence 4, Appli
336	78	4.7	564	4	US-10-069-540A-2	Sequence 2, Appli	427	75.5	4.6	430	1	US-08-504-511A-4	Sequence 4, Appli
337	78	4.7	609	4	US-09-198-452A-579	Sequence 579, App	428	75.5	4.6	451	3	US-09-134-001C-4461	Sequence 4461, Ap
338	78	4.7	1006	4	US-09-949-016-7897	Sequence 7897, Ap	429	75.5	4.6	451	4	US-09-230-225B-4	Sequence 4, Appli
339	78	4.7	1442	1	US-08-015-986A-3	Sequence 3, Appli	430	75.5	4.6	510	4	US-09-270-767-43633	Sequence 43633, A
340	78	4.7	1442	2	US-08-446-363-3	Sequence 3, Appli	431	75.5	4.6	511	1	US-08-220-151-17	Sequence 17, Appl
349	78	4.7	1744	4	US-09-438-185A-542	Sequence 542, App	432	75.5	4.6	511	3	US-08-413-118-17	Sequence 17, Appl
350	78	4.7	2176	4	US-09-949-016-9923	Sequence 9923, App	433	75.5	4.6	511	3	US-08-473-446-17	Sequence 17, Appl
351	78	4.7	514	3	US-09-377-557-10	Sequence 10, Appl	434	75.5	4.6	565	3	US-08-961-083-218	Sequence 218, App
352	77.5	4.7	514	3	US-08-738-168B-15	Sequence 15, Appl	435	75.5	4.6	565	4	US-09-536-784-218	Sequence 218, App
353	77.5	4.7	182	4	US-09-107-433-5067	Sequence 5067, Ap	436	75.5	4.6	639	4	US-09-949-016-6812	Sequence 6812, Ap
354	77.5	4.7	1475	4	US-09-538-092-1160	Sequence 1160, Ap	437	75.5	4.6	641	4	US-10-164-595-46	Sequence 46, Appl
355	77.5	4.7	1475	4	US-09-538-092-1160	Sequence 1160, Ap	438	75.5	4.6	652	4	US-09-949-016-7323	Sequence 7323, Ap
356	77.5	4.7	3969	4	US-09-538-092-1262	Sequence 1262, Ap	438	75.5	4.6				

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441	75	4.5	421	1	US-08-419-414-2	Sequence 2, Appli	514	74	4.5	339	1	US-08-174-745A-4	Sequence 4, Appli
442	75	4.5	425	4	US-09-748-537-14	Sequence 14, Appli	515	74	4.5	339	2	US-08-195-947-4	Sequence 4, Appli
443	75	4.5	554	2	US-08-524-051-2	Sequence 2, Appli	516	74	4.5	339	2	US-08-433-885-4	Sequence 4, Appli
444	75	4.5	554	3	US-09-052-778-16	Sequence 16, Appli	517	74	4.5	339	2	US-08-433-908B-4	Sequence 4, Appli
445	75	4.5	557	4	US-09-248-796A-26892	Sequence 26892, A	518	74	4.5	339	3	US-08-410-614-4	Sequence 4, Appli
446	75	4.5	904	3	US-09-198-484-2	Sequence 2, Appli	519	74	4.5	370	4	US-09-270-767-37418	Sequence 37418, A
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449	75	4.5	1038	4	US-07-757-022B-74	Sequence 74, Appli	522	74	4.5	422	4	US-09-949-016-8251	Sequence 8251, Ap
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451	75	4.5	1140	4	US-07-757-022B-104	Sequence 104, App	524	74	4.5	472	3	US-09-625-188-6	Sequence 6, Appli
452	75	4.5	1151	1	US-08-286-889-37	Sequence 37, Appli	525	74	4.5	493	4	US-09-248-796A-17819	Sequence 17819, A
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454	75	4.5	1151	1	US-08-362-652-37	Sequence 37, Appli	527	74	4.5	681	4	US-09-336-910A-2	Sequence 2, Appli
455	75	4.5	1151	2	US-08-605-672-37	Sequence 37, Appli	528	74	4.5	778	4	US-09-248-796A-16358	Sequence 16358, A
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463	75	4.5	1161	4	US-09-350-259-55	Sequence 55, Appli	536	74	4.5	1693	4	US-08-316-765-1	Sequence 1, Appli
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465	75	4.5	1162	3	US-09-298-568-2	Sequence 2, Appli	538	74	4.5	1693	5	PCT-US93-08849A-1	Sequence 1, Appli
466	75	4.5	1162	4	US-09-410-393-2	Sequence 2, Appli	539	74	4.5	1693	5	PCT-US93-08849-1	Sequence 1, Appli
467	75	4.5	1162	4	US-09-894-273-2	Sequence 2, Appli	540	74	4.5	1729	4	US-09-134-000C-5675	Sequence 5675, Ap
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469	75	4.5	1311	4	US-07-757-022B-42	Sequence 42, Appli	542	74	4.5	2414	4	US-09-538-092-1289	Sequence 1289, Ap
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471	75	4.5	1314	4	US-07-757-022B-50	Sequence 50, Appli	544	74	4.5	124	3	US-08-700-651-11	Sequence 11, Appli
472	75	4.5	1320	4	US-07-757-022B-46	Sequence 46, Appli	545	73.5	4.4	124	3	US-08-928-361B-16	Sequence 16, Appli
473	75	4.5	1320	4	US-07-757-022B-60	Sequence 60, Appli	546	73.5	4.4	124	4	US-09-588-995A-1	Sequence 16, Appli
474	75	4.5	1320	4	US-10-164-595-58	Sequence 48, Appli	547	73.5	4.4	128	3	US-08-700-651-7	Sequence 7, Appli
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476	75	4.5	1361	4	US-07-757-022B-40	Sequence 40, Appli	549	73.5	4.4	128	4	US-09-588-995A-12	Sequence 12, Appli
477	75	4.5	1363	4	US-07-757-022B-52	Sequence 52, Appli	550	73.5	4.4	130	3	US-08-700-651-8	Sequence 8, Appli
478	75	4.5	1404	4	US-07-757-022B-2	Sequence 2, Appli	551	73.5	4.4	130	3	US-08-928-361B-13	Sequence 13, Appli
479	75	4.5	1404	4	US-07-757-022B-62	Sequence 62, Appli	552	73.5	4.4	130	4	US-09-588-995A-13	Sequence 10, Appli
480	75	4.5	1404	4	US-10-164-595-78	Sequence 78, Appli	553	73.5	4.4	138	3	US-08-700-651-10	Sequence 10, Appli
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482	75	4.5	1411	4	US-09-949-016-10827	Sequence 10827, A	555	73.5	4.4	138	4	US-09-588-995A-15	Sequence 15, Appli
483	74.5	4.5	109	4	US-09-107-532A-4999	Sequence 4999, Ap	556	73.5	4.4	262	4	US-09-248-796A-21451	Sequence 21451, A
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485	74.5	4.5	186	4	US-09-252-991A-20433	Sequence 20433, A	558	73.5	4.4	382	4	US-09-248-796A-17276	Sequence 17276, A
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487	74.5	4.5	270	4	US-09-134-000C-3553	Sequence 3553, Ap	560	73.5	4.4	397	3	US-09-143-470-4	Sequence 4, Appli
488	74.5	4.5	312	4	US-09-248-796A-20143	Sequence 20143, A	561	73.5	4.4	397	4	US-08-649-006A-4	Sequence 4, Appli
489	74.5	4.5	333	4	US-09-107-532A-6475	Sequence 6475, Ap	562	73.5	4.4	397	4	US-09-771-023-4	Sequence 4, Appli
490	74.5	4.5	386	4	US-09-270-767-44120	Sequence 44120, A	563	73.5	4.4	427	2	US-08-282-197C-53	Sequence 53, Appli
491	74.5	4.5	429	4	US-09-949-016-8183	Sequence 8183, Ap	564	73.5	4.4	499	4	US-09-561-763-2	Sequence 2, Appli
492	74.5	4.5	429	4	US-09-949-016-8184	Sequence 8184, Ap	565	73.5	4.4	499	4	US-09-431-367B-2	Sequence 2, Appli
493	74.5	4.5	478	2	US-08-456-670B-40	Sequence 40, Appli	566	73.5	4.4	540	4	US-09-583-110-3685	Sequence 3685, Ap
494	74.5	4.5	530	4	US-09-912-935-38	Sequence 38, Appli	567	73.5	4.4	570	4	US-09-565-501A-104	Sequence 104, App
495	74.5	4.5	564	4	US-09-949-016-6898	Sequence 6898, Ap	568	73.5	4.4	570	4	US-09-633-286A-104	Sequence 104, App
496	74.5	4.5	565	4	US-09-949-016-6902	Sequence 6902, Ap	569	73.5	4.4	570	4	US-08-874-923-104	Sequence 104, App
497	74.5	4.5	587	4	US-09-815-923-4	Sequence 4, Appli	570	73.5	4.4	638	1	US-08-463-262A-11	Sequence 11, Appli
498	74.5	4.5	639	4	US-09-248-796A-20583	Sequence 20583, A	571	73.5	4.4	638	1	US-08-463-989-11	Sequence 11, Appli
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500	74.5	4.5	794	4	US-09-252-991A-28569	Sequence 28569, A	573	73.5	4.4	638	3	US-09-003-570-11	Sequence 11, Appli
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502	74.5	4.5	998	2	US-08-702-367A-20	Sequence 20, Appli	575	73.5	4.4	641	4	US-09-613-303-51	Sequence 51, Appli
503	74.5	4.5	998	5	PCT-US95-04681-20	Sequence 20, Appli	576	73.5	4.4	641	4	US-10-267-311-51	Sequence 51, Appli
504	74.5	4.5	1638	4	US-09-071-035-258	Sequence 258, App	577	73.5	4.4	646	4	US-09-902-540-12044	Sequence 12044, A
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506	74.5	4.5	1638	4	US-09-071-035-266	Sequence 266, App	579	73.5	4.4	712	4	US-09-949-016-10600	Sequence 10600, A
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508	74	4.5	197	4	US-09-513-995C-7852	Sequence 7852, Ap	581	73.5	4.4	713	3	US-09-126-121-2	Sequence 2, Appli
509	74	4.5	257	4	US-09-567-458A-2	Sequence 2, Appli	582	73.5	4.4	763	3	US-08-961-083-66	Sequence 66, Appli
510	74	4.5	279	4	US-09-248-796A-16859	Sequence 16859, A	583	73.5	4.4	763	4	US-09-536-784-66	Sequence 66, Appli
511	74	4.5	299	4	US-09-107-433-3811	Sequence 3811, Ap	584	73.5	4.4	780	4	US-09-248-796A-16702	Sequence 16702, A

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586	73.5	4.4	795	4	US-10-055-412B-11	Sequence 11, Appl	659	72.5	4.4	315	4	US-09-328-352-5948	Sequence 5948, Ap
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594	73.5	4.4	1101	4	US-09-561-709B-5	Sequence 5, Appli	667	72.5	4.4	463	2	US-09-902-540-9960	Sequence 9960, Ap
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596	73.5	4.4	1876	4	US-09-418-710-71	Sequence 70, Appl	669	72.5	4.4	510	3	US-09-949-016-11148	Sequence 11148, A
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599	73.5	4.4	1878	4	US-09-418-710-13	Sequence 13, Appl	672	72.5	4.4	608	4	US-09-949-016-11151	Sequence 11151, A
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601	73	4.4	162	3	US-08-700-651-13	Sequence 13, Appl	674	72.5	4.4	652	3	US-08-310-463-4	Sequence 4, Appli
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611	73	4.4	488	4	US-09-094-410-5	Sequence 5, Appli	684	72.5	4.4	878	4	US-09-724-418A-2	Sequence 2, Appli
612	73	4.4	488	4	US-08-708-123B-5	Sequence 5, Appli	685	72.5	4.4	907	3	US-08-783-774-2	Sequence 2, Appli
613	73	4.4	488	4	US-08-583-153A-5	Sequence 5, Appli	686	72.5	4.4	907	4	US-09-328-599A-1	Sequence 1, Appli
614	73	4.4	488	4	US-08-638-524B-5	Sequence 5, Appli	687	72.5	4.4	907	5	PCT-US95-04611A-19	Sequence 19, Appl
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616	73	4.4	497	4	US-08-781-986A-5234	Sequence 5234, Ap	689	72.5	4.4	2308	1	US-08-015-973-1	Sequence 1, Appli
617	73	4.4	502	4	US-09-248-796A-15481	Sequence 15481, A	690	72.5	4.4	2308	2	US-08-448-164-1	Sequence 1, Appli
618	73	4.4	579	4	US-09-198-452A-918	Sequence 918, App	691	72.5	4.4	2308	3	US-08-081-929-2	Sequence 2, Appli
619	73	4.4	606	4	US-09-438-185A-853	Sequence 853, App	692	72.5	4.4	2308	4	US-10-000-954-2	Sequence 2, Appli
620	73	4.4	645	4	US-09-270-767-42233	Sequence 42233, A	693	72.5	4.4	2314	4	US-09-816-703A-2	Sequence 2, Appli
621	73	4.4	650	3	US-08-362-525-2	Sequence 2, Appli	694	72.5	4.4	3256	4	US-09-919-039-21	Sequence 21, Appl
622	73	4.4	658	2	US-08-825-558-4	Sequence 4, Appli	695	72.5	4.4	3256	4	US-09-976-594-22	Sequence 22, Appl
623	73	4.4	658	3	US-09-312-611-4	Sequence 4, Appli	696	72.5	4.4	3256	4	US-09-919-039-21	Sequence 21, Appl
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633	73	4.4	852	4	US-09-206-551-19	Sequence 19, Appl	706	72	4.3	456	4	US-09-611-781-2	Sequence 2, Appli
634	73	4.4	859	2	US-08-825-558-6	Sequence 7, Appli	707	72	4.3	457	4	US-09-949-016-7211	Sequence 7211, Ap
635	73	4.4	918	2	US-08-825-558-6	Sequence 6, Appli	708	72	4.3	462	2	US-08-865-997A-2	Sequence 2, Appli
636	73	4.4	918	3	US-09-312-611-6	Sequence 3, Appli	709	72	4.3	489	4	US-09-545-814-29	Sequence 29, Appl
637	73	4.4	933	2	US-09-853-180B-3	Sequence 3, Appli	710	72	4.3	559	4	US-09-545-814-14	Sequence 14, Appl
638	73	4.4	933	2	US-08-682-847-2	Sequence 2, Appli	711	72	4.3	583	4	US-09-545-814-2	Sequence 2, Appli
639	73	4.4	951	4	US-09-313-942-9	Sequence 9, Appli	712	72	4.3	583	4	US-09-545-814-5	Sequence 5, Appli
640	73	4.4	1158	4	US-09-313-942-26	Sequence 26, Appl	713	72	4.3	599	2	US-08-910-551B-2	Sequence 2, Appli
641	73	4.4	1168	4	US-09-313-942-24	Sequence 24, Appl	714	72	4.3	635	4	US-09-545-814-32	Sequence 32, Appl
642	73	4.4	1702	3	US-08-296-791-5	Sequence 5, Appli	715	72	4.3	785	3	US-08-374-077C-3	Sequence 3, Appli
643	73	4.4	1702	4	US-09-839-996-5	Sequence 5, Appli	716	72	4.3	785	3	US-08-895-590-3	Sequence 3, Appli
644	73	4.4	1702	4	US-10-080-505-5	Sequence 5, Appli	717	72	4.3	785	4	US-09-539-879A-3	Sequence 3, Appli
645	73	4.4	1702	4	US-08-655-5-5	Sequence 5, Appli	718	72	4.3	801	1	US-08-725-012-2	Sequence 2, Appli
646	73	4.4	2285	5	PCT-US95-10661A-5	Sequence 5, Appli	719	72	4.3	903	3	US-09-193-562D-46	Sequence 46, Appl
647	73	4.4	2285	4	US-09-308-375-2	Sequence 2, Appli	720	72	4.3	903	4	US-09-623-624-18	Sequence 18, Appl
648	73	4.4	2285	4	US-09-932-183A-2	Sequence 2, Appli	721	72	4.3	903	4	US-10-055-412B-46	Sequence 46, Appl
649	73	4.4	2736	4	US-09-252-991A-30227	Sequence 30227, A	722	72	4.3	903	4	US-10-270-595-18	Sequence 18, Appl
650	72.5	4.4	150	3	US-08-528-361B-18	Sequence 18, Appl	723	72	4.3	915	4	US-09-270-767-43656	Sequence 43656, A
651	72.5	4.4	150	4	US-09-588-995A-18	Sequence 18, Appl	724	72	4.3	1129	3	US-09-023-905A-2	Sequence 2, Appli
652	72.5	4.4	167	4	US-08-956-171B-5216	Sequence 5216, App	725	72	4.3	1203	3	US-09-351-200-2	Sequence 2, Appli
653	72.5	4.4	167	4	US-08-781-986A-5316	Sequence 5216, App	726	72	4.3	1389	2	US-08-619-198-5	Sequence 5, Appli
654	72.5	4.4	185	4	US-09-248-796A-18311	Sequence 18311, A	727	72	4.3	1512	3	US-09-443-184-48	Sequence 48, Appl
655	72.5	4.4	204	4	US-09-302-540-14080	Sequence 14080, A	728	72	4.3	2441	1	US-08-194-468-2	Sequence 2, Appli
656	72.5	4.4	206	4	US-09-198-452A-879	Sequence 879, App	729	72	4.3	2441	3	US-08-961-739-2	Sequence 2, Appli
657	72.5	4.4	206	4	US-09-438-185A-822	Sequence 822, App	730	72	4.3	2441	3	US-09-514-247A-8	Sequence 8, Appli

731	2441	4	US-09-686-316-2	Sequence 2, Appli	804	70.5	4.3	292	1	US-08-286-888B-6	Sequence 6, Appli
732	135	4	US-09-252-991A-17514	Sequence 17514, A	805	70.5	4.3	319	4	US-09-270-767-44343	Sequence 44343, A
733	142	4	US-09-107-532A-6315	Sequence 6315, Ap	806	70.5	4.3	330	4	US-09-248-796A-14853	Sequence 14853, A
734	232	4	US-09-333-809-217	Sequence 217, App	807	70.5	4.3	330	4	US-09-949-016-7956	Sequence 7956, Ap
735	232	4	US-09-746-311B-366	Sequence 366, App	808	70.5	4.3	432	4	US-09-134-000C-3498	Sequence 3498, Ap
736	240	4	US-09-107-532A-4430	Sequence 4430, Ap	809	70.5	4.3	441	4	US-09-248-796A-20171	Sequence 20171, A
737	326	4	US-09-134-000C-5607	Sequence 5607, Ap	810	70.5	4.3	445	4	US-09-270-767-44629	Sequence 44629, A
738	386	4	US-09-248-796A-18312	Sequence 18312, A	811	70.5	4.3	462	1	US-08-417-330A-16	Sequence 16, Appl
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740	442	1	US-08-363-255-11	Sequence 11, Appli	813	70.5	4.3	522	4	US-09-538-092-1096	Sequence 1096, Ap
741	442	2	US-08-687-559-6	Sequence 6, Appli	814	70.5	4.3	574	4	US-09-248-796A-16162	Sequence 16162, A
742	442	4	US-09-401-415-6	Sequence 6, Appli	815	70.5	4.3	639	4	US-09-252-991A-24474	Sequence 24474, A
743	540	4	US-09-538-092-793	Sequence 793, App	816	70.5	4.3	636	3	US-09-003-574-34	Sequence 34, Appl
744	650	4	US-09-134-000C-5177	Sequence 5177, Ap	817	70.5	4.3	676	3	US-09-003-570-34	Sequence 34, Appl
745	732	4	US-09-134-000C-6359	Sequence 6359, Ap	818	70.5	4.3	676	3	US-09-864-541A-34	Sequence 34, Appl
746	920	4	US-09-538-092-1197	Sequence 1197, Ap	819	70.5	4.3	793	3	US-09-588-256-10	Sequence 10, Appl
747	1709	4	US-09-538-092-1197	Sequence 1197, Ap	820	70.5	4.3	942	4	US-09-538-092-602	Sequence 602, App
748	1724	4	US-09-607-510-2	Sequence 2, Appli	821	70.5	4.3	979	4	US-09-538-092-990	Sequence 990, App
749	1751	3	US-09-136-574A-44	Sequence 44, Appli	822	70.5	4.3	1014	4	US-09-949-016-8229	Sequence 8229, Ap
750	3174	2	US-08-477-451-3	Sequence 3, Appli	823	70.5	4.3	1168	4	US-09-762-311-5	Sequence 5, Appli
751	144	4	US-09-252-991A-23388	Sequence 23388, A	824	70.5	4.3	1187	4	US-09-949-016-6513	Sequence 6513, Ap
752	169	4	US-09-252-991A-32019	Sequence 32019, A	825	70.5	4.3	1591	4	US-09-270-767-45698	Sequence 45698, A
753	188	4	US-09-248-796A-14699	Sequence 14699, A	826	70.5	4.3	1980	4	US-09-914-272A-3	Sequence 3, Appli
754	71	4	US-09-270-767-39457	Sequence 39457, A	827	70.5	4.3	1980	4	US-10-638-333-3	Sequence 3, Appli
755	189	4	US-09-270-767-54674	Sequence 54674, A	828	70.5	4.3	2169	4	US-09-949-016-6930	Sequence 6930, Ap
756	230	4	US-09-328-352-7443	Sequence 7443, Ap	829	70.5	4.3	2442	3	US-09-514-247A-10	Sequence 10, Appl
757	230	4	US-09-248-796A-22910	Sequence 22910, A	830	70.5	4.3	2442	3	US-09-538-092-1370	Sequence 1370, Ap
758	239	4	US-09-248-796A-16743	Sequence 16743, A	831	70	4.2	118	4	US-09-252-991A-18728	Sequence 18728, A
759	251	4	US-09-248-796A-20695	Sequence 20695, A	832	70	4.2	135	4	US-09-270-767-35728	Sequence 35728, A
760	271	4	US-09-248-796A-14774	Sequence 14774, A	833	70	4.2	135	4	US-09-270-767-50945	Sequence 50945, A
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762	316	4	US-09-954-314-10	Sequence 10, Appl	835	70	4.2	232	4	US-09-492-709A-350	Sequence 350, App
763	316	4	US-10-230-562-10	Sequence 10, Appl	836	70	4.2	236	4	US-09-270-767-58225	Sequence 58225, A
764	385	4	US-09-248-796A-23097	Sequence 23097, A	837	70	4.2	265	3	US-08-918-288-39	Sequence 39, Appl
765	401	6	5252556-1	Patent No. 5252556	838	70	4.2	265	3	US-08-918-288-39	Sequence 39, Appl
766	401	6	5252556-1	Patent No. 5252556	839	70	4.2	312	4	US-10-101-464A-930	Sequence 930, App
767	437	3	US-09-353-332-2	Sequence 2, Appli	840	70	4.2	317	6	5340934-11	Patent No. 5340934
768	554	4	US-09-599-360B-78	Sequence 78, Appl	841	70	4.2	352	3	5340934-11	Patent No. 5340934
769	610	1	US-07-821-717B-6	Sequence 6, Appli	842	70	4.2	352	3	US-09-413-814-24	Sequence 24, Appl
770	610	1	US-08-119-262B-6	Sequence 6, Appli	843	70	4.2	352	3	US-09-902-540-9867	Sequence 9867, Ap
771	610	1	US-08-135-929A-11	Sequence 11, Appl	844	70	4.2	355	2	US-08-458-555-2	Sequence 2, Appli
772	610	1	US-08-234-265A-11	Sequence 11, Appl	845	70	4.2	376	4	US-09-248-796A-19334	Sequence 19334, A
773	630	4	US-09-485-529-8	Sequence 8, Appli	846	70	4.2	410	4	US-09-543-681A-5962	Sequence 5962, Ap
774	633	4	US-09-248-796A-20407	Sequence 20407, A	847	70	4.2	413	4	US-09-248-796A-15624	Sequence 15624, A
775	646	4	US-09-248-796A-16701	Sequence 16701, A	848	70	4.2	423	4	US-09-902-540-13157	Sequence 13157, A
776	983	4	US-09-538-092-1320	Sequence 1320, Ap	849	70	4.2	461	4	US-09-248-796A-17227	Sequence 17227, A
777	1835	3	US-08-836-325-15	Sequence 15, Appl	850	70	4.2	523	4	US-09-270-767-43823	Sequence 43823, A
778	1938	4	US-09-457-571-15	Sequence 15, Appl	851	70	4.2	525	4	US-09-107-532A-5095	Sequence 5095, Ap
779	2035	1	US-09-949-016-6609	Sequence 6609, Ap	852	70	4.2	552	4	US-09-248-796A-22710	Sequence 22710, A
780	2035	1	US-08-046-585-5	Sequence 5, Appli	853	70	4.2	584	4	US-09-693-746-22	Sequence 22, Appl
781	2035	1	US-08-393-703-5	Sequence 5, Appli	854	70	4.2	631	4	US-09-107-532A-4548	Sequence 4548, Ap
782	2035	5	FCT-US93-11721-5	Sequence 5, Appli	855	70	4.2	692	3	US-09-003-574-31	Sequence 31, Appl
783	2045	4	US-09-949-016-10491	Sequence 10491, A	856	70	4.2	692	3	US-09-003-570-31	Sequence 31, Appl
784	2090	4	US-09-538-092-1081	Sequence 1081, Ap	857	70	4.2	692	3	US-09-864-541A-31	Sequence 31, Appl
785	2120	4	US-09-949-016-9768	Sequence 9768, Ap	858	70	4.2	722	4	US-09-252-991A-26452	Sequence 26452, A
786	157	4	US-09-270-767-38100	Sequence 38100, A	859	70	4.2	843	4	US-09-252-991A-32668	Sequence 32668, A
787	157	4	US-09-270-767-53317	Sequence 53317, A	860	70	4.2	915	2	US-08-480-917-2	Sequence 2, Appli
788	173	4	US-09-107-532A-4115	Sequence 4115, Ap	861	70	4.2	915	3	US-09-138-736-2	Sequence 2, Appli
789	198	4	US-09-489-039A-9988	Sequence 9988, Ap	862	70	4.2	915	3	US-08-988-242-2	Sequence 2, Appli
790	213	4	US-09-244-805-11	Sequence 11, Appl	863	70	4.2	3892	4	US-09-328-352-5503	Sequence 5503, Ap
791	213	4	US-09-538-092-1255	Sequence 1255, Ap	864	69.5	4.2	51	4	US-09-902-540-15148	Sequence 15148, A
792	220	4	US-09-198-452A-461	Sequence 461, App	865	69.5	4.2	139	4	US-09-248-796A-14268	Sequence 14268, A
793	220	4	US-09-438-185A-442	Sequence 442, App	866	69.5	4.2	184	4	US-09-893-737-14	Sequence 14, Appl
794	232	4	US-09-333-809-214	Sequence 214, App	867	69.5	4.2	219	1	US-08-463-115-91	Sequence 91, Appl
795	232	4	US-09-333-809-215	Sequence 215, App	868	69.5	4.2	219	1	US-08-463-388-91	Sequence 91, Appl
796	232	4	US-09-333-809-216	Sequence 216, App	869	69.5	4.2	290	2	US-08-903-801-1	Sequence 1, Appli
797	232	4	US-09-746-311B-363	Sequence 363, App	870	69.5	4.2	290	3	US-09-295-035-1	Sequence 1, Appli
798	232	4	US-09-746-311B-364	Sequence 364, App	871	69.5	4.2	291	6	5194600-2	Patent No. 5194600
799	232	4	US-09-746-311B-365	Sequence 365, App	872	69.5	4.2	291	6	5194600-2	Patent No. 5194600
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801	244	4	US-09-107-532A-4536	Sequence 4536, Ap	874	69.5	4.2	312	4	US-09-254-465A-9	Sequence 9, Appli
802	256	4	US-09-248-796A-14185	Sequence 14185, A	884	69.5	4.2	312	4	US-09-953-499-9	Sequence 9, Appli
803	267	4	US-09-270-767-60080	Sequence 60080, A	885	69.5	4.2	338	4	US-09-538-092-144	Sequence 144, App

886	69.5	4.2	339	1	US-08-431-080-18	Sequence 18, Appl	959	68.5	4.1	253	4	US-09-543-681A-8042	Sequence 8042, Ap
887	69.5	4.2	339	2	US-08-938-534-18	Sequence 18, Appl	960	68.5	4.1	291	4	US-09-270-767-45280	Sequence 45280, A
888	69.5	4.2	339	3	US-09-345-294-18	Sequence 18, Appl	961	68.5	4.1	325	1	US-08-233-788A-55	Sequence 55, Appl
889	69.5	4.2	385	4	US-09-370-767-42966	Sequence 42966, A	962	68.5	4.1	331	4	US-09-248-796A-20795	Sequence 20795, A
890	69.5	4.2	406	4	US-09-248-796A-20860	Sequence 20860, A	963	68.5	4.1	338	4	US-09-328-352-4529	Sequence 4529, Ap
891	69.5	4.2	567	4	US-09-773-877B-12	Sequence 12, Appl	964	68.5	4.1	371	4	US-09-533-029-110	Sequence 110, App
892	69.5	4.2	633	4	US-09-248-796A-18427	Sequence 18427, A	965	68.5	4.1	391	4	US-09-200-090-4	Sequence 4, Appl
893	69.5	4.2	644	4	US-09-248-796A-23441	Sequence 23441, A	966	68.5	4.1	402	1	US-08-444-734A-6	Sequence 6, Appl
894	69.5	4.2	651	4	US-09-248-796A-18743	Sequence 18743, A	967	68.5	4.1	402	1	US-08-087-772A-15	Sequence 15, Appl
895	69.5	4.2	812	4	US-09-248-796A-20875	Sequence 20875, A	968	68.5	4.1	408	1	US-07-916-901-2	Sequence 2, Appl
896	69.5	4.2	1020	4	US-09-248-796A-17115	Sequence 17115, A	969	68.5	4.1	408	3	US-08-450-962-2	Sequence 2, Appl
897	69.5	4.2	1059	4	US-09-248-796A-15164	Sequence 15164, A	970	68.5	4.1	408	3	US-08-450-962-5	Sequence 5, Appl
898	69.5	4.2	1105	3	US-08-999-774A-2	Sequence 2, Appl	971	68.5	4.1	408	3	US-08-848-631-2	Sequence 2, Appl
899	69.5	4.2	1308	4	US-09-134-000C-6588	Sequence 6588, Ap	972	68.5	4.1	408	4	US-08-848-631-5	Sequence 5, Appl
900	69.5	4.2	1323	3	US-09-770-170-2	Sequence 2, Appl	973	68.5	4.1	440	4	US-09-270-767-37864	Sequence 37864, A
901	69.5	4.2	1619	4	US-09-328-352-7347	Sequence 7347, Ap	974	68.5	4.1	440	4	US-09-270-767-53081	Sequence 53081, A
902	69.5	4.2	2468	4	US-09-976-594-726	Sequence 726, App	975	68.5	4.1	498	4	US-09-309-572-4	Sequence 4, Appl
903	69.5	4.2	2468	4	US-09-538-092-1135	Sequence 1135, Ap	976	68.5	4.1	498	4	US-09-718-096-4	Sequence 4, Appl
904	69.5	4.2	2522	4	US-09-949-016-10237	Sequence 10237, A	977	68.5	4.1	499	3	US-09-049-672A-1	Sequence 1, Appl
905	69	4.2	88	4	US-09-252-991A-23868	Sequence 23868, A	978	68.5	4.1	529	3	US-09-291-922-28	Sequence 28, Appl
906	69	4.2	111	4	US-09-248-796A-14291	Sequence 14291, A	979	68.5	4.1	557	4	US-09-773-877B-14	Sequence 14, Appl
907	69	4.2	153	4	US-09-489-039A-12486	Sequence 12486, A	980	68.5	4.1	567	4	US-09-773-877B-20	Sequence 20, Appl
908	69	4.2	171	4	US-09-248-796A-19229	Sequence 19229, A	981	68.5	4.1	600	4	US-09-693-746-2	Sequence 2, Appl
909	69	4.2	184	4	US-09-252-991A-25661	Sequence 25661, A	982	68.5	4.1	600	6	5240706-1	Patent No. 5240706
910	69	4.2	189	4	US-09-489-039A-11063	Sequence 11063, A	983	68.5	4.1	600	6	5240706-1	Patent No. 5240706
911	69	4.2	211	4	US-09-248-796A-26891	Sequence 26891, A	984	68.5	4.1	680	2	US-08-674-351-2	Sequence 2, Appl
912	69	4.2	218	1	US-08-463-115-92	Sequence 92, Appl	985	68.5	4.1	687	4	US-09-248-796A-23026	Sequence 23026, A
913	69	4.2	218	1	US-08-465-388-92	Sequence 92, Appl	986	68.5	4.1	697	4	US-09-270-767-41650	Sequence 41650, A
914	69	4.2	226	4	US-09-721-908-3	Sequence 3, Appl	987	68.5	4.1	744	4	US-09-021-560-2	Sequence 2, Appl
915	69	4.2	237	4	US-09-721-908-4	Sequence 4, Appl	988	68.5	4.1	744	4	US-09-021-560-2	Sequence 2, Appl
916	69	4.2	265	3	US-08-918-288-3	Sequence 3, Appl	989	68.5	4.1	756	3	US-09-085-199B-9	Sequence 9, Appl
917	69	4.2	265	3	US-09-282-357-3	Sequence 3, Appl	990	68.5	4.1	756	4	US-09-963-137-184	Sequence 184, App
918	69	4.2	288	4	US-09-902-540-14377	Sequence 14377, A	991	68.5	4.1	763	4	US-09-949-016-10382	Sequence 10382, A
919	69	4.2	341	4	US-09-902-540-14167	Sequence 14167, A	992	68.5	4.1	773	4	US-09-489-039A-11160	Sequence 11160, A
920	69	4.2	347	4	US-09-252-991A-15903	Sequence 15903, A	993	68.5	4.1	887	4	US-09-540-236-2911	Sequence 2911, Ap
921	69	4.2	347	4	US-09-540-236-3586	Sequence 3586, Ap	994	68.5	4.1	888	4	US-09-134-000C-5886	Sequence 5886, Ap
922	69	4.2	423	4	US-09-248-796A-26813	Sequence 26813, A	995	68.5	4.1	906	4	US-09-863-901-6	Sequence 6, Appl
923	69	4.2	430	4	US-09-949-016-8782	Sequence 8782, Ap	996	68.5	4.1	1167	4	US-10-274-409-2	Sequence 2, Appl
924	69	4.2	490	4	US-09-292-225-41	Sequence 41, Appl	997	68.5	4.1	1167	4	US-09-803-671B-2	Sequence 2, Appl
925	69	4.2	490	4	US-09-248-796A-20112	Sequence 20112, A	998	68.5	4.1	1187	4	US-09-949-016-7933	Sequence 7933, Ap
926	69	4.2	509	4	US-09-292-225-35	Sequence 35, Appl	999	68.5	4.1	1325	4	US-09-270-767-43789	Sequence 43789, A
927	69	4.2	509	4	US-09-292-225-38	Sequence 38, Appl	1000	68	4.1	147	4	US-09-252-991A-21137	Sequence 21137, A
928	69	4.2	552	4	US-09-540-236-2610	Sequence 2610, Ap	1001	68	4.1	155	4	US-10-101-464A-573	Sequence 573, App
929	69	4.2	556	4	US-09-538-092-712	Sequence 712, App	1002	68	4.1	183	4	US-09-270-767-35830	Sequence 35830, A
930	69	4.2	642	2	US-08-245-511-48	Sequence 48, Appl	1003	68	4.1	183	4	US-09-270-767-51047	Sequence 51047, A
931	69	4.2	642	2	US-08-600-993A-48	Sequence 48, Appl	1004	68	4.1	191	3	US-08-745-404-4	Sequence 4, Appl
932	69	4.2	696	3	US-08-899-437-23	Sequence 23, Appl	1005	68	4.1	203	4	US-09-059-625-85	Sequence 85, Appl
933	69	4.2	696	3	US-09-126-121-23	Sequence 23, Appl	1006	68	4.1	204	4	US-09-252-991A-29026	Sequence 29026, A
934	69	4.2	720	3	US-08-899-437-6	Sequence 6, Appl	1007	68	4.1	269	3	US-08-646-265A-109	Sequence 109, App
935	69	4.2	720	3	US-09-126-121-6	Sequence 6, Appl	1008	68	4.1	284	4	US-09-248-796A-18924	Sequence 18924, A
936	69	4.2	801	4	US-09-248-796A-18375	Sequence 18375, A	1009	68	4.1	292	4	US-09-248-796A-15095	Sequence 15095, A
937	69	4.2	813	3	US-08-836-325-8	Sequence 8, Appl	1010	68	4.1	294	4	US-09-248-796A-15817	Sequence 15817, A
938	69	4.2	813	3	US-09-457-571-8	Sequence 8, Appl	1011	68	4.1	306	4	US-09-107-532A-5552	Sequence 5552, Ap
939	69	4.2	817	4	US-09-248-796A-20276	Sequence 20276, A	1012	68	4.1	307	4	US-09-270-767-31716	Sequence 31716, A
940	69	4.2	845	3	US-08-804-439A-94	Sequence 94, Appl	1013	68	4.1	312	4	US-09-774-639-145	Sequence 145, App
941	69	4.2	845	3	US-08-720-229-94	Sequence 94, Appl	1014	68	4.1	330	4	US-09-248-796A-20142	Sequence 20142, A
942	69	4.2	861	4	US-09-784-316-2	Sequence 2, Appl	1015	68	4.1	354	4	US-09-949-016-10392	Sequence 10392, A
943	69	4.2	861	4	US-10-229-124-2	Sequence 2, Appl	1016	68	4.1	374	4	US-09-248-796A-16008	Sequence 16008, A
944	69	4.2	882	4	US-09-328-352-5232	Sequence 5232, Ap	1017	68	4.1	380	4	US-09-902-540-10846	Sequence 10846, A
945	69	4.2	903	1	US-08-220-151-8	Sequence 8, Appl	1018	68	4.1	387	4	US-09-570-778A-11	Sequence 11, Appl
946	69	4.2	903	1	US-08-413-118-8	Sequence 8, Appl	1019	68	4.1	387	4	US-09-991-138-11	Sequence 11, Appl
947	69	4.2	903	2	US-08-473-446-8	Sequence 19, Appl	1020	68	4.1	422	3	US-08-872-979-8	Sequence 8, Appl
948	69	4.2	988	3	US-08-286-819A-19	Sequence 19, Appl	1021	68	4.1	431	4	US-09-252-991A-27034	Sequence 8, Appl
949	69	4.2	988	3	US-08-980-357-19	Sequence 19, Appl	1022	68	4.1	516	2	US-08-762-106-8	Sequence 2, Appl
950	69	4.2	1163	4	US-09-949-016-11047	Sequence 11047, A	1023	68	4.1	516	3	US-08-745-404-2	Sequence 8, Appl
951	69	4.2	1311	1	US-08-340-011-5	Sequence 5, Appl	1024	68	4.1	516	3	US-09-320-774-8	Sequence 8, Appl
952	69	4.2	1311	3	US-08-901-710-5	Sequence 5, Appl	1025	68	4.1	527	2	US-08-762-106-9	Sequence 9, Appl
953	69	4.2	1311	4	US-09-169-079-5	Sequence 5, Appl	1026	68	4.1	527	2	US-08-823-516-144	Sequence 144, App
954	69	4.2	1455	3	US-08-840-062-5	Sequence 5, Appl	1027	68	4.1	527	3	US-09-320-774-9	Sequence 9, Appl
955	69	4.2	1650	4	US-09-252-991A-21798	Sequence 21798, A	1028	68	4.1	527	3	US-09-940-244-144	Sequence 144, App
956	68.5	4.1	189	4	US-09-949-016-6682	Sequence 6682, Ap	1029	68	4.1	552	3	US-08-745-404-3	Sequence 3, Appl
957	68.5	4.1	206	4	US-09-949-016-10049	Sequence 10049, A	1030	68	4.1	562	6	5258502-2	Patent No. 5258502
958	68.5	4.1	213	4	US-09-949-016-6681	Sequence 6681, Ap	1031	68	4.1	562	6	5258502-2	Patent No. 5258502

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1063	68	4.1	1155	1	US-08-286-889-46	Sequence 46, Appli	1136	67.5	4.1	498	4	US-09-583-110-2949	Sequence 2949, Ap
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1068	68	4.1	1155	2	US-08-943-363-46	Sequence 46, Appli	1141	67.5	4.1	555	4	US-09-107-532A-6422	Sequence 6422, Ap
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1070	68	4.1	1155	4	US-09-688-307A-46	Sequence 46, Appli	1143	67.5	4.1	591	4	US-09-949-016-10915	Sequence 10915, A
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1075	68	4.1	1161	1	US-08-362-652-55	Sequence 55, Appli	1148	67.5	4.1	630	4	US-09-269-939A-10	Sequence 10, Appli
1076	68	4.1	1161	2	US-08-605-672-53	Sequence 53, Appli	1149	67.5	4.1	649	4	US-09-493-522-14	Sequence 14, Appli
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1079	68	4.1	1161	2	US-08-482-293A-55	Sequence 55, Appli	1152	67.5	4.1	650	3	US-08-461-004A-63	Sequence 63, Appli
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1095	68	4.1	1545	4	US-09-839-996-4	Sequence 4, Appli	1168	67.5	4.1	1020	4	US-09-538-092-911	Sequence 911, App
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1097	68	4.1	1545	4	US-10-645-655-4	Sequence 4, Appli	1170	67.5	4.1	1150	3	US-09-206-800-3	Sequence 3, Appli
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1099	68	4.1	1675	2	US-09-540-236-1994	Sequence 1994, Ap	1172	67.5	4.1	1301	4	US-09-071-035-234	Sequence 234, App
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1101	68	4.1	8991	4	US-08-714-741-32	Sequence 32, Appli	1174	67.5	4.1	1301	4	US-09-071-035-242	Sequence 242, App
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1103	67.5	4.1	107	4	US-09-536-784-150	Sequence 150, App	1176	67.5	4.1	1978	4	US-09-302-626B-60	Sequence 60, Appli
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1179	67	4.0	135	4	US-09-908-322-51	Sequence 51, Appl	1252	67	4.0	668	4	US-09-134-000C-5289	Sequence 5289, Ap
1180	67	4.0	149	4	US-09-513-999C-4813	Sequence 4813, Ap	1253	67	4.0	784	4	US-09-538-092-1254	Sequence 1254, Ap
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1182	67	4.0	197	4	US-09-107-532A-7229	Sequence 7229, Ap	1255	67	4.0	863	2	US-08-380-182-19	Sequence 19, Appl
1183	67	4.0	206	4	US-09-328-352-6224	Sequence 6224, Ap	1256	67	4.0	886	4	US-09-784-316-4	Sequence 4, Appl
1184	67	4.0	210	1	US-07-667-276A-2	Sequence 2, Appl	1257	67	4.0	886	4	US-10-229-124-4	Sequence 4, Appl
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1187	67	4.0	246	1	US-08-294-386C-3	Sequence 3, Appl	1260	67	4.0	908	3	US-08-666-221B-12	Sequence 12, Appl
1188	67	4.0	246	1	US-08-299-249A-1	Sequence 1, Appl	1261	67	4.0	908	3	US-08-666-221B-14	Sequence 14, Appl
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1191	67	4.0	246	1	US-08-590-708-1	Sequence 1, Appl	1264	67	4.0	915	4	US-09-949-016-7025	Sequence 7025, Ap
1192	67	4.0	246	5	PCT-US94-06543-1	Sequence 1, Appl	1265	67	4.0	915	4	US-09-949-016-9697	Sequence 9697, Ap
1193	67	4.0	246	5	PCT-US95-10224-1	Sequence 1, Appl	1266	67	4.0	976	2	US-08-449-645A-18	Sequence 18, Appl
1194	67	4.0	246	5	PCT-US95-10224-3	Sequence 3, Appl	1267	67	4.0	976	2	US-08-702-367A-18	Sequence 18, Appl
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1196	67	4.0	272	4	US-09-248-796A-16689	Sequence 16689, A	1269	67	4.0	976	5	PCT-US95-04661-18	Sequence 18, Appl
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1198	67	4.0	273	3	US-09-224-681-54	Sequence 54, Appl	1271	67	4.0	1132	4	US-09-528-784A-87	Sequence 87, Appl
1199	67	4.0	273	4	US-09-635-251-54	Sequence 54, Appl	1272	67	4.0	1132	4	US-09-569-098A-87	Sequence 87, Appl
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1201	67	4.0	289	3	US-08-961-083-20	Sequence 20, Appl	1274	67	4.0	1265	4	US-09-071-035-418	Sequence 418, App
1202	67	4.0	289	4	US-09-536-78A-2	Sequence 20, Appl	1275	67	4.0	1278	4	US-09-134-000C-6043	Sequence 6043, Ap
1203	67	4.0	309	4	US-09-270-767-46802	Sequence 20, Appl	1276	67	4.0	1278	4	US-09-710-279-3188	Sequence 3188, Ap
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1205	67	4.0	342	4	US-09-107-433-3903	Sequence 20167, A	1278	67	4.0	1339	4	US-09-949-016-10448	Sequence 10448, A
1206	67	4.0	373	4	US-09-270-767-46313	Sequence 3903, Ap	1279	67	4.0	1478	4	US-09-949-016-8315	Sequence 8315, Ap
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Db      181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAAFKNEAAGFGGVP 240
      |||||||
QY      241 LVLALLFFGAAAGLGFYVRYVKAFFPTNKNQKQKEMIETKVVKEEKANDSNPNESKKT 300
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Db      241 LVLALLFFGAAAGLGFYVRYVKAFFPTNKNQKQKEMIETKVVKEEKANDSNPNESKKT 300
      |||||||
QY      301 DKNPEESKSPSKTIVRCLEAEV 322
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Db      301 DKNPEESKSPSKTIVRCLEAEV 322
      |||||||

RESULT 5
; Sequence 201, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTPEAKEA 60
DB 1 MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTPEAKEA 60
QY 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNKCGKNGVGLWKVPV 120
DB 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNKCGKNGVGLWKVPV 120
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DB 121 SRQFAAYCYNSSDWTNNSCIPEIITTKDPIFNTQTATQTTEFIIVSDSTYSVASPYSTIPA 180
QY 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMTSTETEPVENKAAAFKNEAAGFGVPTAL 240
DB 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMTSTETEPVENKAAAFKNEAAGFGVPTAL 240
QY 241 LVLLALLFCAAGAGLCYKRVYKAPFPFTNKNQCKEMIETKVVKKEKANDSNPNESKKT 300
DB 241 LVLLALLFCAAGAGLCYKRVYKAPFPFTNKNQCKEMIETKVVKKEKANDSNPNESKKT 300
QY 301 DKNPEESKSPSKTTVRCLAEAV 322
DB 301 DKNPEESKSPSKTTVRCLAEAV 322

RESULT 6
; Sequence 201, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fillaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTPEAKEA 60
DB 1 MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTPEAKEA 60
QY 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNKCGKNGVGLWKVPV 120
DB 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNKCGKNGVGLWKVPV 120
QY 121 SRQFAAYCYNSSDWTNNSCIPEIITTKDPIFNTQTATQTTEFIIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDWTNNSCIPEIITTKDPIFNTQTATQTTEFIIVSDSTYSVASPYSTIPA 180
QY 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMTSTETEPVENKAAAFKNEAAGFGVPTAL 240

Db 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMTEPFFVENKAAFNENAGGGVPTAL 240
Qy 241 LVLALLFFGAAAGLFCYVKRYKAPFPFTNKNOQKEMIETKVVKERKANDSNPNEESKKT 300
Db 241 LVLALLFFGAAAGLFCYVKRYKAPFPFTNKNOQKEMIETKVVKERKANDSNPNEESKKT 300
Qy 301 DKNPEESKSPSKTTVRCLEAEV 322
Db 301 DKNPEESKSPSKTTVRCLEAEV 322

RESULT 7

; Sequence 201, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARCFSLVLLLTSIWTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTKEA 60
Db 1 MARCFSLVLLLTSIWTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTKEA 60

Qy 61 CRLGLSLAGKDOVETALKASFETCSYGWVGDFVVISRISPNKCGKNGVGLWKVPV 120
Db 61 CRLGLSLAGKDOVETALKASFETCSYGWVGDFVVISRISPNKCGKNGVGLWKVPV 120

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Db 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNQTATOTTEFIVSDSYVASPYSTIPA 180

Qy 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMTEPFFVENKAAFNENAGGGVPTAL 240
Db 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMTEPFFVENKAAFNENAGGGVPTAL 240

Qy 241 LVLALLFFGAAAGLFCYVKRYKAPFPFTNKNOQKEMIETKVVKERKANDSNPNEESKKT 300
Db 241 LVLALLFFGAAAGLFCYVKRYKAPFPFTNKNOQKEMIETKVVKERKANDSNPNEESKKT 300

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Db 301 DKNPEESKSPSKTTVRCLEAEV 322

RESULT 8

; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCSFLVLLLSIWTRLLVQGSRAEELSIOVSCRINGITLVSKKANQQLNFTAEKEA 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 121 SRQFAAYCYNSSDTWNSCIPRIITTKDPINFNTQTATQTEFIVSDSYSVASPYSTIPA 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 PTTTPAPASTSIPRRKLLICYTEVFMETSTSTETEPVENKAAFKQEAAGFGVPTAL 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 LVLALLFFGAAGLFCYVKRVKAPFPFTNKQKQKEMIETKVVKBEKANDSNPNESKKT 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 DKNPEESKSPSKTTVRCLAEAV 322
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 DKNPEESKSPSKTTVRCLAEAV 322
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
; Sequence 201, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match      100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTSTWTRLLVQGSRAEELSIQVSCRIMGITLVSKKANQQLNFTTAKEA 60
DB 1 MARCFSLVLLLTSTWTRLLVQGSRAEELSIQVSCRIMGITLVSKKANQQLNFTTAKEA 60

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DB 61 CRLLGLSLAGKQOVETALKASFETCSYGWGDFVVISRISPNPKCGKNGVGLIWKVPV 120

QY 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNTQTATOTTEFIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNTQTATOTTEFIVSDSTYSVASPYSTIPA 180

QY 181 PTTTPPAPASTSIIPRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGGGVPTAL 240
DB 181 PTTTPPAPASTSIIPRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGGGVPTAL 240

QY 241 LVLALLFFGAAAGLGFYKRYVKAFPPFTNKNQOKEMIEIKVVKEEKANDSNPNESKKT 300
DB 241 LVLALLFFGAAAGLGFYKRYVKAFPPFTNKNQOKEMIEIKVVKEEKANDSNPNESKKT 300

QY 301 DKNPEESKSPSKTTVRCLEAEV 322
DB 301 DKNPEESKSPSKTTVRCLEAEV 322
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RESULT 10

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; Sequence 201, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
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; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match      100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTSTWTRLLVQGSRAEELSIQVSCRIMGITLVSKKANQQLNFTTAKEA 60
DB 1 MARCFSLVLLLTSTWTRLLVQGSRAEELSIQVSCRIMGITLVSKKANQQLNFTTAKEA 60

QY 61 CRLLGLSLAGKQOVETALKASFETCSYGWGDFVVISRISPNPKCGKNGVGLIWKVPV 120
DB 61 CRLLGLSLAGKQOVETALKASFETCSYGWGDFVVISRISPNPKCGKNGVGLIWKVPV 120

QY 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNTQTATOTTEFIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNTQTATOTTEFIVSDSTYSVASPYSTIPA 180

QY 181 PTTTPPAPASTSIIPRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGGGVPTAL 240
DB 181 PTTTPPAPASTSIIPRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGGGVPTAL 240

QY 241 LVLALLFFGAAAGLGFYKRYVKAFPPFTNKNQOKEMIEIKVVKEEKANDSNPNESKKT 300
DB 241 LVLALLFFGAAAGLGFYKRYVKAFPPFTNKNQOKEMIEIKVVKEEKANDSNPNESKKT 300

QY 301 DKNPEESKSPSKTTVRCLEAEV 322
DB 301 DKNPEESKSPSKTTVRCLEAEV 322

RESULT 11
US-09-949-016-7765
; Sequence 7765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 7765
;; LENGTH: 344
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-7765

Query Match 100.0%; Score 1657; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTSTWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEA 60
DB 23 MARCFSLVLLLTSTWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEA 82

QY 61 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLWKVPV 120
DB 83 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLWKVPV 142

QY 121 SRQFAAYCYNSSDWTNNSCIPETITTKDPIFNQTATQTFEIVSDSTYSVASPYSTIPA 180
DB 143 SRQFAAYCYNSSDWTNNSCIPETITTKDPIFNQTATQTFEIVSDSTYSVASPYSTIPA 202

QY 181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAAFKNEAAGFGGVP 240
DB 203 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAAFKNEAAGFGGVP 262

QY 241 LVALLFFGAAAGLFCYVKRYKAFPPFNKNQOKEMIETKVVEEKANDSNPNESKKT 300
DB 263 LVALLFFGAAAGLFCYVKRYKAFPPFNKNQOKEMIETKVVEEKANDSNPNESKKT 322

QY 301 DKNPEESKSPSKTTVRCLAEV 322
DB 323 DKNPEESKSPSKTTVRCLAEV 344

RESULT 12
US-08-892-880-2
; Sequence 2, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/021,762
;; FILING DATE: 15-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEFFE, ERIC K
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.0490001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 322 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-892-880-2

Query Match 99.6%; Score 1651; DB 2; Length 322;
Best Local Similarity 99.7%; Pred. No. 8.1e-159;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTSTWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEA 60
DB 1 MARCFSLVLLLTSTWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEA 60

QY 61 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLWKVPV 120
DB 61 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLWKVPV 120

QY 121 SRQFAAYCYNSSDWTNNSCIPETITTKDPIFNQTATQTFEIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDWTNNSCIPETITTKDPIFNQTATQTFEIVSDSTYSVASPYSTIPA 180

QY 181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAAFKNEAAGFGGVP 240
DB 181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAAFKNEAAGFGGVP 240

QY 241 LVALLFFGAAAGLFCYVKRYKAFPPFNKNQOKEMIETKVVEEKANDSNPNESKKT 300
DB 241 LVALLFFGAAAGLFCYVKRYKAFPPFNKNQOKEMIETKVVEEKANDSNPNESKKT 300

QY 301 DKNPEESKSPSKTTVRCLAEV 322
DB 301 DKNPEESKSPSKTTVRCLAEV 322

RESULT 13
US-09-724-864-60
; Sequence 60, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-60

Query Match 66.6%; Score 1103; DB 3; Length 318;
Best Local Similarity 69.7%; Pred. No. 2.6e-103;
Matches 221; Conservative 30; Mismatches 62; Indels 4; Gaps 3;

QY 6 SLVLLTSTWTRLLVQGSRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACRLILG 65
Db 6 SLVLLTSTWTRLLVQGSRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACRLILG 64
QY 66 LSLAGDQVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPSRQFA 125
Db 65 LTLASRDQVESAKSFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPSRQFA 124
QY 126 AYCNSSDTWNSCIPEIITTKDPIFNQTATOTTEFIVSDSTYSVASPYSTIPAPTTTP 185
Db 125 AYCNSSDTWNSCIPEIITTKDPIFNQTATOTTEFIVSDSTYSVASPYSTIPAPTTTP 181
QY 186 PAPASTISPRKKLICVTEFVMTSTMTSTETEFVFNKAAPVNEAAGFGVPTALLVLAL 245
Db 182 RAPPLTSMARKTKICITTEYTEPIETATETAFVAGAAFKNEAAGFGVPTALLVLAL 241
QY 246 LRFGAAGLFGFCVVKRYKAFPTNKNQOKEMILETKVKEEKANDSNPNESKKTDKNPE 305
Db 242 LRFGAAGLFGFCVVKRYKAFPTNKNQOKEMILETKVKEEKANDSNPNESKKTDKNPE 301
QY 306 ESKSPSKTTVRCLAEV 322
Db 302 EAKSPKTTVRCLAEV 318

RESULT 14
US-07-946-497-7
; Sequence 7, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mCD44
US-07-946-497-7

Query Match 14.0%; Score 231.5; DB 1; Length 363;
Best Local Similarity 24.9%; Pred. No. 6.2e-15;

Matches 89; Conservative 57; Mismatches 148; Indels 63; Gaps 14;
QY 15 WTR---LIVQGSRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACRLILGSLACK 71
Db 6 WTAGLCLLQLSLAHQQLDNLVTRYAGVFCVCKNGRYSISRTAEADLCQAFNSTLPTM 65
QY 72 DQVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPSRQFAAYCYN 131
Db 66 DQKLALSKGFETCRGYFI-EGNVVPIRHPNAICAAHNTGVVILVTSNTHYDTCFNA 124
QY 132 SDTWNSCIPEIITTKDPIFNQTATOTTEFIVSDSTYSVASPYSTIPAPT--- 182
Db 125 SAPPEDC-----TSVTDLPNSFDGPFVITIVNRDGRYKKGVEYRTHOEDIDASNI 179
QY 183 -----TTPPA-PASTSIPRAKKLICVTEFVMTSTMTST-ETEPFVFNKAAPK--- 227
Db 180 DVSSGSTTEKSTPEGYILHTYLTQPTGDDDSFFIRSTLATRDSDSKDRGSRRTWT 239
QY 228 --NEAGFGG-----VPTALLVLALFFGAAAGLFGFCVVKRYKRYKAPF 267
Db 240 HGSSELAGHSSANQDSGVTTTSGPMRRPQIPEWLIILASL-LALALILAVC----- 293
QY 268 PTNKNQOKEMI---ETKVKEEKANDSNPNESKKTDKNPEESKSPSKTTVRCLAE 321
Db 294 RRRCGKKLVINGNGTVEDRKPSLN-GEASKSQEMVHLVYNKPSPTPDQCMTAD 349

RESULT 15
US-08-483-322-7
; Sequence 7, Application US/08483322
; Patent No. 5760178
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,322
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,497
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

OM protein - protein search, using sw model
 Run on: October 5, 2005, 17:07:32 ; Search time 138.341 Seconds
 (without alignments)
 900.218 Million cell updates/sec

Title: US-10-063-510-6
 Perfect score: 1657
 Sequence: 1 MARCSLVLLTSIWTRLL.....NPESKSPKTTVRCLAEV 322
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 2105692 segs, 386760381 residues
 Total number of hits satisfying Chosen parameters: 2105692
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%

Database :
 Listing first 1500 summaries
 A_Geneseq_16Dec04: *
 1: Geneseq1980s: *
 2: Geneseq1990s: *
 3: Geneseq2000s: *
 4: Geneseq2001s: *
 5: Geneseq2002s: *
 6: Geneseq2003as: *
 7: Geneseq2003bs: *
 8: Geneseq2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	DB	ID	Description
RESULT 1					
ID	AAI13379	standard; protein; 322 AA.			
DE	Amino acid sequence of protein PRO263.				
PN	WO9914328-A2.				
PD	25-MAR-1999.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1657;	DB 2;	Length 322;	
Best Local Similarity	100.0%;	Pred. No. 8.7e-148;			
RESULT 2					
ID	AAI87287	standard; protein; 322 AA.			
DE	Human signal peptide containing protein HSP-64				
PN	WO20000610-A2.				
PD	06-JAN-2000.				
PA	(INCY-) INCYTE PHARM INC.				
Query Match	100.0%;	Score 1657;	DB 3;	Length 322;	
Best Local Similarity	100.0%;	Pred. No. 8.7e-148;			
RESULT 3					
ID	ADC78521	standard; protein; 322 AA.			
DE	Human PRO263 protein.				
PN	WO200015796-A2.				
PD	23-MAR-2000.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1657;	DB 3;	Length 322;	
Best Local Similarity	100.0%;	Pred. No. 8.7e-148;			
RESULT 4					
ID	AAB80247	standard; protein; 322 AA.			
DE	Human PRO263 protein.				
PN	WO200104311-A1.				
PD	18-JAN-2001.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1657;	DB 4;	Length 322;	
Best Local Similarity	100.0%;	Pred. No. 8.7e-148;			
RESULT 5					
ID	AAB87528	standard; protein; 322 AA.			
DE	Human PRO263.				
PN	WO200116318-A2.				
PD	08-MAR-2001.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1657;	DB 4;	Length 322;	
Best Local Similarity	100.0%;	Pred. No. 8.7e-148;			
RESULT 6					
ID	AAB88391	standard; protein; 322 AA.			

DE Human membrane or secretory protein clone PSEC0135.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 100.0%; Score 1657; DB 4; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 7
 ID ABG95853 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein PRO263.
 PN US2002119130-A1.
 PD 29-AUG-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 5; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 8
 ID ABB84832 standard; protein; 322 AA.
 DE Human PRO263 protein sequence SEQ ID NO:32.
 PN WO200200690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 5; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 9
 ID ABB95438 standard; protein; 322 AA.
 DE Human angiogenesis related protein PRO263 SEQ ID NO: 32.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 1657; DB 5; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 10
 ID ABU71625 standard; protein; 322 AA.
 DE Human PRO polypeptide #36.
 PN US2002146709-A1.
 PD 10-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 6; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 11
 ID ABU71480 standard; protein; 322 AA.
 DE Human PRO polypeptide #36.
 PN US2002192659-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 6; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 12
 ID ABU71926 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein PRO263.
 PN US2003003530-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 6; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 13
 ID ABO01809 standard; protein; 322 AA.
 DE Novel human secreted and transmembrane protein PRO263.
 PN US2002197671-A1.

PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 14
ID ABU90878 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 15
ID ABO33937 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 16
ID ABO33937 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 17
ID ABO47397 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 18
ID ABO47397 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 19
ID ABO71508 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 20
ID ABU7289 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 21
ID ABU90962 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 22
ID ABO27283 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 23
ID ABU64534 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 24
ID ABU67380 standard; protein; 322 AA.
DE Human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 25
ID ABU92478 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 26
ID ABO14900 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 27
ID ABU81148 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 28
ID ABO33263 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 29
ID ABU98265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 30
ID ABU99270 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 31
ID ABU82477 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 32
ID ABU69657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 33
ID ABU96441 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 34
ID ABU72111 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 35
ID ABO14839 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 36
ID ADB29406 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 37
ID ADB17063 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 38
ID ABO44241 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 39
ID ADA18262 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 40
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 41
ID ADA19868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 42
ID ADB17251 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 43
ID ABO34851 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 44
ID ADA16237 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 45
ID ADA20040 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 46
ID ABO34169 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 47
ID ADA42382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 48
ID ABO17529 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 49
ID ADA00337 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
RESULT 50
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 6; Length 322;
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RESULT 50
ID ADA16661 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US200303969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 51
ID ADA13090 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 52
ID ADA1958 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 53
ID ADA17305 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 54
ID ADA42808 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 55
ID ABO17590 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 56
ID ADB85579 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 57
ID ADB77727 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 58
ID ADB74863 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 59
ID ADB68258 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 60
ID ADB68065 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 61
ID ADB90882 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 62
ID ADC28509 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 63
ID ADC39709 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 64
ID ADC40223 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 65
ID ADC19047 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 66
ID ADC34347 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 67
ID ADC29402 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 68
ID ADC28933 standard; protein; 322 AA.
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DE Human secreted/transmembrane protein, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 69
ID ADC40818 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 70
ID ADC19475 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 71
ID ADC06962 standard; protein; 322 AA.
DE Human secreted/transmembrane protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 72
ID ADC17141 standard; protein; 322 AA.
DE Mammalian PRO polypeptide (SeqID 6).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 73
ID ADC33923 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 74
ID ADC12993 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 75
ID ADC14839 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 76
ID ADC52334 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 77
ID ADC12445 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003078387-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 78
ID ADC10321 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 79
ID ADD05000 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 80
ID ADD11281 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 81
ID ADD04006 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 82
ID ADD03582 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 83
ID ADD37074 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 84
ID ADD36010 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 85
ID ADE34834 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 86
ID ADG01011 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003078387-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 87
ID ADG08564 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 88
ID ADP95185 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 89
ID ADH24038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 90
ID ADH34064 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 91
ID ADH29897 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 92
ID ADH23868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 93
ID ADG85272 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 94
ID ADH24548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 95
ID ADH37404 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181646-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 96
ID ADH01993 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 97
ID ADH37574 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 98
ID ADG85612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 99
ID ADH24208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 100
ID ADH38502 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 101
ID ADG83623 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 102
ID ADH29431 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 103
ID ADH27547 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 104
ID ADH37744 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 105
ID ADH37921 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 106
ID ADH57341 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 107
ID ADH59317 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 108
ID ADH53483 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 109
ID ADH3653 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 110
ID ADH51989 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 111
ID ADH49844 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 112
ID ADI25354 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 113
ID ADH90147 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;

Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 114
ID ADI25524 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181659-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 115
ID ADH97698 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 116
ID ADI38096 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 117
ID ADI03546 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 118
ID ADI11903 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 119
ID ADH89977 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 120
ID ADH98378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 121
ID ADI11053 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 122
ID ADI11563 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
RESULT 123
ID ADH90147 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;

DE Novel human secreted and transmembrane protein PRO263.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 142
ID ADH79442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 143
ID ADI19399 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 144
ID ADI05200 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 145
ID ADH79612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 146
ID ADI01438 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 147
ID ADI01608 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 148
ID ADI01778 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 149
ID ADH79782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 150
ID ADI04600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.

PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 151
ID ADI02736 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 152
ID ADH78055 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 153
ID ADI25694 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 154
ID ADI25864 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 155
ID ADK65376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 156
ID ADH98718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 157
ID ADH79959 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 158
ID ADJ26364 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 159
ID ADJ93690 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003040013-A1.

Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 177
ID ADG25058 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 178
ID ADH33690 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 179
ID ADG92297 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 180
ID ADH02333 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 181
ID ADH07940 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 182
ID ADG9337 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 183
ID ADH39158 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 184
ID ADG22724 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 185
ID ADG3898 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 186
ID ADG5442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 187
ID ADH06236 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 188
ID ADH30066 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 189
ID ADH24378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 190
ID ADG69507 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 191
ID ADH07770 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 192
ID ADG85782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 193
ID ADH39328 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 194
ID ADH33520 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 195
ID ADH33520 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;

ID ADH33860 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 196
ID ADH01070 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 197
ID ADG69677 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 198
ID ADH02163 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 199
ID ADG93167 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 200
ID ADG95952 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 201
ID ADH24888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 202
ID ADH39505 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 203
ID ADH02503 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 204
ID ADG68997 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 205
ID ADH07600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 206
ID ADG86122 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 207
ID ADH24718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 208
ID ADH25766 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 209
ID ADH38332 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 210
ID ADH20513 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 211
ID ADH57171 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 212
ID ADH43465 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 213
ID ADH07368 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.

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PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 214
ID ADH52159 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 215
ID ADH59913 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 216
ID ADH49525 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 217
ID ADH06941 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 218
ID ADH90487 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 219
ID ADI11223 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 220
ID ADI18683 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 221
ID ADH98888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 222
ID ADI65403 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 223
ID ADI02118 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 224
ID ADH90657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 225
ID ADI37666 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 226
ID ADH97462 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 227
ID ADI65830 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 228
ID ADH60573 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 229
ID ADJ99630 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
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PN US2003187238-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 230
ID ADL08823 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 231
ID ADJ98532 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 232
ID ADJ98702 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 233
ID ADH78861 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 234
ID ADJ99095 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 235
ID ADJ99265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 236
ID ADJ98883 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 237
ID ADH79031 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 238
ID ADK00891 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003186407-A1.

PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 239
ID ADK14412 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 240
ID ADM25164 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 241
ID ADM29914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 242
ID ADK82810 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 243
ID ADM80861 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 244
ID AD006236 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 245
ID ADL11088 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 246
ID ADL17997 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.

PA (ZERR/) ZERHUSEN B D.
Query Match 90.6%; Score 1500.5; DB 8; Length 297;
Best Local Similarity 91.9%; Pred. No. 4.9e-133;
RESULT 257
ID AAB34702 standard; protein; 250 AA.
DE Human secreted protein encoded by DNA clone vb28 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 73.5%; Score 1218.5; DB 3; Length 250;
Best Local Similarity 92.0%; Pred. No. 1.8e-106;
RESULT 258
ID AAE05364 standard; protein; 318 AA.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 66.6%; Score 1103; DB 4; Length 318;
Best Local Similarity 69.7%; Pred. No. 2e-95;
RESULT 259
ID ABB72376 standard; protein; 255 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 700.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 49.5%; Score 821; DB 5; Length 255;
Best Local Similarity 65.0%; Pred. No. 6.9e-69;
RESULT 260
ID AAY12323 standard; protein; 116 AA.
DE Human 5' EST secreted protein SEQ ID NO:354.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 35.7%; Score 592; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1e-47;
RESULT 261
ID AAY12853 standard; protein; 58 AA.
DE Human 5' EST secreted protein SEQ ID NO:443.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 16.7%; Score 277; DB 2; Length 58;
Best Local Similarity 98.3%; Pred. No. 2.5e-18;
RESULT 262
ID AAY12170 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO: 483.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 15.8%; Score 261; DB 2; Length 69;
Best Local Similarity 96.4%; Pred. No. 1e-16;
RESULT 263
ID ABB81033 standard; protein; 364 AA.
DE Rat glycoprotein CD44 polypeptide.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (EGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 13.8%; Score 229; DB 5; Length 364;
Best Local Similarity 24.3%; Pred. No. 1.1e-12;
RESULT 264
ID AAR07355 standard; protein; 362 AA.
DE B7 adhesion receptor.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.
Query Match 13.4%; Score 222.5; DB 2; Length 362;
Best Local Similarity 25.5%; Pred. No. 4.3e-12;
RESULT 265
ID ABU79109 standard; protein; 365 AA.
DE CD44 protein.
PN US200217551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.

Query Match 13.4%; Score 222.5; DB 6; Length 365;
Best Local Similarity 24.5%; Pred. No. 4.4e-12;
RESULT 266
ID ADF43353 standard; protein; 365 AA.
DE CD44 receptor polypeptide seq id 73.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.
Query Match 13.4%; Score 222.5; DB 7; Length 365;
Best Local Similarity 24.5%; Pred. No. 4.4e-12;
RESULT 267
ID AAR14768 standard; protein; 503 AA.
DE Metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Query Match 13.4%; Score 222; DB 2; Length 503;
Best Local Similarity 25.7%; Pred. No. 7.5e-12;
RESULT 268
ID ADE57911 standard; protein; 503 AA.
DE Rat Protein P26051, SEQ ID NO 3777.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.4%; Score 222; DB 7; Length 503;
Best Local Similarity 25.7%; Pred. No. 7.5e-12;
RESULT 269
ID ABU04619 standard; protein; 658 AA.
DE Human expressed protein tag (EPT) #1285.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.6%; Score 208.5; DB 6; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.1e-10;
RESULT 270
ID ADQ39384 standard; protein; 668 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.6%; Score 208.5; DB 8; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.1e-10;
RESULT 271
ID AAR20816 standard; protein; 361 AA.
DE Haematopoietic CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GHO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 272
ID AAR91444 standard; protein; 361 AA.
DE Human haematopoietic CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GHO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 273
ID AAW80453 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GHO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 274
ID AAW86200 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).

PN US5849898-A.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 275
ID AAY96139 standard; protein; 361 AA.
DE Human haematopoietic CD44.5.
PN US611093-A.
PD 29-AUG-2000.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 3; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 276
ID AAU02448 standard; protein; 361 AA.
DE Human haematopoietic antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 4; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 277
ID ABU04632 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1298.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 278
ID ABU04610 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 279
ID ABU04638 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1304.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 280
ID ABU04634 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1300.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 281
ID ABU04626 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1292.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 282
ID ABU04630 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1296.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 283
ID ABU04636 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1302.
PN WO200278524-A2.

PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 284
ID ADO49373 standard; protein; 361 AA.
DE Human CD44 #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUE/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (COUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 12.5%; Score 207; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 285
ID AAY9851 standard; protein; 361 AA.
DE Human CD44 cell surface adhesion receptor.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 12.4%; Score 205; DB 3; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.9e-10;
RESULT 286
ID ABU04643 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1309.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.9e-10;
RESULT 287
ID ABU04609 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.9e-10;
RESULT 288
ID ABU04644 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1310.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.9e-10;
RESULT 289
ID ABU04622 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1288.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 204; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.4e-10;
RESULT 290
ID AAE30338 standard; protein; 361 AA.
DE Human CD44 antigen.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 12.3%; Score 204; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.4e-10;
RESULT 291
ID ADQ39385 standard; protein; 361 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.
PN WO2004058052-A2.

PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.3%; Score 204; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.4e-10;
RESULT 292
ID ABP72424 standard; protein; 608 AA.
DE Human CD44 variant CD44VRA associated with rheumatoid arthritis.
PN WO2003014160-A2.
PD 20-FEB-2003.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203.5; DB 6; Length 608;
Best Local Similarity 21.8%; Pred. No. 5.5e-10;
RESULT 293
ID AAY97579 standard; protein; 700 AA.
DE Human CD44 splice variant (RA-CD44) protein sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Query Match 12.3%; Score 203.5; DB 4; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.7e-10;
RESULT 294
ID ABU04640 standard; protein; 700 AA.
DE Human expressed protein tag (EPT) #1306.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203.5; DB 6; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.7e-10;
RESULT 295
ID ADD90594 standard; protein; 700 AA.
DE Human CD44v glycoprotein SEQ ID NO:4.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 12.3%; Score 203.5; DB 7; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.7e-10;
RESULT 296
ID ADD90592 standard; protein; 361 AA.
DE Human CD44std glycoprotein SEQ ID NO:2.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203; DB 7; Length 361;
Best Local Similarity 24.4%; Pred. No. 3e-10;
RESULT 297
ID AAY97651 standard; protein; 436 AA.
DE CD44Hextra/tmfAScyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 12.3%; Score 203; DB 4; Length 436;
Best Local Similarity 25.4%; Pred. No. 3.9e-10;
RESULT 298
ID ABU04642 standard; protein; 436 AA.
DE Human expressed protein tag (EPT) #1308.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203; DB 6; Length 436;
Best Local Similarity 25.4%; Pred. No. 3.9e-10;
RESULT 299
ID ABU04653 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1319.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 300
ID ABU04616 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1282.
Query Match 12.2%; Score 202; DB 6; Length 361;
Best Local Similarity 25.1%; Pred. No. 2.9e-10;
RESULT 301
ID ADP65295 standard; protein; 742 AA.
DE Human CD44 antigen (homing function and Indian blood group system), CD44.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 12.3%; Score 203; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 302
ID ADL61252 standard; protein; 742 AA.
DE Human protein tyrosine kinase biomarker CD44 antigen protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 303
ID ADQ39391 standard; protein; 742 AA.
DE Human mvocardial infarction-associated gene derived protein, SEQ ID 1054.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 304
ID ADG67253 standard; protein; 742 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 305
ID ADH18898 standard; protein; 330 AA.
DE Human cell adhesion and extracellular matrix CADECM-25 protein - SEQ 25.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 12.2%; Score 202.5; DB 8; Length 330;
Best Local Similarity 25.1%; Pred. No. 2.9e-10;
RESULT 306
ID AAY97650 standard; protein; 431 AA.
DE CD44HextraFAScm/cyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 12.2%; Score 202.5; DB 4; Length 431;
Best Local Similarity 24.7%; Pred. No. 4.3e-10;
RESULT 307
ID ABU04641 standard; protein; 431 AA.
DE Human expressed protein tag (EPT) #1307.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202.5; DB 6; Length 431;
Best Local Similarity 24.7%; Pred. No. 4.3e-10;
RESULT 308
ID ABU04607 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1273.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 361;

Best Local Similarity 24.4%; Pred. No. 3.7e-10;
RESULT 309
ID ADL93508 standard; protein; 361 AA.
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.2%; Score 202; DB 8; Length 361;
Best Local Similarity 24.1%; Pred. No. 3.7e-10;
RESULT 310
ID ABU04618 standard; protein; 675 AA.
DE Human expressed protein tag (EPT) #1284.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 675;
Best Local Similarity 26.0%; Pred. No. 8.8e-10;
RESULT 311
ID ABU04621 standard; protein; 691 AA.
DE Human expressed protein tag (EPT) #1287.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 691;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 312
ID ADQ39390 standard; protein; 691 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.2%; Score 202; DB 8; Length 691;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 313
ID ABU04620 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1286.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 314
ID ABU04645 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1311.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 315
ID ADN95511 standard; protein; 742 AA.
DE Human BCC/LEC-related protein sequence SeqID434.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 12.2%; Score 202; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 316
ID ADL93506 standard; protein; 742 AA.
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 317
ID ADO55181 standard; protein; 742 AA.
DE Protein #83 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 12.2%; Score 202; DB 8; Length 742;

Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 318
ID ADQ39383 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 319
ID ADQ39386 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 320
ID ABU04617 standard; protein; 425 AA.
DE Human expressed protein tag (EPT) #1283.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.1%; Score 201; DB 6; Length 425;
Best Local Similarity 22.0%; Pred. No. 5.8e-10;
RESULT 321
ID ADD90596 standard; protein; 699 AA.
DE Human CD44v glycoprotein SEQ ID NO:6.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.1%; Score 200.5; DB 7; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.3e-09;
RESULT 322
ID AAR20817 standard; protein; 493 AA.
DE Epithelial CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 323
ID AAR91445 standard; protein; 493 AA.
DE Human epithelial CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 324
ID AAW80454 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 325
ID AAW89151 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 326
ID AAY96140 standard; protein; 493 AA.
DE Human epithelial CD44.
PN US6111033-A.
PD 29-AUG-2000.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 3; Length 493;

Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 327
ID ABU04635 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1301.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 328
ID AAU99123 standard; protein; 493 AA.
DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.
PN WO200244342-A2.
PD 06-JUN-2002.
PA (EGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 12.0%; Score 199.5; DB 5; Length 493;
Best Local Similarity 22.2%; Pred. No. 9.8e-10;
RESULT 329
ID ABU04637 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1303.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 330
ID ABU04627 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1293.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 331
ID ABU04639 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1305.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 332
ID ABU04623 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1289.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 22.2%; Pred. No. 9.8e-10;
RESULT 333
ID ABU04631 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1297.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 334
ID ABU04633 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1299.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 335
ID ABU04612 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1278.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 22.2%; Pred. No. 9.8e-10;
RESULT 336
ID ABU04635 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1301.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 337
ID ABU04613 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1279.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 338
ID ADL93507 standard; protein; 493 AA.
DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.0%; Score 199.5; DB 8; Length 493;
Best Local Similarity 22.2%; Pred. No. 9.8e-10;
RESULT 339
ID ADO49375 standard; protein; 493 AA.
DE Human CD44 #2.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 12.0%; Score 199.5; DB 8; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 340
ID ABU04649 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1315.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199; DB 6; Length 338;
Best Local Similarity 24.6%; Pred. No. 6.5e-10;
RESULT 341
ID ABU04605 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1271.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199; DB 6; Length 338;
Best Local Similarity 24.6%; Pred. No. 6.5e-10;
RESULT 342
ID ABU04615 standard; protein; 395 AA.
DE Human expressed protein tag (EPT) #1281.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 198; DB 6; Length 395;
Best Local Similarity 23.0%; Pred. No. 1e-09;
RESULT 343
ID ABU04604 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1270.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 2.8e-09;

RESULT 344
ID ABU04650 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1316.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 2.8e-09;
RESULT 345
ID ABM83594 standard; protein; 535 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.9%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.1e-09;
RESULT 346
ID ADQ39381 standard; protein; 535 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.9%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.1e-09;
RESULT 347
ID ABU56470 standard; protein; 699 AA.
DE Lung cancer-associated polypeptide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3e-09;
RESULT 348
ID ABU04647 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1313.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3e-09;
RESULT 349
ID ABU04614 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1280.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3e-09;
RESULT 350
ID ABU04608 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1274.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3e-09;
RESULT 351
ID ADI60182 standard; protein; 261 AA.
DE Secreted polypeptide #66.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 196; DB 7; Length 261;
Best Local Similarity 30.9%; Pred. No. 8.8e-10;
RESULT 352
ID ABU04611 standard; protein; 293 AA.
DE Human expressed protein tag (EPT) #1277.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.8%; Score 196; DB 6; Length 293;
Best Local Similarity 30.9%; Pred. No. 1e-09;
RESULT 353
ID ABU04602 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1290.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.8%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1e-09;
RESULT 354
ID ABU04646 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1312.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.8%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1e-09;
RESULT 355
ID ADQ39389 standard; protein; 395 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.8%; Score 196; DB 8; Length 395;
Best Local Similarity 30.9%; Pred. No. 1.6e-09;
RESULT 356
ID ADQ39382 standard; protein; 425 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.8%; Score 196; DB 8; Length 425;
Best Local Similarity 30.9%; Pred. No. 1.7e-09;
RESULT 357
ID ADQ39388 standard; protein; 493 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.8%; Score 196; DB 8; Length 493;
Best Local Similarity 30.9%; Pred. No. 2.1e-09;
RESULT 358
ID ABG17071 standard; protein; 742 AA.
DE Novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 194.5; DB 4; Length 742;
Best Local Similarity 25.4%; Pred. No. 5.1e-09;
RESULT 359
ID AAM48306 standard; protein; 194 AA.
DE Protein R2 SEQ ID 29.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.7%; Score 194; DB 5; Length 194;
Best Local Similarity 30.8%; Pred. No. 9e-10;
RESULT 360
ID AAM48307 standard; protein; 200 AA.
DE Protein R3 SEQ ID 30.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.7%; Score 194; DB 5; Length 200;
Best Local Similarity 30.8%; Pred. No. 9.4e-10;
RESULT 361
ID AAM48308 standard; protein; 273 AA.
DE Protein R4 SEQ ID 31.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.7%; Score 194; DB 5; Length 273;
Best Local Similarity 30.8%; Pred. No. 1.4e-09;
RESULT 362
ID ABU04602 standard; protein; 676 AA.

DE Human expressed protein tag (EPT) #1268.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match 11.6%; Score 191.5; DB 6; Length 676;
 Best Local Similarity 25.8%; Pred. No. 8.6e-09;
 RESULT 363
 ID ABU04652 standard; protein; 676 AA.
 DE Human expressed protein tag (EPT) #1318.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match 11.6%; Score 191.5; DB 6; Length 676;
 Best Local Similarity 25.8%; Pred. No. 8.6e-09;
 RESULT 364
 ID ABU04648 standard; protein; 271 AA.
 DE Human expressed protein tag (EPT) #1314.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match 11.5%; Score 191; DB 6; Length 271;
 Best Local Similarity 31.5%; Pred. No. 2.7e-09;
 RESULT 365
 ID ABU04606 standard; protein; 271 AA.
 DE Human expressed protein tag (EPT) #1272.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match 11.5%; Score 191; DB 6; Length 271;
 Best Local Similarity 31.5%; Pred. No. 2.7e-09;
 RESULT 366
 ID ABU04651 standard; protein; 470 AA.
 DE Human expressed protein tag (EPT) #1317.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match 11.5%; Score 191; DB 6; Length 470;
 Best Local Similarity 31.5%; Pred. No. 5.9e-09;
 RESULT 367
 ID ASU04603 standard; protein; 470 AA.
 DE Human expressed protein tag (EPT) #1269.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match 11.5%; Score 191; DB 6; Length 470;
 Best Local Similarity 31.5%; Pred. No. 5.9e-09;
 RESULT 368
 ID AAM48305 standard; protein; 170 AA.
 DE Protein R1 SEQ ID 28.
 PN WO200192507-A1.
 PD 06-DEC-2001.
 PA (FUJI-) FUJICHEMICO LTD.
 Query Match 11.3%; Score 188; DB 5; Length 170;
 Best Local Similarity 35.7%; Pred. No. 2.8e-09;
 RESULT 369
 ID ABP73148 standard; protein; 112 AA.
 DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.
 PN WO2003018044-A1.
 PD 06-MAR-2003.
 PA (STRO/) STROEMBLAD S.
 PA (KOGE/) KOGERMAN P.
 PA (PAEL/) PAELL T.
 Query Match 11.3%; Score 187; DB 6; Length 112;
 Best Local Similarity 36.0%; Pred. No. 2e-09;
 RESULT 370
 ID ABP73150 standard; protein; 113 AA.
 DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.
 PN WO2003018044-A1.
 PD 06-MAR-2003.
 PA (STRO/) STROEMBLAD S.
 PA (KOGE/) KOGERMAN P.
 PA (PAEL/) PAELL T.
 Query Match 11.3%; Score 186.5; DB 6; Length 113;
 Best Local Similarity 36.0%; Pred. No. 2.2e-09;
 RESULT 371
 ID ABP73151 standard; protein; 112 AA.
 DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
 PN WO2003018044-A1.
 PD 06-MAR-2003.
 PA (STRO/) STROEMBLAD S.
 PA (KOGE/) KOGERMAN P.
 PA (PAEL/) PAELL T.
 Query Match 11.2%; Score 185; DB 6; Length 112;
 Best Local Similarity 36.0%; Pred. No. 3e-09;
 RESULT 372
 ID ABP73152 standard; protein; 112 AA.
 DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
 PN WO2003018044-A1.
 PD 06-MAR-2003.
 PA (STRO/) STROEMBLAD S.
 PA (KOGE/) KOGERMAN P.
 PA (PAEL/) PAELL T.
 Query Match 11.0%; Score 183; DB 6; Length 112;
 Best Local Similarity 36.0%; Pred. No. 4.7e-09;
 RESULT 373
 ID ABP73149 standard; protein; 112 AA.
 DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.
 PN WO2003018044-A1.
 PD 06-MAR-2003.
 PA (STRO/) STROEMBLAD S.
 PA (KOGE/) KOGERMAN P.
 PA (PAEL/) PAELL T.
 Query Match 11.0%; Score 182; DB 6; Length 112;
 Best Local Similarity 34.2%; Pred. No. 5.8e-09;
 RESULT 374
 ID ABP73153 standard; protein; 112 AA.
 DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
 PN WO2003018044-A1.
 PD 06-MAR-2003.
 PA (STRO/) STROEMBLAD S.
 PA (KOGE/) KOGERMAN P.
 PA (PAEL/) PAELL T.
 Query Match 10.9%; Score 181; DB 6; Length 112;
 Best Local Similarity 36.0%; Pred. No. 7.2e-09;
 RESULT 375
 ID ABG17067 standard; protein; 920 AA.
 DE Novel human diagnostic protein #17058.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 10.9%; Score 180; DB 4; Length 920;
 Best Local Similarity 25.6%; Pred. No. 1.6e-07;
 RESULT 376
 ID ADI60410 standard; protein; 920 AA.
 DE Secreted polypeptide encoded by gene splice variant #46.
 PN WO2003025142-A2.
 PD 27-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 10.9%; Score 180; DB 7; Length 920;
 Best Local Similarity 25.6%; Pred. No. 1.6e-07;
 RESULT 377
 ID AAM28056 standard; protein; 34 AA.
 DE Peptide #2093 encoded by probe for measuring placental gene expression.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 10.3%; Score 170; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.5e-08;
 RESULT 378
 ID ABG37308 standard; peptide; 34 AA.
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.
 PN WO200186003-A2.
 PD 15-NOV-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 10.3%; Score 170; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.5e-08;

RESULT 379
ID ADB64426 standard; protein; 510 AA.
DE Human protein encoded by clone FEBRA20038970.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.1%; Score 150; DB 7; Length 510;
Best Local Similarity 23.6%; Pred. No. 4.9e-05;
RESULT 380
ID ABP73154 standard; protein; 80 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 9.0%; Score 148.5; DB 6; Length 80;
Best Local Similarity 37.0%; Pred. No. 5.4e-06;
RESULT 381
ID ADP07712 standard; protein; 162 AA.
DE Human secreted protein, seq id 195.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.8%; Score 145; DB 8; Length 162;
Best Local Similarity 33.0%; Pred. No. 3e-05;
RESULT 382
ID ADM80807 standard; protein; 237 AA.
DE Human CADECM-36 protein SEQ ID NO:36.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.8%; Score 145; DB 8; Length 237;
Best Local Similarity 33.0%; Pred. No. 5.1e-05;
RESULT 383
ID AAR26044 standard; protein; 277 AA.
DE Tumour necrosis factor-induced glycoprotein TSG-6.
PN WO9212175-A1.
PD 23-JUL-1992.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 384
ID AAW3654 standard; protein; 277 AA.
DE Tumour necrosis factor-stimulated gene-6 protein.
PN WO9704075-A1.
PD 06-FEB-1997.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 385
ID AAW84087 standard; protein; 277 AA.
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.
PN US5846763-A.
PD 08-DEC-1998.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 386
ID AAQ02361 standard; protein; 277 AA.
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.
PN US6210905-B1.
PD 03-APR-2001.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 4; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 387
ID ABG70870 standard; protein; 277 AA.
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.
PN US2002090708-A1.
PD 11-JUL-2002.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 0.0014;
RESULT 388
ID ABR58556 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:213.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 389
ID ABUS6653 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #246.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 390
ID ADE25781 standard; protein; 277 AA.
DE Human protein differentially expressed in foam cells #58.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 391
ID ADN39919 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 392
ID ADN38974 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 393
ID ADQ21506 standard; protein; 277 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4326.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 8.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 394
ID ADR51534 standard; protein; 277 AA.
DE Human lipopolysaccharide-sensitive polypeptide #14.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 8.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 395
ID ADK67822 standard; protein; 2626 AA.
DE Human BRCC300 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match 8.8%; Score 145; DB 8; Length 2626;
Best Local Similarity 33.0%; Pred. No. 0.0014;
RESULT 396
ID ADS85081 standard; protein; 275 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID83.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.

RESULT 406
ID AAM47675 standard; protein; 1431 AA.
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match
Best Local Similarity 8.0%; Score 133; DB 5; Length 1431;
Best Local Similarity 18.5%; Pred. No. 0.0082;
RESULT 407
ID ARG72498 standard; protein; 1431 AA.
DE Rat 175RDa Hyaluronan receptor for endocytosis (HARE).
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match
Best Local Similarity 8.0%; Score 133; DB 6; Length 1431;
Best Local Similarity 18.5%; Pred. No. 0.0082;
RESULT 408
ID ADH71358 standard; protein; 1510 AA.
DE Human protein of the invention NOV9x SEQ ID NO:254.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.0%; Score 133; DB 8; Length 1510;
Best Local Similarity 20.7%; Pred. No. 0.0088;
RESULT 409
ID ABG72514 standard; protein; 1653 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match
Best Local Similarity 8.0%; Score 133; DB 6; Length 1653;
Best Local Similarity 20.7%; Pred. No. 0.01;
RESULT 410
ID ADM90835 standard; protein; 1895 AA.
DE Human pharmaceutically useful protein SeqID 228.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAP-) DNAPFORM KK.
Query Match
Best Local Similarity 8.0%; Score 133; DB 8; Length 1895;
Best Local Similarity 20.7%; Pred. No. 0.012;
RESULT 411
ID ADH71360 standard; protein; 2551 AA.
DE Human protein of the invention NOV9y SEQ ID NO:256.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.0%; Score 133; DB 8; Length 2551;
Best Local Similarity 20.7%; Pred. No. 0.018;
RESULT 412
ID ABM84174 standard; protein; 2285 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4423.
PN WO20040231973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 8.0%; Score 132.5; DB 8; Length 2285;
Best Local Similarity 27.4%; Pred. No. 0.017;
RESULT 413
ID ABM84173 standard; protein; 2384 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4422.
PN WO20040231973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 8.0%; Score 132.5; DB 8; Length 2384;
Best Local Similarity 27.4%; Pred. No. 0.018;
RESULT 414
ID ABP72603 standard; protein; 883 AA.
DE Rat mutant brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match
Best Local Similarity 7.9%; Score 131.5; DB 6; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0059;
RESULT 415
ID ADK67779 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match
Best Local Similarity 7.9%; Score 131.5; DB 8; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0059;
RESULT 416
ID AAB61236 standard; protein; 649 AA.
DE Mature human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 4; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 417
ID ABO32673 standard; protein; 649 AA.
DE Secreted polypeptide-related protein #74.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match
Best Local Similarity 7.9%; Score 131; DB 6; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 418
ID ADB90778 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003082596-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 7; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 419
ID ADP71513 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 7; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 420
ID ADQ10331 standard; protein; 649 AA.
DE Human polypeptide #167.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 421
ID AAB61234 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 4; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;

RESULT 422
ID ABO32671 standard; protein; 671 AA.
DE Secreted polypeptide-related protein #73.
PN US200302229-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIg/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 7.9%; Score 131; DB 6; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;
RESULT 423
ID ADB90776 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 7; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;
RESULT 424
ID ADF1511 standard; protein; 671 AA.
DE Human TANGO 332.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 7; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;
RESULT 425
ID ADQ10329 standard; protein; 671 AA.
DE Human polypeptide #165.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 8; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;
RESULT 426
ID ADH18892 standard; protein; 806 AA.
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 7.9%; Score 131; DB 8; Length 806;
Best Local Similarity 20.4%; Pred. No. 0.0058;
RESULT 427
ID AAY97583 standard; protein; 911 AA.
DE Human secreted protein PRO6018.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 4; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 428
ID ABG34055 standard; protein; 911 AA.
DE Human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 5; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 429
ID ADI28032 standard; protein; 911 AA.
DE ECMCAD protein 6755002CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.9%; Score 131; DB 5; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 430
ID ADA01320 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 431
ID ADA43749 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 432
ID ADA43517 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 433
ID ADA01192 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 434
ID ADA01076 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 435
ID ADA43633 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 436
ID ADA06895 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 437
ID ADA08383 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 438
ID ADB99676 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;

RESULT 439
ID ADB86959 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 440
ID ADB66114 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 441
ID ADB99792 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 442
ID ADB99447 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 443
ID ADB65998 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 444
ID ADC23396 standard; protein; 911 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 445
ID ADC26089 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 446
ID ADE62583 standard; protein; 911 AA.
DE Human Protein NP_068767, SEQ ID NO 8514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 447
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;

RESULT 448
ID ADE11222 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 449
ID ADD88153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 450
ID ADD95448 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 451
ID ADE06378 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 452
ID ADE38153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 453
ID ADD88259 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 454
ID ADD90850 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 455
ID ADF99405 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 456
ID ADG06498 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 457
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;

ID ADG05449 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 458
ID ADG82450 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US200307744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 459
ID ADE51703 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 460
ID ADE51819 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 461
ID ADE37677 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 462
ID ADE37561 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 463
ID ADD95332 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 464
ID ADE38032 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 465
ID ADE76121 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 466
ID ADE39444 standard; protein; 911 AA.

ID Human PRO polypeptide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 467
ID ADE04248 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 468
ID ADE39845 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 469
ID ADE19710 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 470
ID ADE77288 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 471
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 472
ID ADE76005 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 473
ID ADE37916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 474
ID ADE64526 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 475
ID ADE38861 standard; protein; 911 AA.
DE Human PRO polypeptide #26.

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PN US2003096363-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 476
ID ADE51935 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 477
ID ADD90966 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 478
ID ADE38745 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 479
ID ADE37445 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 480
ID ADE06262 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 481
ID ADD90121 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 482
ID ADE38629 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 483
ID ADE39560 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 484
ID ADD89165 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138897-A1.

PN US2003096363-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 485
ID ADD88932 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 486
ID ADE19826 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 487
ID ADE77404 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 488
ID ADE65280 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 489
ID ADE39328 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 490
ID ADE38513 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 491
ID ADG11066 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 492
ID ADG10950 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 493
ID ADH31478 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
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PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 494
ID ADH38726 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 495
ID ADH29361 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 496
ID ADH23664 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 497
ID ADH26994 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 498
ID ADH38262 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 499
ID ADH26878 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 500
ID ADH38146 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 501
ID ADH38842 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 502
ID ADH23780 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 503
ID ADH40156 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 504
ID ADH40040 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 505
ID ADH31362 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 506
ID ADH29240 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 507
ID ADH49455 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 508
ID ADH51919 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 509
ID ADH49774 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 510
ID ADH52375 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 511
ID ADH52491 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 512
ID ADH23780 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 512
ID ADH5488 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 513
ID ADH51803 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 514
ID ADH58364 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 515
ID ADI13561 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 516
ID ADK00817 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 517
ID ADL08558 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 518
ID ABM80156 standard; protein; 911 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 519
ID RAB61242 standard; protein; 883 AA.
DE Murine brevidin protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 4; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 520
ID ABO32678 standard; protein; 883 AA.
DE Secreted polypeptide-related protein #119.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.

PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (WACK/) WACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 7.9%; Score 130.5; DB 6; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 521
ID ASP72604 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (WATT/) MATTHEWS R T.
Query Match 7.9%; Score 130.5; DB 6; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0073;
RESULT 522
ID ADB90787 standard; protein; 883 AA.
DE Mouse brevicin protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 523
ID ADE62581 standard; protein; 883 AA.
DE Rat Protein P55068, SEQ ID NO 8512.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEOH) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.9%; Score 130.5; DB 7; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0073;
RESULT 524
ID ADF71522 standard; protein; 883 AA.
DE Murine brevidin protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 525
ID ADK67782 standard; protein; 883 AA.
DE Rat glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match 7.9%; Score 130.5; DB 8; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0073;
RESULT 526
ID ADQ10338 standard; protein; 883 AA.
DE Human polypeptide #172.
PN US2004121356-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 8; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 527
ID ABB90349 standard; protein; 1082 AA.
DE Human polypeptide SEQ ID NO 2725.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.9%; Score 130.5; DB 5; Length 1082;
Best Local Similarity 20.6%; Pred. No. 0.0096;
RESULT 528
ID ABM80463 standard; protein; 2570 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.
PN WO2004030615-A2.

PD 15-APR-2004.
 PA (GETH) GENENTECH INC. 7.9%; Score 130.5; DB 8; Length 2570;
 Query Match
 Best Local Similarity 20.6%; Pred. No. 0.032;
 RESULT 529
 ID AAY93911 standard; protein; 457 AA.
 DE A human hyaluronan-binding protein, designated WF-HABP.
 PN WO200039166-A1.
 PD 06-JUL-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (AMNA-) AMERICAN NAT RED CROSS.
 Query Match
 Best Local Similarity 20.9%; Pred. No. 0.0037;
 RESULT 530
 ID ABM83434 standard; protein; 761 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 7.8%; Score 129.5; DB 8; Length 761;
 RESULT 531
 ID AAY93910 standard; protein; 2157 AA.
 DE A human hyaluronan-binding protein, designated WF-HABP.
 PN WO200039166-A1.
 PD 06-JUL-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (AMNA-) AMERICAN NAT RED CROSS.
 Query Match
 Best Local Similarity 7.8%; Score 129.5; DB 3; Length 2157;
 RESULT 532
 ID ABR82200 standard; protein; 2570 AA.
 DE Human CLEVER-1 protein SEQ ID NO:1.
 PN WO20003057130-A2.
 PD 17-JUL-2003.
 PA (JALK/) JALKANEN S.
 PA (IRJA/) IRJALA H.
 PA (SALM/) SALMI M.
 Query Match
 Best Local Similarity 7.8%; Score 129.5; DB 6; Length 2570;
 RESULT 533
 ID AAB08023 standard; protein; 95 AA.
 DE The domain of hyaluronic acid which interacts with CD44.
 PN WO200047163-A2.
 PD 17-AUG-2000.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 Query Match
 Best Local Similarity 28.7%; Pred. No. 0.00053;
 RESULT 534
 ID ABU04625 standard; protein; 95 AA.
 DE Human expressed protein tag (EPT) #1291.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match
 Best Local Similarity 7.8%; Score 128.5; DB 6; Length 95;
 RESULT 535
 ID AAR85442 standard; protein; 912 AA.
 DE Bovine brevican core protein.
 PN WO9526201-A1.
 PD 05-OCT-1995.
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 Query Match
 Best Local Similarity 22.0%; Pred. No. 0.012;
 RESULT 536
 ID ABM83431 standard; protein; 825 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3680.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 8; Length 825;
 RESULT 537
 ID ADB47827 standard; protein; 457 AA.
 ID ABM83430 standard; protein; 863 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3679.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 8; Length 863;
 RESULT 538
 ID AAE30340 standard; protein; 911 AA.
 DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.
 PN WO200276510-A1.
 PD 03-OCT-2002.
 PA (AGYT-) AGY THERAPEUTICS INC.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 6; Length 911;
 RESULT 539
 ID ADN38942 standard; protein; 911 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 7; Length 911;
 RESULT 540
 ID ADK67784 standard; protein; 911 AA.
 DE Human glycosylation-variant BEHAB isoform.
 PN WO2004013356-A1.
 PD 12-FEB-2004.
 PA (UYVA) UNIV YALE.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 8; Length 911;
 RESULT 541
 ID ABR58557 standard; protein; 277 AA.
 DE Human cancer related protein SEQ ID NO:214.
 PN WO2003025138-A2.
 PD 27-MAR-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 7.7%; Score 127; DB 6; Length 277;
 RESULT 542
 ID ABUS6654 standard; protein; 277 AA.
 DE Lung cancer-associated polypeptide #247.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 7.7%; Score 127; DB 6; Length 277;
 RESULT 543
 ID ADN38976 standard; protein; 277 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 7.7%; Score 127; DB 7; Length 277;
 RESULT 544
 ID ADO24439 standard; protein; 277 AA.
 DE Human PRO87335 protein SEQ ID NO:78.
 PN WO2004043397-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 30.7%; Pred. No. 0.0032;
 RESULT 545
 ID ADRI4117 standard; protein; 277 AA.
 DE Human NF-kappaB pathway-associated protein SegID118.
 PN WO2004065577-A2.
 PD 05-AUG-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match
 Best Local Similarity 7.7%; Score 127; DB 8; Length 277;
 RESULT 546
 ID ADB47827 standard; protein; 457 AA.

DE Novel human secreted protein #3.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NIJU/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C E.
Query Match
Best Local Similarity 7.6%; Score 126.5; DB 7; Length 457;
RESULT 547
ID ADJ5382 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.6%; Score 126.5; DB 8; Length 457;
RESULT 548
ID ADO24485 standard; protein; 277 AA.
DE Human PRO87343 protein SEQ ID NO:124.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 126; DB 8; Length 277;
RESULT 549
ID ADB65640 standard; protein; 482 AA.
DE Human protein encoded by clone THYMU20143230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 7.5%; Score 124.5; DB 7; Length 482;
RESULT 550
ID ADM80804 standard; protein; 259 AA.
DE Human CADECM-33 protein SEQ ID NO:33.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 259;
RESULT 551
ID AAY13381 standard; protein; 360 AA.
DE Amino acid sequence of protein PRO271.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 2; Length 360;
RESULT 552
ID ADC78533 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 3; Length 360;
RESULT 553
ID AAB80249 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 4; Length 360;
RESULT 554
ID AAU29037 standard; protein; 360 AA.
DE Human PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 4; Length 360;
RESULT 555
ID AAM38965 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 2110.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 4; Length 360;
RESULT 556
ID ABUS8413 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 557
ID ABU71627 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 558
ID ABUS7961 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 559
ID ABUS4276 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 560
ID ABR66150 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 561
ID ABR65540 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 562
ID ABUS9480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 563
ID ABUS2719 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.

Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 564
ID ABU9840 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 565
ID ABU71482 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 566
ID ABR68089 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027284-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 567
ID ABU96142 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 568
ID ABU92573 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 569
ID ABO08650 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 570
ID ABO02702 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 571
ID ABR74856 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 572
ID ABR94618 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 573
ID ABU95591 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 574
ID ABU98751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 575
ID ABU97966 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 576
ID ABU91672 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 577
ID ABU71928 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 578
ID ABU89365 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 579
ID ABU86206 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 580
ID ABU67419 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 581
ID ABU80447 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 582
ID ABO01811 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 583
ID ABR99365 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040063-A1.

PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 584
ID ABU98755 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 585
ID ABO16278 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 586
ID ABR92178 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 587
ID ABO18819 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 588
ID ABR78240 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 589
ID ABU84976 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 590
ID ABO00115 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 591
ID ABO11447 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 592
ID ABO02092 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 593
ID ABU54384 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.

Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 594
ID ABU98666 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 595
ID ABU83361 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 596
ID ABO06162 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 597
ID ABR59198 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 598
ID ABO09260 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 599
ID ABO19124 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 600
ID ABO11142 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 601
ID ABR66760 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 602
ID ABO15973 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 603
ID ABO13679 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 604
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 605
ID ABUS582 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, SEQ ID 28.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 606
ID ABO07430 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 607
ID ABO3617 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 608
ID ABR67065 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 609
ID ABO15668 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 610
ID ABUS5949 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 611
ID ABUS5277 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 612
ID ABUS9522 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 613
ID ABU71125 standard; protein; 360 AA.
DE Human PRO271 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 614
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

ID ABO07735 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 615
ID ABR69976 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 616
ID ABR69309 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 617
ID ABO01450 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 618
ID ABU81252 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 619
ID ABR60049 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 620
ID ABR67784 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 621
ID ABR65172 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 622
ID ABR68394 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 623
ID ABR71806 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 624
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

ID ABU85286 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 625
ID ABU88976 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 626
ID ABU83056 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 627
ID ABU94912 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 628
ID ABU90460 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 629
ID ABU83971 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 630
ID ABU93622 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 631
ID ABR64867 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 632
ID ABR68699 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 633
ID ABO06515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 634
ID ABR99060 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 635
ID ABU56944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 636
ID ABU64536 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 637
ID ABU85896 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 638
ID ABU67382 standard; protein; 360 AA.
DE Human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 639
ID ABU82183 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 640
ID ABU87194 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 641
ID ABU83666 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 642
ID ABO08040 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 643
ID ABO14902 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 644
ID ABU81751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.

PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 645
ID ABU65915 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 646
ID ABR59744 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 647
ID ABU93932 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 648
ID ABU99785 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 649
ID ABR66455 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 650
ID ABR90873 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 651
ID ABU94300 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 652
ID ABU79182 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 653
ID ABU86511 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 654
ID ABU86816 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 655
ID ABU94605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 656
ID ABO04532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 657
ID ABR70281 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 658
ID ABU98446 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 659
ID ABR65845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 660
ID ABR64562 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 661
ID ABU79487 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 662
ID ABU92878 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 663
ID ABU95837 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 664
ID ABU91057 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 665
ID ABU90150 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 666
ID ABO09565 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 667
ID ABO10837 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 668
ID ABR70891 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 669
ID ABU87499 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 670
ID ABU91367 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 671
ID ABU84581 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 672
ID ABR69671 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 673
ID ABU80048 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 674
ID ABU69659 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 675
ID ABU93317 standard; protein; 360 AA.

DE Human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 676
ID ABO09870 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 677
ID ABO08955 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 678
ID ABU10523 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 679
ID ABU95532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 680
ID ABU96741 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 681
ID ABR70586 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 682
ID ABO04937 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 683
ID ABO08345 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 684
ID ABO14841 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 685

ID ABO5552 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 686
ID ABR73941 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 687
ID ABR95533 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 688
ID ABR80830 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 689
ID ABR81135 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 690
ID ABO00831 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 691
ID ABR88433 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 692
ID ABR77254 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 693
ID ABO28738 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 694
ID ABO31483 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068725-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 695
ID ABO07900 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 696
ID ABO40380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 697
ID ABO35805 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 698
ID ABO43944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 699
ID ADA77780 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 700
ID ABO24739 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 701
ID ADB29418 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 702
ID ABO03007 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 703
ID ABR90263 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 704
ID ABM17177 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 705
ID ABR94923 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 706
ID ABR95228 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 707
ID ABO21466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 708
ID ABR97730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 709
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 710
ID ABM77559 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 711
ID ABM27789 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 712
ID ABM06070 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 713
ID ABM03576 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 714
ID ABM35027 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 715
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 716
ID ABO48046 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 717
ID ABR92788 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 718
ID ABO24549 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 719
ID ABM1560 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 720
ID ABM02661 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 721
ID ABM15957 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 722
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 723
ID ABM25654 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 732
ID ABM25959 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 733
ID ABO031312 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 735
ID ABO02397 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 736
ID ABR90568 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 737
ID ABR73636 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 738
ID ABO16888 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 739
ID ABR94313 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 740
ID ABR75820 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 741
ID ADA18274 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

PD 03-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 723
ID ABM29009 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 724
ID ABM06985 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 725
ID ABM21079 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 726
ID ABM09425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 727
ID ABO41295 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 728
ID ABO36110 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 729
ID ABO43639 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 730
ID ABM76339 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 6; Length 360;
Query Match 34.9%; Pred. No. 0.015;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 731
ID ABM76035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

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Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 742
ID ABO32793 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 743
ID ABR71196 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 744
ID ABR93093 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 745
ID ABR93398 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 746
ID ABR7823 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 747
ID ABO27823 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 748
ID ABO29958 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003084461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 749
ID ABO33167 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 750
ID ABO4855 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 751
ID ABO8815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 752
ID ABO36415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 753
ID ABO35500 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 754
ID ABO39465 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 755
ID ABM10340 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 756
ID ABM1865 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 757
ID ABO52011 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 758
ID ABO52316 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 759
ID ABO23634 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 760
ID ABO23634 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 760
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ID ABR97120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 761
ID ABR6908 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 762
ID ABM10950 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 763
ID ABM28094 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 764
ID ABO32093 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 765
ID ABM15220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 766
ID ABM06375 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 767
ID ABM04186 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 768
ID ABM22299 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 769
ID ABM07595 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 770
ID ABO40685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 771
ID ABM35332 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 772
ID ABM33095 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 773
ID ABO52621 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 774
ID ABO50181 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 775
ID ABU99175 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 776
ID ABO04227 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 777
ID ABO05857 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 778
ID ABO34853 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 779
ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 780
ID ADA16249 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 781
ID ABR97425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 782
ID ABR80525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 783
ID ABM01136 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 784
ID ABR88738 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 785
ID ABM13390 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 786
ID ABM20774 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 787
ID ABO41905 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 788

ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 789
ID ABM10035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 790
ID ABO38550 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003088773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 791
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 792
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 793
ID ABM74815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 794
ID ADA79572 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 795
ID ABR96205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 796
ID ABM02356 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 797
ID ABR86298 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 798
ID ABR86603 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 799
ID ABM16567 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 800
ID ABM29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 801
ID ABO29043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 802
ID ABM23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 803
ID ABM23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 804
ID ABM21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 805
ID ABO37635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 806
ID ABM28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 807
ID ABM28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 808
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 809
ID ABM75730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 810
ID ABM34010 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 811
ID ABM34315 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 812
ID ABO20246 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 813
ID ABO21161 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 814
ID ABO22076 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 815
ID ABR96510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 816
ID ABR85688 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049753-A1.
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PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 817
ID ABR99670 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 818
ID ABM00221 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 819
ID ABM00526 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 820
ID ABO29653 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 821
ID ABM23519 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 822
ID ABM29314 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 823
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 824
ID ABO45545 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 825
ID ABM20469 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 826
ID ADA42394 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 827
ID ADA81299 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 828
ID ABO16583 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 829
ID ABO18209 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 830
ID ABO22636 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027285-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 831
ID ABO22941 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 832
ID ABR92483 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 833
ID ABR81440 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 834
ID ABO17531 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 835
ID ABM77864 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

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PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 845
ID ABO35195 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 846
ID ABM25044 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 847
ID ABO47436 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 848
ID ABO47741 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 849
ID ABO48351 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 850
ID ABO51401 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 851
ID ABO51706 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 852
ID ABO50486 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 853
ID ABR79610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 854
ID ABO41600 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 836
ID ABR89653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 837
ID ABM26569 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 838
ID ABM13695 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 839
ID ABO28433 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 840
ID ABO30263 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 841
ID ABM07290 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 842
ID ABM03881 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 843
ID ABO37025 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 844
ID ABO41600 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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ID ABM16872 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 855
ID ABO17904 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 856
ID ABO20856 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 857
ID ABR96815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 858
ID ABM12170 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 859
ID ABM16262 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 860
ID ABM24129 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 861
ID ABM14610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 862
ID ABM04491 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 863
ID ABM06680 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068730-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 864
ID ABM09120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 865
ID ABO39160 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 866
ID ABM75425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 867
ID ABM25349 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 868
ID ABM19859 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 869
ID ABO46765 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 870
ID ABO47070 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 871
ID ADA83097 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 872
ID ABR71501 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 873

ID ABR72111 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 874
ID ABR98450 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 875
ID ABO06820 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 876
ID ABR84773 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 877
ID ABR73331 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054467-A1.
PD 20-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 878
ID ABR76425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 879
ID ABR73026 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 880
ID ABM18092 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054469-A1.
PD 20-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 881
ID ABO20551 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 882
ID ABO25294 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054463-A1.
PD 20-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 883

ID ABO25599 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 884
ID ABR94008 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059879-A1.
PD 27-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 885
ID ABR79915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 886
ID ABM11255 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064469-A1.
PD 03-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 887
ID ABO32862 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 888
ID ABO30568 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064466-A1.
PD 03-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 889
ID ABO30873 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064468-A1.
PD 03-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 890
ID ABM27179 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068760-A1.
PD 10-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 891
ID ABM29924 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068769-A1.
PD 10-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 892
ID ABM05460 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003045700-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 893
 ID ABO49571 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003068698-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 894
 ID ABO49571 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003068759-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 895
 ID ABO42210 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049748-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 896
 ID ABO37940 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003068765-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 897
 ID ABO45850 standard; protein; 360 AA.
 DE Human PRO polypeptide #14.
 PN US2003049754-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 898
 ID ABO66653 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068688-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 899
 ID ABO20140 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003082767-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 900
 ID ABO19554 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003104552-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 901
 ID ABO49266 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049774-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 902
 ID ABO49571 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049775-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 903
 ID ADA78392 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003073181-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 904
 ID ABR88128 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068720-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 905
 ID ABM26874 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068739-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 906
 ID ABM03271 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068763-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 907
 ID ABO39770 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003068689-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 908
 ID ABO49876 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049776-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 909
 ID ABO50791 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049780-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 910
 ID ABO05247 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003061266-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 911
ID ABR74551 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 912
ID ABR77030 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 913
ID ADA16673 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 914
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 915
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 916
ID ADA13102 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 917
ID ABO21771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 918
ID ABO19941 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 919
ID ABO24244 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 920
ID ABR85993 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049759-A1.
PD 13-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 921
ID ABR10645 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 922
ID ABR76644 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 923
ID ABR9348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 924
ID ABM12475 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 925
ID ABM05765 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 926
ID ABO34890 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 927
ID ABM02966 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 928
ID ABM18944 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 929
ID ABM19249 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 930
ID ABO46460 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 931
ID ABO48961 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 932
ID ADA41970 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 933
ID ABR69004 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 934
ID ABR89043 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 935
ID ABR72416 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 936
ID ABR74246 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 937
ID ABO18514 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 938
ID ADA17317 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 939
ID ABR80220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049739-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 940
ID ABM01441 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 941
ID ABM02051 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 942
ID ABR87213 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003086887-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 943
ID ABM12780 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 944
ID ABM30534 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 945
ID ABM24434 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 946
ID ABO29348 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 947
ID ABO31178 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 948
ID ABM14305 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068686-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 949
ID ABM09730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 950
ID ABO38855 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 951
ID ABM34620 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 952
ID ABO51096 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 953
ID ADA42820 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 954
ID ABO03922 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 955
ID ABO10392 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 956
ID ABR77635 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 957
ID ABR78845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 958
ID ABO23939 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.

PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 959
ID ABR93703 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 960
ID ABM01746 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 961
ID ABM78169 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 962
ID ABR89958 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 963
ID ABM27484 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 964
ID ABM13085 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 965
ID ABO31788 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;
Query Match 34.9%; Pred. No. 0.015;
RESULT 966
ID ABM14000 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 967
ID ABM08205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068754-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 968
ID ABO40075 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 969
ID ABO74510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 970
ID ABO33705 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 971
ID ABO20164 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 972
ID ABO48656 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 973
ID ABR72721 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 974
ID ABO15363 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 975
ID ABR85078 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 976
ID ABO15058 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 977
ID ABO17193 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 978
ID ABO17482 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 979
ID ABR85383 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 980
ID ABO17592 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 981
ID ABO76949 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 982
ID ABO28128 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 983
ID ABO22909 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 984
ID ABO30229 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 985
ID ABO21689 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 986
ID ABO21384 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068744-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 987
ID ABM14915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 988
ID ABO40990 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 989
ID ABO36720 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 990
ID ABO37330 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 991
ID ABM75120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 992
ID ABM33400 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 993
ID ABO46155 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 994
ID ADA82463 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 995
ID ABM31754 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 996
ID ABM31144 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 997
ID ADB77739 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 998
ID ADB74875 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 999
ID ADB85771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1000
ID ABM32059 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1001
ID ABM32364 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1002
ID ABM31449 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1003
ID ABM30839 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1004
ID ADC28521 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 1005
ID ADC39721 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1006
ID ADC40235 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1007
ID ADC19059 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1008
ID ADC34359 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1009
ID ADC29414 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1010
ID ADC28945 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1011
ID ADC40830 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1012
ID ADC19487 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1013
ID ADC33935 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1014

ID ADC13005 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1015
ID ADC12457 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1016
ID ADD05501 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1017
ID ADD05012 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1018
ID ADD04018 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1019
ID ADD03594 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1020
ID ADE34846 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1021
ID ADG02496 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1022
ID ADG01203 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1023
ID ADF95378 standard; protein; 360 AA.

DE Novel human secreted and transmembrane protein PRO271.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1024
ID ADG12193 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1025
ID ADH08853 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1026
ID ADH59329 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1027
ID ADI38108 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1028
ID ADJ26376 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1029
ID ADL32634 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1030
ID ADM30168 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1031
ID ADE79291 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1032
ID ADE79715 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003130489-A1.

PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1033
ID ADE73391 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1034
ID ADE74165 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1035
ID ADE73926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1036
ID ADE74777 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1037
ID ADE99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1038
ID ADE98599 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1039
ID ADE99026 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1040
ID ADG40496 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GUEN/) GUERNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
RESULT 1041

ID ADF73890 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1042
ID ADF95990 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1043
ID ADF73466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1044
ID ADG04261 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1045
ID ADG00421 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1046
ID ADG82677 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1047
ID ADG92309 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1048
ID ADG92736 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1049
ID ADH25958 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1050
ID ADH32927 standard; protein; 360 AA.
DE Human PRO polypeptide #14.

PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1051
ID ADH20525 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1052
ID ADH07380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1053
ID ADH59925 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1054
ID ADH06953 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1055
ID ADI18695 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1056
ID ADI65415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1057
ID ADI37678 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1067
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1068
ID ADM36380 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1069
ID ADM40185 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1070
ID ADL91793 standard; protein; 360 AA.
DE Human PRO271 protein SEQ ID NO:14.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1071
ID ADO06248 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1072
ID ADM37793 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1073
ID ADRI1100 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1074
ID ADRI8009 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.

PA (GAOW/) GAO W. 7.3%; Score 121.5; DB 8; Length 360;
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 34.9%; Pred. No. 0.015; Length 360;
RESULT 1075
ID ADT03685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 34.9%; Pred. No. 0.015; Length 360;
RESULT 1076
ID ADS74648 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #42.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOVERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 34.9%; Pred. No. 0.015; Length 360;
RESULT 1077
ID AAW5982 standard; protein; 528 AA.
DE Amino acid sequence of the cDNA clone BEF (HSXCK41).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVISES LTD.
Query Match
Best Local Similarity 24.1%; Pred. No. 0.029; Length 528;
RESULT 1078
ID AAB61241 standard; protein; 528 AA.
DE Human BEF protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match
Best Local Similarity 7.3%; Score 121; DB 4; Length 528;
RESULT 1079
ID ABO32677 standard; protein; 528 AA.
DE Secreted polypeptide-related protein #75.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GODDEARL A D J.
Query Match
Best Local Similarity 7.3%; Score 121; DB 6; Length 528;
RESULT 1080
ID ADB90786 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.3%; Score 121; DB 7; Length 528;
RESULT 1081
ID ADF71521 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.3%; Score 121; DB 7; Length 528;
RESULT 1082
ID ADQ10337 standard; protein; 528 AA.
DE Human polypeptide #171.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.3%; Score 121; DB 8; Length 528;
RESULT 1083
ID AAR46627 standard; protein; 1257 AA.
DE Neurocan core protein.
PN WO9403601-A2.
PD 17-FEB-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match
Best Local Similarity 7.3%; Score 120.5; DB 2; Length 1257;
RESULT 1084
ID ADQ39513 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 7.2%; Score 118.5; DB 8; Length 1642;
RESULT 1085
ID ADQ39515 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 7.2%; Score 118.5; DB 8; Length 1642;
RESULT 1086
ID ADN04531 standard; protein; 2000 AA.
DE Antipsoriatic protein sequence #458.
PN WO2004028479-A2.
PD 08-APR-2004.

PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.31;
RESULT 1087
ID ADP23738 standard; protein; 2000 AA.
DE PRO polypeptide SEQ ID NO:916.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.31;
RESULT 1088
ID ADD48597 standard; protein; 3396 AA.
DE Human Protein P13611, SEQ ID NO 14303.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1089
ID ADN95526 standard; protein; 3396 AA.
DE Human BEC/LEC-related protein sequence SeqID449.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.2%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1090
ID ADJ75521 standard; protein; 3396 AA.
DE Marker gene related amino acid sequence SEQ ID NO:773.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1091
ID ADQ39509 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1092
ID ADQ39510 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1093
ID ADR99164 standard; protein; 3396 AA.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1094
ID ADP71273 standard; protein; 191 AA.
DE Human Lf2 protein B-B' domain SeqID8.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 7.1%; Score 117; DB 8; Length 191;
Best Local Similarity 26.5%; Pred. No. 0.017;
RESULT 1095
ID ADM87304 standard; protein; 340 AA.
DE Human protein SEQ ID NO:397.
PN WO2004009834-A2.

PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.1%; Score 117; DB 8; Length 340;
Best Local Similarity 26.5%; Pred. No. 0.037;
RESULT 1096
ID ABUI1635 standard; protein; 343 AA.
DE Human MDDT polypeptide SEQ ID 582.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.1%; Score 117; DB 6; Length 343;
Best Local Similarity 26.5%; Pred. No. 0.038;
RESULT 1097
ID ADJ76266 standard; protein; 2397 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1518.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.0%; Score 116; DB 8; Length 2397;
Best Local Similarity 28.4%; Pred. No. 0.68;
RESULT 1098
ID AAR85443 standard; protein; 908 AA.
DE Rat brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 6.9%; Score 115; DB 2; Length 908;
Best Local Similarity 22.2%; Pred. No. 0.22;
RESULT 1099
ID ADO31200 standard; protein; 1257 AA.
DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 6.9%; Score 114.5; DB 8; Length 1257;
Best Local Similarity 23.1%; Pred. No. 0.39;
RESULT 1100
ID ADD48595 standard; protein; 656 AA.
DE Rat Protein AF072892, SEQ ID NO 14301.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.9%; Score 114; DB 7; Length 656;
Best Local Similarity 28.4%; Pred. No. 0.18;
RESULT 1101
ID ABB10268 standard; protein; 287 AA.
DE Human cDNA SEQ ID NO: 576.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.8%; Score 112.5; DB 4; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.079;
RESULT 1102
ID ABP66855 standard; protein; 287 AA.
DE Human polypeptide SEQ ID NO 576.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.8%; Score 112.5; DB 5; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.079;
RESULT 1103
ID ABU36285 standard; protein; 402 AA.
DE Protein encoded by Prokaryotic essential gene #21812.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 111.5; DB 6; Length 402;
Best Local Similarity 22.5%; Pred. No. 0.16;
RESULT 1104
ID ADP71271 standard; protein; 200 AA.

DE Human aggrecan protein B-B' domain SeqID6.
PN JF2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIRAGAKU KOGYO CO LTD.
Query Match 6.7%; Score 111; DB 8; Length 200;
Best Local Similarity 37.4%; Pred. No. 0.066;
RESULT 1105
ID AAM52242 standard; protein; 655 AA.
DE Human versican isoform V3 SEQ ID NO 2.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH/) WIGHT T N.
PA (MERR/) MERRILEES M.
Query Match
Best Local Similarity 6.7%; Score 111; DB 5; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.34;
RESULT 1106
ID ADQ39511 standard; protein; 655 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 6.7%; Score 111; DB 8; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.34;
RESULT 1107
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match
Best Local Similarity 6.7%; Score 111; DB 2; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1108
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence SEQ ID NO:90.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match
Best Local Similarity 6.7%; Score 111; DB 6; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1109
ID ADQ39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 6.7%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1110
ID ADQ39512 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 6.7%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1111
ID AAB12304 standard; protein; 341 AA.
DE Human secreted protein encoded by gene 4 clone HPXHC41.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.6%; Score 110; DB 3; Length 341;
Best Local Similarity 28.5%; Pred. No. 0.17;
RESULT 1112
ID AAY93913 standard; protein; 353 AA.
DE A human hyaluronan-binding protein, designated BM-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match
Best Local Similarity 6.6%; Score 109; DB 3; Length 353;
Best Local Similarity 24.3%; Pred. No. 0.22;

RESULT 1113
ID ABP97200 standard; protein; 1321 AA.
DE Tumour-associated antigenic target protein TAT185 SEQ ID NO:82.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.6%; Score 109; DB 6; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1114
ID ADJ69615 standard; protein; 1321 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1421.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 6.6%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1115
ID ADN38944 standard; protein; 1321 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 6.6%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1116
ID ADO31196 standard; protein; 1321 AA.
DE Human neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match
Best Local Similarity 6.6%; Score 109; DB 8; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1117
ID ABJ56909 standard; protein; 322 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.25;
RESULT 1118
ID ABJ56908 standard; protein; 322 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.25;
RESULT 1119
ID ABJ56918 standard; protein; 353 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 353;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1120
ID AAY57081 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 6.5%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1121
ID AAY57084 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor #2.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 6.5%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;

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RESULT 1122
ID ABJ56902 standard; protein; 354 AA.
DE 151P3D4 v-1 354aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1123
ID ABJ56906 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1124
ID ABJ56914 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1125
ID ABJ56898 standard; protein; 354 AA.
DE 151P3D4 v-8 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1126
ID ABJ56895 standard; protein; 354 AA.
DE 151P3D4 v-5 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1127
ID ABJ56897 standard; protein; 354 AA.
DE 151P3D4 v-7 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1128
ID ABJ56901 standard; protein; 354 AA.
DE 151P3D4 v-11 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1129
ID ABJ56894 standard; protein; 354 AA.
DE 151P3D4 v-4 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1130
ID ABJ56905 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1131
ID AAR77034 standard; protein; 355 AA.
DE 151P3D4 v-9 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1132
ID ABJ56912 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1133
ID ABJ56893 standard; protein; 354 AA.
DE 151P3D4 v-3 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1134
ID ABJ56891 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1135
ID ABJ56896 standard; protein; 354 AA.
DE 151P3D4 v-6 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1136
ID ABJ56900 standard; protein; 354 AA.
DE 151P3D4 v-10 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1137
ID ABJ56889 standard; protein; 354 AA.
DE Transcript variant 121PIF1 v-1.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1138
ID ABJ56904 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 354;
RESULT 1139
ID ADP07795 standard; protein; 354 AA.
DE Human secreted protein, seq id 278.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 8; Length 354;
RESULT 1140
ID AAR77034 standard; protein; 355 AA.
```

DE Rat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYU) UNIV YALE.
Query Match 6.5%; Score 108; DB 2; Length 355;
Best Local Similarity 28.9%; Pred. No. 0.28;
RESULT 1141
ID ADH71348 standard; protein; 552 AA.
DE Human protein of the invention NOV9s SEQ ID NO:244.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 108; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.51;
RESULT 1142
ID ABJ56890 standard; protein; 721 AA.
DE Transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.74;
RESULT 1143
ID ABJ56892 standard; protein; 721 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.8%; Pred. No. 0.74;
RESULT 1144
ID ABJ56903 standard; protein; 721 AA.
DE 151P3D4 v-1 721aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.74;
RESULT 1145
ID ABG72500 standard; protein; 93 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) LINK domain.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 6.5%; Score 107; DB 6; Length 93;
Best Local Similarity 29.2%; Pred. No. 0.055;
RESULT 1146
ID AAB83358 standard; protein; 315 AA.
DE NOV2 protein sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 4; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.3;
RESULT 1147
ID ADH71316 standard; protein; 315 AA.
DE Human protein of the invention NOV9c SEQ ID NO:212.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.3;
RESULT 1148
ID AAY57083 standard; protein; 339 AA.
DE Rat proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.5%; Score 107; DB 3; Length 339;
Best Local Similarity 28.8%; Pred. No. 0.33;
RESULT 1149
ID ABJ56915 standard; protein; 354 AA.

DE Rat cartilage-link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 107; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.35;
RESULT 1150
ID AAY57082 standard; protein; 355 AA.
DE Chicken proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.5%; Score 107; DB 3; Length 355;
Best Local Similarity 34.9%; Pred. No. 0.35;
RESULT 1151
ID ABJ56907 standard; protein; 355 AA.
DE Mouse cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 107; DB 6; Length 355;
Best Local Similarity 28.6%; Pred. No. 0.35;
RESULT 1152
ID ADH71336 standard; protein; 533 AA.
DE Human protein of the invention NOV9m SEQ ID NO:232.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.61;
RESULT 1153
ID ADH71334 standard; protein; 533 AA.
DE Human protein of the invention NOV9l SEQ ID NO:230.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.61;
RESULT 1154
ID ADH71340 standard; protein; 552 AA.
DE Human protein of the invention NOV9o SEQ ID NO:236.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1155
ID ADH71346 standard; protein; 552 AA.
DE Human protein of the invention NOV9r SEQ ID NO:242.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1156
ID ADH71354 standard; protein; 552 AA.
DE Human protein of the invention NOV9v SEQ ID NO:250.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1157
ID ADH71344 standard; protein; 552 AA.
DE Human protein of the invention NOV9q SEQ ID NO:240.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1158
ID ADH71342 standard; protein; 552 AA.
DE Human protein of the invention NOV9p SEQ ID NO:238.

PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1159
ID ADH71350 standard; protein; 552 AA.
DE Human protein of the invention NOV9t SEQ ID NO:246.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1160
ID ADH71314 standard; protein; 556 AA.
DE Human protein of the invention NOV9b SEQ ID NO:210.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 556;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1161
ID ABM83433 standard; protein; 774 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3682.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.5%; Score 107; DB 8; Length 774;
Best Local Similarity 21.5%; Pred. No. 1;
RESULT 1162
ID ABM83432 standard; protein; 822 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3681.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.5%; Score 107; DB 8; Length 822;
Best Local Similarity 21.5%; Pred. No. 1.1;
RESULT 1163
ID ADO31202 standard; protein; 1268 AA.
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 6.5%; Score 107; DB 8; Length 1268;
Best Local Similarity 26.2%; Pred. No. 2;
RESULT 1164
ID ABB69806 standard; protein; 1795 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.5%; Score 107; DB 4; Length 1795;
Best Local Similarity 24.1%; Pred. No. 3.2;
RESULT 1165
ID ADH71332 standard; protein; 2417 AA.
DE Human protein of the invention NOV9k SEQ ID NO:228.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 2417;
Best Local Similarity 29.2%; Pred. No. 4.8;
RESULT 1166
ID ABJ10587 standard; protein; 2420 AA.
DE Human novel protein NOV1b SEQ ID NO: 4.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 5; Length 2420;
Best Local Similarity 29.2%; Pred. No. 4.9;
RESULT 1167
ID ADO09838 standard; protein; 2420 AA.
DE Human NOV1b.
PN US2004018970-A1.

PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATI/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOV S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCH/) TCHERNEV V T.
PA (SIJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 6.5%; Score 107; DB 8; Length 2420;
Best Local Similarity 29.2%; Pred. No. 4.9;
RESULT 1168
ID ADH71338 standard; protein; 552 AA.
DE Human protein of the invention NOV9n SEQ ID NO:234.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 106; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.79;
RESULT 1169
ID AAY57080 standard; protein; 354 AA.
DE Human link protein precursor amino acid sequence.
PN WO9556763-A1.
PD 11-NOV-1999.
PA (REGC-) UNIV CALIFORNIA.
Query Match 6.3%; Score 105; DB 3; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.54;
RESULT 1170
ID ABJ56913 standard; protein; 354 AA.
DE Bovine cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.3%; Score 105; DB 6; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.54;
RESULT 1171
ID AAB42164 standard; protein; 330 AA.
DE Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 104.5; DB 3; Length 330;
Best Local Similarity 18.7%; Pred. No. 0.54;
RESULT 1172
ID ABU07339 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2040.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.3%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.18;
RESULT 1173
ID ABU07336 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2037.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.

Query Match 6.3%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.18;
RESULT 1174
ID ADQ39387 standard; protein; 139 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.3%; Score 104; DB 8; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.18;
RESULT 1175
ID ADP71269 standard; protein; 195 AA.
DE Human LPI protein B-B' domain SeqID4.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 6.3%; Score 104; DB 8; Length 195;
Best Local Similarity 33.7%; Pred. No. 0.29;
RESULT 1176
ID ADP71267 standard; protein; 200 AA.
DE Human versican protein B-B' domain SeqID2.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 6.3%; Score 104; DB 8; Length 200;
Best Local Similarity 32.5%; Pred. No. 0.3;
RESULT 1177
ID ADH71352 standard; protein; 552 AA.
DE Human protein of the invention NOV9u SEQ ID NO:248.
PN WO200171042-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 104; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 1.2;
RESULT 1178
ID ABB60536 standard; protein; 1712 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8400.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 104; DB 4; Length 1712;
Best Local Similarity 22.7%; Pred. No. 5.8;
RESULT 1179
ID ABB65987 standard; protein; 183 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.2%; Score 102.5; DB 4; Length 183;
Best Local Similarity 29.7%; Pred. No. 0.37;
RESULT 1180
ID ADN23553 standard; protein; 380 AA.
DE Bacterial polypeptide #6206.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.1%; Score 101.5; DB 8; Length 380;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 1181
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 101.5; DB 3; Length 590;
Best Local Similarity 20.6%; Pred. No. 2.3;
RESULT 1182
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 101.5; DB 6; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1183
ID AAU76528 standard; protein; 402 AA.
DE Human LP polypeptide #1.
PN WO200216578-A2.
PD 28-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 6.1%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1184
ID AAU09883 standard; protein; 402 AA.
DE Novel human secreted protein #23.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.1%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1185
ID ADF59259 standard; protein; 402 AA.
DE Human polypeptide sequence SEQ ID NO:1667.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 100.5; DB 7; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1186
ID ADF74155 standard; protein; 412 AA.
DE Human novel brain/hippocampus protein #43.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match 6.1%; Score 100.5; DB 7; Length 412;
Best Local Similarity 30.9%; Pred. No. 1.8;
RESULT 1187
ID ABB68940 standard; protein; 1379 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33612.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 100.5; DB 4; Length 1379;
Best Local Similarity 20.2%; Pred. No. 9.2;
RESULT 1188
ID AAR77035 standard; protein; 378 AA.
DE Cat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV VALE.
Query Match 6.0%; Score 100; DB 2; Length 378;
Best Local Similarity 24.1%; Pred. No. 1.7;
RESULT 1189
ID ABP57346 standard; protein; 402 AA.
DE Human secreted protein SECP-17 SEQ ID NO:17.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUYV/) LU Y.
Query Match 6.0%; Score 99.5; DB 6; Length 402;
Best Local Similarity 30.9%; Pred. No. 2.1;
RESULT 1190
ID ABJ56917 standard; protein; 201 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.0%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.91;

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RESULT 1191
ID ABJ56916 standard; protein; 201 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PA (AGEN-) AGENSYS INC.
Query Match 6.0%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.91;
RESULT 1192
ID ADO29463 standard; protein; 410 AA.
DE Mouse GPCR GPRC5B, SEQ ID NO:565.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.0%; Score 99; DB 8; Length 410;
Best Local Similarity 22.0%; Pred. No. 2.4;
RESULT 1193
ID ABJ56919 standard; protein; 600 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.0%; Score 99; DB 6; Length 600;
Best Local Similarity 28.0%; Pred. No. 4.1;
RESULT 1194
ID ABB70377 standard; protein; 1428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37923.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 6.0%; Score 99; DB 4; Length 1428;
Best Local Similarity 28.4%; Pred. No. 13;
RESULT 1195
ID ABB69720 standard; protein; 1126 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35952.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 5.9%; Score 98.5; DB 4; Length 1126;
Best Local Similarity 25.0%; Pred. No. 11;
RESULT 1196
ID AAY95559 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 3; Length 2870;
Best Local Similarity 23.1%; Pred. No. 39;
RESULT 1197
ID ADN07634 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV -1 deletion mutant protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 8; Length 2870;
Best Local Similarity 23.1%; Pred. No. 39;
RESULT 1198
ID AAY95556 standard; protein; 3178 AA.
DE Caenorhabditis elegans LOV-1 (location of vulva) protein.
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 3; Length 3178;
Best Local Similarity 23.1%; Pred. No. 45;
RESULT 1199
ID ADN07623 standard; protein; 3178 AA.
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 8; Length 3178;
Best Local Similarity 23.1%; Pred. No. 45;
RESULT 1200
ID ABB60403 standard; protein; 2112 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 5.9%; Score 98; DB 4; Length 2112;
Best Local Similarity 25.9%; Pred. No. 29;
RESULT 1201
ID AAB75555 standard; protein; 298 AA.
DE Gene 1 human secreted protein homologous amino acid sequence #109.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 5.9%; Score 97.5; DB 4; Length 298;
Best Local Similarity 19.8%; Pred. No. 2.2;
RESULT 1202
ID ADE58456 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4331.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1203
ID ADE58468 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4343.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1204
ID ADE58460 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4335.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1205
ID ADE58464 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4339.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1206
ID ADE58472 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4347.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1207
ID ADE58476 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4351.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1208
ID ADO41972 standard; protein; 231 AA.
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.

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PN WO2004048529-A2.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 95.5; DB 8; Length 231;
Best Local Similarity 30.2%; Pred. No. 2.4;
RESULT 1209
ID ADQ67145 standard; protein; 803 AA.
DE Novel human protein sequence #2118.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 94; DB 8; Length 803;
Best Local Similarity 21.9%; Pred. No. 18;
RESULT 1210
ID AAU18060 standard; protein; 258 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 205.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.2;
RESULT 1211
ID ABB10532 standard; protein; 258 AA.
DE Human cDNA SEQ ID NO: 840.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.2;
RESULT 1212
ID ABP67119 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 840.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.6%; Score 93.5; DB 5; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.2;
RESULT 1213
ID ADB31684 standard; protein; 258 AA.
DE Human novel protein SEQ ID NO 205.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 7; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.2;
RESULT 1214
ID AAU17999 standard; protein; 261 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 144.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.3;
RESULT 1215
ID ABB10361 standard; protein; 261 AA.
DE Human cDNA SEQ ID NO: 669.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.3;
RESULT 1216
ID ABP66948 standard; protein; 261 AA.
DE Human polypeptide SEQ ID NO 669.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.6%; Score 93.5; DB 5; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.3;
RESULT 1217
ID ADB31623 standard; protein; 261 AA.
DE Human novel protein SEQ ID NO 144.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 7; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.3;
RESULT 1218
ID ABG01510 standard; protein; 320 AA.
DE Novel human diagnostic protein #1501.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 93.5; DB 4; Length 320;
Best Local Similarity 23.2%; Pred. No. 5.7;
RESULT 1219
ID ADE36618 standard; protein; 339 AA.
DE Plasmid pCR2.1-CG57008-03-S943 15B protein insert SEQ ID NO:28.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 93.5; DB 7; Length 339;
Best Local Similarity 23.1%; Pred. No. 6.2;
RESULT 1220
ID ADE36592 standard; protein; 339 AA.
DE Human NOV1a protein SEQ ID NO:2.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 93.5; DB 7; Length 339;
Best Local Similarity 23.1%; Pred. No. 6.2;
RESULT 1221
ID ABR58582 standard; protein; 359 AA.
DE Human cancer related protein SEQ ID NO:239.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1222
ID ABP70439 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1223
ID ABP70441 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 4.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1224
ID ABP70438 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1225
ID ABR48174 standard; protein; 359 AA.
DE Human bladder cancer associated protein sequence SEQ ID NO:64.
PN WO2003003906-A2.
PD 16-JAN-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1226
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ID AAO26680 standard; protein; 359 AA.
 DE KIM-1 related protein, SEQ ID NO 8.
 PN WO200298920-A1.
 PD 12-DEC-2002.
 PA (BIOJ) BIOGEN INC.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 5.6%; Score 93.5; DB 6; Length 359;
 Best Local Similarity 23.1%; Pred. No. 6.7;
 RESULT 1227
 ID ADE36594 standard; protein; 359 AA.
 DE Human NOV1B protein SEQ ID NO:4.
 PN WO2003080856-A2.
 PD 02-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.6%; Score 93.5; DB 7; Length 359;
 Best Local Similarity 23.1%; Pred. No. 6.7;
 RESULT 1228
 ID ADN38984 standard; protein; 359 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 5.6%; Score 93.5; DB 7; Length 359;
 Best Local Similarity 23.1%; Pred. No. 6.7;
 RESULT 1229
 ID ADQ76690 standard; protein; 359 AA.
 DE Human kidney injury molecule-1 (KIM-1).
 PN WO2004060041-A2.
 PD 22-JUL-2004.
 PA (BIOG-) BIOGEN IDEC MA INC.
 Query Match 5.6%; Score 93.5; DB 8; Length 359;
 Best Local Similarity 23.1%; Pred. No. 6.7;
 RESULT 1230
 ID ABG07923 standard; protein; 366 AA.
 DE Novel human diagnostic protein #7914.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.6%; Score 93.5; DB 4; Length 366;
 Best Local Similarity 23.2%; Pred. No. 6.9;
 RESULT 1231
 ID ADP04445 standard; protein; 1381 AA.
 DE Sea squirt protein with tissue specific expression in development Seq40.
 PN JP2004057129-A.
 PD 26-FEB-2004.
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
 Query Match 5.6%; Score 93.5; DB 8; Length 1381;
 Best Local Similarity 22.9%; Pred. No. 42;
 RESULT 1232
 ID ABR63235 standard; protein; 2055 AA.
 DE Glucanase sequence from strain KG15.
 PN WO2003008618-A2.
 PD 30-JAN-2003.
 PA (NEDE-) NEDERLANDSE ORG TOEGEPAST.
 Query Match 5.6%; Score 93.5; DB 6; Length 2055;
 Best Local Similarity 23.3%; Pred. No. 73;
 RESULT 1233
 ID AAR88466 standard; protein; 629 AA.
 DE Drosophila scavenger receptor class CI.
 PN WO9600288-A2.
 PD 04-JAN-1996.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 5.6%; Score 93; DB 2; Length 629;
 Best Local Similarity 19.9%; Pred. No. 16;
 RESULT 1234
 ID ABG33057 standard; protein; 629 AA.
 DE Fruit fly scavenger receptor type CI (dsr-CI).
 PN US6429289-B1.
 PD 06-AUG-2002.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 5.6%; Score 93; DB 5; Length 629;
 Best Local Similarity 19.9%; Pred. No. 16;
 RESULT 1235

ID AAE21524 standard; protein; 629 AA.
 DE Drosophila melanogaster scavenger receptor class CI (dsr-CI).
 PN US6350859-B1.
 PD 26-FEB-2002.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 5.6%; Score 93; DB 5; Length 629;
 Best Local Similarity 19.9%; Pred. No. 16;
 RESULT 1236
 ID ABP73157 standard; protein; 40 AA.
 DE Deletion mutant of a CD44-hyaluronic acid binding domain.
 PN WO2003018044-A1.
 PD 06-MAR-2003.
 PA (STRO/) STROEMBLAD S.
 PA (KOGE/) KOGERMAN P.
 PA (PAEL/) PAELL T.
 Query Match 5.6%; Score 92.5; DB 6; Length 40;
 Best Local Similarity 54.1%; Pred. No. 0.41;
 RESULT 1237
 ID AAW61380 standard; protein; 300 AA.
 DE Mouse junctional adhesion molecule protein.
 PN WO9824897-A1.
 PD 11-JUN-1998.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Query Match 5.6%; Score 92.5; DB 2; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1238
 ID AAY23325 standard; protein; 300 AA.
 DE A33 related antigen JAM.
 PN WO9927098-A2.
 PD 03-JUN-1999.
 PA (GETH) GENENTECH INC.
 Query Match 5.6%; Score 92.5; DB 2; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1239
 ID ADH62537 standard; protein; 300 AA.
 DE Murine JAM protein used in the exemplification of the invention.
 PN US2003171568-A1.
 PD 11-SEP-2003.
 PA (ASHK/) ASHKENAZI A.
 PA (FONG/) FONG S.
 PA (GODD/) GODDARD A.
 PA (GURN/) GURNEY A L.
 PA (NAPI/) NAPIER M A.
 PA (TUMA/) TUMAS D.
 PA (WOOD/) WOOD W I.
 Query Match 5.6%; Score 92.5; DB 7; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1240
 ID ADK40853 standard; protein; 300 AA.
 DE Mouse junction adhesion molecule (JAM).
 PN US6699688-B1.
 PD 02-MAR-2004.
 PA (UYNY) UNIV NEW YORK STATE RES FOUND.
 Query Match 5.6%; Score 92.5; DB 8; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1241
 ID ADN35293 standard; protein; 300 AA.
 DE Human JAM protein.
 PN WO2004031105-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.6%; Score 92.5; DB 8; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1242
 ID ABP70440 standard; protein; 365 AA.
 DE Amino acid sequence of human TIM-1 allele 3.
 PN WO2003002722-A2.
 PD 09-JAN-2003.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 Query Match 5.6%; Score 92.5; DB 6; Length 365;
 Best Local Similarity 22.6%; Pred. No. 8.5;
 RESULT 1243
 ID ABB50001 standard; protein; 569 AA.

DE Listeria monocytogenes protein #2705.
PN WO200177335-A2.
PA (INSP) INST PASTEUR.
Query Match 5.6%; Score 92.5; DB 5; Length 569;
Best Local Similarity 21.4%; Pred. No. 16;
RESULT 1244
ID ABU32518 standard; protein; 569 AA.
DE Protein encoded by Prokaryotic essential gene #18045.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 92.5; DB 6; Length 569;
Best Local Similarity 21.4%; Pred. No. 16;
RESULT 1245
ID AAU48553 standard; protein; 706 AA.
DE Propionibacterium acnes immunogenic protein #9449.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.6%; Score 92.5; DB 4; Length 706;
Best Local Similarity 25.4%; Pred. No. 21;
RESULT 1246
ID ABM45072 standard; protein; 706 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9748.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.6%; Score 92.5; DB 6; Length 706;
Best Local Similarity 25.4%; Pred. No. 21;
RESULT 1247
ID ADN18863 standard; protein; 994 AA.
DE Bacterial polypeptide #1516.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.6%; Score 92.5; DB 8; Length 994;
Best Local Similarity 19.7%; Pred. No. 34;
RESULT 1248
ID ABR53566 standard; protein; 1636 AA.
DE Protein sequence #SEQ ID 1997.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 5.6%; Score 92.5; DB 6; Length 1636;
Best Local Similarity 19.7%; Pred. No. 67;
RESULT 1249
ID ADK64364 standard; protein; 1636 AA.
DE Disease treating protein complex-derived protein #1193.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 5.6%; Score 92.5; DB 7; Length 1636;
Best Local Similarity 19.7%; Pred. No. 67;
RESULT 1250
ID ABP70442 standard; protein; 364 AA.
DE Amino acid sequence of human TIM-1 allele 5.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 92; DB 6; Length 364;
Best Local Similarity 21.8%; Pred. No. 9.4;
RESULT 1251
ID ABG93047 standard; protein; 966 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 52.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 5.6%; Score 92; DB 5; Length 966;

Best Local Similarity 20.3%; Pred. No. 36;
RESULT 1252
ID ADL72180 standard; protein; 2829 AA.
DE X. laevis mutated adenomatous polyposis coli (APC) protein.
PN WO2004018677-A1.
PD 04-MAR-2004.
PA (EISA) EISAI CO LTD.
Query Match 5.6%; Score 92; DB 8; Length 2829;
Best Local Similarity 20.7%; Pred. No. 1.6e+02;
RESULT 1253
ID AAU18036 standard; protein; 166 AA.
DE Human immunoglobulin polypeptide SEQ ID No 181.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.6;
RESULT 1254
ID ABB10469 standard; protein; 166 AA.
DE Human cDNA SEQ ID NO: 777.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.6;
RESULT 1255
ID ABP67056 standard; protein; 166 AA.
DE Human polypeptide SEQ ID NO 777.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.5%; Score 91.5; DB 5; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.6;
RESULT 1256
ID ADB31660 standard; protein; 166 AA.
DE Human novel protein SEQ ID NO 181.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 91.5; DB 7; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.6;
RESULT 1257
ID ADR46581 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 5.5%; Score 91.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 8.1;
RESULT 1258
ID AAM52302 standard; protein; 350 AA.
DE ActA protein fragment #2.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.5%; Score 91.5; DB 4; Length 350;
Best Local Similarity 22.0%; Pred. No. 10;
RESULT 1259
ID AAM52301 standard; protein; 376 AA.
DE ActA protein fragment #1.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.5%; Score 91.5; DB 4; Length 376;
Best Local Similarity 22.0%; Pred. No. 11;
RESULT 1260
ID AAM52300 standard; protein; 610 AA.
DE ActA protein.
PN WO200171356-A2.

PD 27-SEP-2001.
 PA (CNRS) CENT NAT RECH SCI.
 PA (CURI-) INST CURIE.
 Query Match 5.5%; Score 91.5; DB 4; Length 610;
 Best Local Similarity 22.0%; Pred. No. 21;
 RESULT 1261
 ID AAG79171 standard; protein; 639 AA.
 DE Amino acid sequence of an ActA fragment.
 PN WO200174858-A2.
 PD 11-OCT-2001.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 Query Match 5.5%; Score 91.5; DB 4; Length 639;
 Best Local Similarity 22.0%; Pred. No. 23;
 RESULT 1262
 ID AAU09142 standard; protein; 639 AA.
 DE Lysteria monocytogenes ActA.
 PN WO200174853-A2.
 PD 11-OCT-2001.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 Query Match 5.5%; Score 91.5; DB 4; Length 639;
 Best Local Similarity 22.0%; Pred. No. 23;
 RESULT 1263
 ID ABB47677 standard; protein; 639 AA.
 DE Listeria monocytogenes protein #381.
 PN WO200177335-A2.
 PD 18-OCT-2001.
 PA (INSP) INST PASTEUR.
 Query Match 5.5%; Score 91.5; DB 5; Length 639;
 Best Local Similarity 22.0%; Pred. No. 23;
 RESULT 1264
 ID ADM48341 standard; protein; 681 AA.
 DE Marburg virus glycoprotein, GP.
 PN US2003215794-A1.
 PD 20-NOV-2003.
 PA (KAWA/) KAWAOKA Y.
 PA (JASE/) JASENOSKY L D.
 PA (NEUM/) NEUMANN G.
 Query Match 5.5%; Score 91.5; DB 8; Length 681;
 Best Local Similarity 19.2%; Pred. No. 25;
 RESULT 1265
 ID ADN20575 standard; protein; 1103 AA.
 DE Bacterial polypeptide #3228.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 5.5%; Score 91.5; DB 8; Length 1103;
 Best Local Similarity 24.3%; Pred. No. 48;
 RESULT 1266
 ID ABP60839 standard; protein; 246 AA.
 DE Caenorhabditis elegans thioredoxin-like protein SEQ ID NO:188.
 PN WO200250289-A1.
 PD 27-JUN-2002.
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 5.5%; Score 91; DB 5; Length 246;
 Best Local Similarity 27.0%; Pred. No. 6.9;
 RESULT 1267
 ID ADG73740 standard; protein; 505 AA.
 DE Aspergillus niger Brea-109.
 PN US2003215950-A1.
 PD 20-NOV-2003.
 PA (IASU/) LASURE L L.
 PA (DAIZ/) DAI Z.
 Query Match 5.5%; Score 90.5; DB 8; Length 505;
 Best Local Similarity 27.0%; Pred. No. 21;
 RESULT 1268
 ID ABB60186 standard; protein; 1714 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 7350.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 5.5%; Score 90.5; DB 4; Length 1714;
 Best Local Similarity 26.7%; Pred. No. 1.1e+02;
 RESULT 1269
 ID ABB69419 standard; protein; 1976 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 35049.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 5.5%; Score 90.5; DB 4; Length 1976;
 Best Local Similarity 38.5%; Pred. No. 1.3e+02;
 RESULT 1270
 ID ABP70443 standard; protein; 364 AA.
 DE Amino acid sequence of human TIM-1 allele 6.
 PN WO2003002722-A2.
 PD 09-JAN-2003.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 Query Match 5.4%; Score 90; DB 6; Length 364;
 Best Local Similarity 21.6%; Pred. No. 15;
 RESULT 1271
 ID ABB59507 standard; protein; 629 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 5313.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 5.4%; Score 90; DB 4; Length 629;
 Best Local Similarity 20.7%; Pred. No. 31;
 RESULT 1272
 ID ADD47260 standard; protein; 957 AA.
 DE Human Protein AAC02272, SEQ ID NO 12954.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 5.4%; Score 90; DB 7; Length 957;
 Best Local Similarity 18.3%; Pred. No. 55;
 RESULT 1273
 ID ADE58049 standard; protein; 957 AA.
 DE Human Protein AAC02272, SEQ ID NO 3917.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 5.4%; Score 90; DB 7; Length 957;
 Best Local Similarity 18.3%; Pred. No. 55;
 RESULT 1274
 ID ADD47264 standard; protein; 957 AA.
 DE Human Protein AAC02272, SEQ ID NO 12958.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 5.4%; Score 90; DB 7; Length 957;
 Best Local Similarity 18.3%; Pred. No. 55;
 RESULT 1275
 ID ADE58045 standard; protein; 957 AA.
 DE Human Protein AAC02272, SEQ ID NO 3913.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 5.4%; Score 90; DB 7; Length 957;
 Best Local Similarity 18.3%; Pred. No. 55;
 RESULT 1276
 ID ADQ29696 standard; protein; 1217 AA.
 DE Human colorectal cancer-associated protein #51.
 PN EP1439993-A2.
 PD 21-JUL-2004.
 PA (FARB) BAYER HEALTHCARE LLC.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

Query Match 5.4%; Score 90; DB 8; Length 1217;
Best Local Similarity 18.3%; Pred. No. 76;
RESULT 1277
ID ABG66756 standard; protein; 1296 AA.
DE Human novel polypeptide #91.
PN WO20024340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 90; DB 5; Length 1296;
Best Local Similarity 18.3%; Pred. No. 83;
RESULT 1278
ID ABG66702 standard; protein; 1296 AA.
DE Human novel polypeptide #37.
PN WO20024340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 90; DB 5; Length 1296;
Best Local Similarity 18.3%; Pred. No. 83;
RESULT 1279
ID ABP70432 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-2 BALB/c allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.4%; Score 89.5; DB 6; Length 305;
Best Local Similarity 24.3%; Pred. No. 13;
RESULT 1280
ID ABP70433 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-2 ES-HBA and DBA/2J allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.4%; Score 89.5; DB 6; Length 305;
Best Local Similarity 24.3%; Pred. No. 13;
RESULT 1281
ID AAR69555 standard; protein; 410 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-2.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 5.4%; Score 89.5; DB 2; Length 410;
Best Local Similarity 21.0%; Pred. No. 19;
RESULT 1282
ID AAR85213 standard; protein; 480 AA.
DE Blowfly larvae PM95 antigen.
PN AU9517609-A.
PD 02-NOV-1995.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 5.4%; Score 89.5; DB 2; Length 480;
Best Local Similarity 22.1%; Pred. No. 24;
RESULT 1283
ID ABO48994 standard; protein; 917 AA.
DE Murine cancer-associated protein (CAP) MP07-101.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.4%; Score 89.5; DB 8; Length 917;
Best Local Similarity 21.4%; Pred. No. 58;
RESULT 1284
ID ABB65879 standard; protein; 307 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24429.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 89; DB 4; Length 307;
Best Local Similarity 31.6%; Pred. No. 14;
RESULT 1285
ID ABP69313 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 1360.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.

Query Match 5.4%; Score 89; DB 5; Length 343;
Best Local Similarity 27.7%; Pred. No. 17;
RESULT 1286
ID AAR69554 standard; protein; 416 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-1.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 5.4%; Score 89; DB 2; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1287
ID AAY52550 standard; protein; 416 AA.
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).
PN WO9958658-A2.
PD 18-NOV-1999.
PA (EPIM-) EPIMUNE INC.
Query Match 5.4%; Score 89; DB 3; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1288
ID ADP65283 standard; protein; 416 AA.
DE Human lysosomal-associated membrane protein 1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 5.4%; Score 89; DB 7; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1289
ID ADN03755 standard; protein; 416 AA.
DE Antipsoriatic protein sequence #74.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1290
ID ADP49321 standard; protein; 416 AA.
DE Human lysosomal associated membrane protein LAMP #1.
PN WO2004048537-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1291
ID ADP3231 standard; protein; 416 AA.
DE PRO polypeptide SEQ ID NO:325.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1292
ID ADR86408 standard; protein; 832 AA.
DE Aspergillus fumigatus essential gene protein #458.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 5.4%; Score 89; DB 8; Length 832;
Best Local Similarity 19.8%; Pred. No. 56;
RESULT 1293
ID ABB70039 standard; protein; 846 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16909.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 89; DB 4; Length 846;
Best Local Similarity 22.5%; Pred. No. 58;
RESULT 1294
ID ABB67102 standard; protein; 882 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28098.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 89; DB 4; Length 882;
Best Local Similarity 22.5%; Pred. No. 61;
RESULT 1295
ID ADQ37103 standard; protein; 951 AA.
DE Cell proliferation-related polypeptide #118.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.4%; Score 89; DB 8; Length 951;
Best Local Similarity 22.1%; Pred. No. 68;
RESULT 1296
ID ADI19804 standard; protein; 1076 AA.
DE Protein encoded by novel human channel/transporter gene #122.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 89; DB 4; Length 1076;
Best Local Similarity 21.1%; Pred. No. 80;
RESULT 1297
ID AAG39194 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48458.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 88.5; DB 3; Length 193;
Best Local Similarity 21.4%; Pred. No. 8.5;
RESULT 1298
ID AAG39193 standard; protein; 199 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48457.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 88.5; DB 3; Length 199;
Best Local Similarity 21.4%; Pred. No. 8.8;
RESULT 1299
ID AAG15314 standard; protein; 358 AA.
DE Novel human diagnostic protein #15305.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.3%; Score 88.5; DB 4; Length 358;
Best Local Similarity 20.2%; Pred. No. 20;
RESULT 1300
ID AAR11605 standard; protein; 392 AA.
DE Human 75KD TNF-binding protein.
PN EP417563-A.
PD 20-MAR-1991.
PA (HOFF) HOFFMANN-LA ROCHE AG.
Query Match 5.3%; Score 88.5; DB 2; Length 392;
Best Local Similarity 21.8%; Pred. No. 22;
RESULT 1301
ID AAY10935 standard; protein; 392 AA.
DE Human tumour necrosis factor binding protein fragment.
PN EP939121-A2.
PD 01-SEP-1999.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.3%; Score 88.5; DB 2; Length 392;
Best Local Similarity 21.8%; Pred. No. 22;
RESULT 1302
ID AAB86818 standard; protein; 392 AA.
DE Human TNFBP-associated protein #2.
PN EP1132471-A2.
PD 12-SEP-2001.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.3%; Score 88.5; DB 4; Length 392;
Best Local Similarity 21.8%; Pred. No. 22;
RESULT 1303
ID ABO68455 standard; protein; 451 AA.
DE Pseudomonas aeruginosa polypeptide #630.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.3%; Score 88.5; DB 7; Length 451;
Best Local Similarity 20.7%; Pred. No. 27;

RESULT 1304
ID ABB63417 standard; protein; 481 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17043.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.3%; Score 88.5; DB 4; Length 481;
Best Local Similarity 21.2%; Pred. No. 30;
RESULT 1305
ID AAG64210 standard; protein; 596 AA.
DE Murine HSP47 interacting protein, M4.
PN JP2001145493-A.
PD 29-MAY-2001.
PA (KACA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 5.3%; Score 88.5; DB 4; Length 596;
Best Local Similarity 21.3%; Pred. No. 40;
RESULT 1306
ID AAY37234 standard; protein; 708 AA.
DE Chlamydia trachomatis cellular envelope protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 5.3%; Score 88.5; DB 2; Length 708;
Best Local Similarity 23.6%; Pred. No. 50;
RESULT 1307
ID AAR63068 standard; protein; 905 AA.
DE Human EAA3b excitatory amino acid receptor.
PN CA2110933-A.
PD 12-JUN-1994.
PA (KAMB/) KAMBOJ R.
Query Match 5.3%; Score 88; DB 2; Length 905;
Best Local Similarity 22.4%; Pred. No. 79;
RESULT 1308
ID ADE86597 standard; protein; 995 AA.
DE Frog tail resorption protein.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Query Match 5.3%; Score 88; DB 8; Length 995;
Best Local Similarity 19.9%; Pred. No. 90;
RESULT 1309
ID ADN23131 standard; protein; 3507 AA.
DE Bacterial polypeptide #5784.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.3%; Score 88; DB 8; Length 3507;
Best Local Similarity 20.1%; Pred. No. 5.1e+02;
RESULT 1310
ID ABP43908 standard; protein; 4315 AA.
DE MUC5B partial gene protein.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.3%; Score 88; DB 5; Length 4315;
Best Local Similarity 23.8%; Pred. No. 6.7e+02;
RESULT 1311
ID ADL23265 standard; protein; 5703 AA.
DE Human WOC5B.
PN WO2004019041-A1.
PD 04-MAR-2004.
PA (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.

PA (PACK/) PACKER N H.
 PA (KARL/) KARLSSON N.
 PA (SCHU/) SCHULZ B L.
 Query Match
 Best Local Similarity 5.3%; Score 88; DB 8; Length 5703;
 RESULT 1312
 ID AAG13468 standard; protein; 310 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 12974.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 3; Length 310;
 RESULT 1313
 ID AAG13467 standard; protein; 331 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 12973.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 3; Length 331;
 RESULT 1314
 ID AAY52525 standard; protein; 536 AA.
 DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
 PN WO9954349-A2.
 PD 28-OCT-1999.
 PA (HESK-) HESKA CORP.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 3; Length 536;
 RESULT 1315
 ID AAU96329 standard; protein; 536 AA.
 DE Der HMW-map polypeptide #16.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 5; Length 536;
 RESULT 1316
 ID AAY52523 standard; protein; 555 AA.
 DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
 PN WO9954349-A2.
 PD 28-OCT-1999.
 PA (HESK-) HESKA CORP.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 3; Length 555;
 RESULT 1317
 ID AAU96327 standard; protein; 555 AA.
 DE Der HMW-map polypeptide #14.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 5; Length 555;
 RESULT 1318
 ID AAU96328 standard; protein; 555 AA.
 DE Der HMW-map polypeptide #15.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 5; Length 555;
 RESULT 1319
 ID ADB64946 standard; protein; 717 AA.
 DE Human protein encoded by clone PROST20036350.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 7; Length 717;
 RESULT 1320
 ID ADH71768 standard; protein; 904 AA.
 DE Human protein of the invention NOV28n SEQ ID NO:664.
 PN WO2003102155-A2.
 PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 8; Length 904;
 RESULT 1321
 ID AAW16313 standard; protein; 906 AA.
 DE Yeast alpha factor-G-alpha protein fusion.
 PN WO9711159-A1.
 PD 27-MAR-1997.
 PA (HEAR-) HEARTLAND BIOTECHNOLOGIES LLC.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 2; Length 906;
 RESULT 1322
 ID AAW54844 standard; protein; 1085 AA.
 DE Bovine parathyroid calcium receptor 1 protein 5kb fragment.
 PN US5763569-A.
 PD 09-JUN-1998.
 PA (NPSP-) NPS PHARM INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 2; Length 1085;
 RESULT 1323
 ID AAY41778 standard; protein; 1085 AA.
 DE Bovine parathyroid calcium receptor 1 protein sequence.
 PN US5962314-A.
 PD 05-OCT-1999.
 PA (NPSP-) NPS PHARM INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 2; Length 1085;
 RESULT 1324
 ID AAW89563 standard; protein; 1085 AA.
 DE Bovine parathyroid calcium receptor BopCar 1.
 PN US5858684-A.
 PD 12-JAN-1999.
 PA (NPSP-) NPS PHARM INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 2; Length 1085;
 RESULT 1325
 ID AAY51825 standard; protein; 1085 AA.
 DE Bovine calcium receptor BopCar1 protein.
 PN US6031003-A.
 PD 29-FEB-2000.
 PA (NPSP-) NPS PHARM INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 3; Length 1085;
 RESULT 1326
 ID AAB47820 standard; protein; 1085 AA.
 DE BopCar1.
 PN US6313146-B1.
 PD 06-NOV-2001.
 PA (NPSP-) NPS PHARM INC.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 5; Length 1085;
 RESULT 1327
 ID ADJ93194 standard; protein; 1085 AA.
 DE Bovine extracellular Ca-sensing receptor.
 PN WO200296946-A1.
 PD 05-DEC-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 7; Length 1085;
 RESULT 1328
 ID ADI40961 standard; protein; 1085 AA.
 DE Bovine GPCR CASR.
 PN US2004018976-A1.
 PD 29-JAN-2004.
 PA (FEDE/) FEDER J N.
 PA (MINT/) MINTIER G.
 PA (RAMA/) RAMANATHAN C S.
 Query Match
 Best Local Similarity 5.3%; Score 87.5; DB 8; Length 1085;
 RESULT 1329

RESULT 1329
ID ADI41015 standard; protein; 1085 AA.
DE Bovine GPCR CASR #2.
PN US2004018976-A1.
PA (MILH/) MILHAUSEN M J.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 5.3%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.1e+02;
RESULT 1330
ID ADS24007 standard; protein; 1322 AA.
DE Bacterial polypeptide #13040.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.3%; Score 87.5; DB 8; Length 1322;
Best Local Similarity 22.9%; Pred. No. 1.5e+02;
RESULT 1331
ID ADD44997 standard; protein; 235 AA.
DE Rat Protein CAA82313, SEQ ID NO 10428.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.3%; Score 87; DB 7; Length 235;
Best Local Similarity 27.8%; Pred. No. 15;
RESULT 1332
ID AAY29082 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1333
ID AAY29081 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1334
ID AAU25553 standard; protein; 288 AA.
DE T. gondii immunogenic protein Ptg1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 5.3%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1335
ID AAU25552 standard; protein; 288 AA.
DE T. gondii immunogenic protein Ptg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 5.3%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1336
ID ADG17391 standard; protein; 288 AA.
DE T. gondii protein #79.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 5.3%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1337
ID ADG17394 standard; protein; 288 AA.

DE T. gondii protein #82.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 5.3%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1338
ID ADJ76313 standard; protein; 363 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1565.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 5.3%; Score 87; DB 8; Length 363;
Best Local Similarity 25.3%; Pred. No. 28;
RESULT 1339
ID AAR01940 standard; protein; 417 AA.
DE Tumour necrosis factor.
PN JP01285191-A.
PD 16-NOV-1989.
PA (GREC) GREEN CROSS CORP.
Query Match 5.3%; Score 87; DB 2; Length 417;
Best Local Similarity 23.6%; Pred. No. 34;
RESULT 1340
ID AAG83274 standard; protein; 631 AA.
DE Chlamydia trachomatis PmpH(N-term) fusion protein.
PN WO200140474-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 4; Length 631;
Best Local Similarity 28.1%; Pred. No. 60;
RESULT 1341
ID ABB94245 standard; protein; 631 AA.
DE Chlamydia trachomatis protein sequence SEQ ID NO:325.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 5; Length 631;
Best Local Similarity 28.1%; Pred. No. 60;
RESULT 1342
ID ADA2755 standard; protein; 664 AA.
DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.
PN WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 7; Length 664;
Best Local Similarity 28.1%; Pred. No. 64;
RESULT 1343
ID AAR63070 standard; protein; 849 AA.
DE Human EAA3d excitatory amino acid receptor.
PN CA2110933-A.
PD 12-JUN-1994.
PA (KAME/) KAMBOJ R.
Query Match 5.3%; Score 87; DB 2; Length 849;
Best Local Similarity 22.4%; Pred. No. 90;
RESULT 1344
ID AAR60563 standard; protein; 862 AA.
DE Yeast 2.6 kb agglutination gene FLO1S.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 5.3%; Score 87; DB 2; Length 862;
Best Local Similarity 19.1%; Pred. No. 92;
RESULT 1345
ID AAR58754 standard; protein; 894 AA.
DE S. cerevisiae FLO1.
PN WO9418330-A1.
PD 18-AUG-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 5.3%; Score 87; DB 2; Length 894;
Best Local Similarity 19.1%; Pred. No. 96;
RESULT 1346

ID AAR47578 standard; protein; 894 AA.
DE Flocculation protein of *Saccharomyces cerevisiae*.
PN W09401567-A1.
PD 20-JAN-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 5.3%; Score 87; DB 2; Length 894;
Best Local Similarity 19.1%; Pred. No. 96;
RESULT 1347
ID AAR60112 standard; protein; 905 AA.
DE Human EAA3a excitatory amino acid receptor.
PN CA2110933-A.
PD 12-JUN-1994.
PA (KAMB/) KAMBOJ R.
Query Match 5.3%; Score 87; DB 2; Length 905;
Best Local Similarity 22.4%; Pred. No. 98;
RESULT 1348
ID AAR75883 standard; protein; 905 AA.
DE Human EAA3 receptor (Q-591).
PN W09517508-A2.
PD 29-JUN-1995.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 5.3%; Score 87; DB 2; Length 905;
Best Local Similarity 22.4%; Pred. No. 98;
RESULT 1349
ID AAB19496 standard; protein; 905 AA.
DE The Q591 form of the human EAA3 receptor.
PN US6136544-A.
PD 24-OCT-2000.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 5.3%; Score 87; DB 4; Length 905;
Best Local Similarity 22.4%; Pred. No. 98;
RESULT 1350
ID AAU38901 standard; protein; 1016 AA.
DE C. trachomatis CT872 protein.
PN W0200181379-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 4; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.1e+02;
RESULT 1351
ID ABG91037 standard; protein; 1016 AA.
DE Chlamydia trachomatis outer membrane protein H protein.
PN W0200262380-A2.
PD 15-AUG-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 5.3%; Score 87; DB 5; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.1e+02;
RESULT 1352
ID .ADD42682 standard; protein; 1016 AA.
DE Chlamydia trachomatis antigen protein SEQ ID NO:95.
PN W02003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 7; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.1e+02;
RESULT 1353
ID ADD43800 standard; protein; 1016 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 95.
PN W02003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 5.3%; Score 87; DB 7; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.1e+02;
RESULT 1354
ID AAR60562 standard; protein; 1537 AA.
DE Yeast 4.7 kD agglutination gene FLO1L.
PN W09419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 5.3%; Score 87; DB 2; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2e+02;

RESULT 1355
ID ADP87475 standard; protein; 1537 AA.
DE *S. cerevisiae* glucan synthase pathway protein YAR050W (FLO1) SeqID17.
PN W02004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match 5.3%; Score 87; DB 8; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2e+02;
RESULT 1356
ID ADN18745 standard; protein; 1537 AA.
DE Bacterial polypeptide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.3%; Score 87; DB 8; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2e+02;
RESULT 1357
ID ABB67362 standard; protein; 1575 AA.
DE *Drosophila melanogaster* polypeptide SEQ ID NO 28878.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.3%; Score 87; DB 4; Length 1575;
Best Local Similarity 20.5%; Pred. No. 2.1e+02;
RESULT 1358
ID AAU39177 standard; protein; 238 AA.
DE *Propionibacterium acnes* immunogenic protein #73.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.2%; Score 86.5; DB 4; Length 238;
Best Local Similarity 22.7%; Pred. No. 17;
RESULT 1359
ID ABM35696 standard; protein; 238 AA.
DE *Propionibacterium acnes* predicted ORF-encoded polypeptide #372.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.2%; Score 86.5; DB 6; Length 238;
Best Local Similarity 22.7%; Pred. No. 17;
RESULT 1360
ID AAP19141 standard; peptide; 400 AA.
DE Sequence of preprospasmolysin.
PN DE3808456-A.
PD 28-SEP-1989.
PA (PLAC) MAX PLANCK GBS FOERDERUNG WISSENSCHAFTEN.
Query Match 5.2%; Score 86.5; DB 1; Length 400;
Best Local Similarity 30.8%; Pred. No. 36;
RESULT 1361
ID ADN19290 standard; protein; 503 AA.
DE Bacterial polypeptide #1943.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.2%; Score 86.5; DB 8; Length 503;
Best Local Similarity 22.1%; Pred. No. 49;
RESULT 1362
ID ABU25742 standard; protein; 687 AA.
DE Protein encoded by *Prokaryotic essential gene #11269*.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 86.5; DB 6; Length 687;
Best Local Similarity 23.2%; Pred. No. 75;
RESULT 1363

ID ABG15647 standard; protein; 714 AA.
DE Novel human diagnostic protein #15638.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 86.5; DB 4; Length 714;
Best Local Similarity 18.2%; Pred. No. 79;
RESULT 1364
ID ABG15147 standard; protein; 714 AA.
DE Novel human diagnostic protein #15138.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 86.5; DB 4; Length 714;
Best Local Similarity 18.2%; Pred. No. 79;
RESULT 1365
ID AAY54466 standard; protein; 788 AA.
DE Amino acid sequence of intestinal insect mucin isoform IIM14.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 5.2%; Score 86.5; DB 3; Length 788;
Best Local Similarity 27.2%; Pred. No. 90;
RESULT 1366
ID AAY54467 standard; protein; 807 AA.
DE Amini acid sequence of intestinal insect mucin isoform IIM22.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 5.2%; Score 86.5; DB 3; Length 807;
Best Local Similarity 27.2%; Pred. No. 93;
RESULT 1367
ID ADA14416 standard; protein; 1579 AA.
DE Mouse spermatogenesis related protein sequence SEQ ID NO:158.
PN WO2003068969-A1.
PD 21-AUG-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.2%; Score 86.5; DB 6; Length 1579;
Best Local Similarity 21.1%; Pred. No. 2.3e+02;
RESULT 1368
ID AAY57453 standard; protein; 2781 AA.
DE Human transcriptional regulatory factor SEQ ID NO:10.
PN WO9957143-A1.
PD 11-NOV-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.2%; Score 86.5; DB 3; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.1e+02;
RESULT 1369
ID ADF42724 standard; protein; 2781 AA.
DE Human BPTF amino acid sequence SEQ ID NO:30.
PN WO2003102163-A2.
PD 11-DEC-2003.
PA (META-) METABOLEX INC.
Query Match 5.2%; Score 86.5; DB 8; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.1e+02;
RESULT 1370
ID ADO0984 standard; protein; 2781 AA.
DE Human homologue of Fruit fly AD-related protein CG17135.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 5.2%; Score 86.5; DB 8; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.1e+02;
RESULT 1371
ID ADQ18653 standard; protein; 2781 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1472.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.2%; Score 86.5; DB 8; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.1e+02;
RESULT 1372
ID AAY57452 standard; protein; 2907 AA.
DE Novel human diagnostic protein #5666.
PN WO9957143-A1.
PD 11-NOV-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.2%; Score 86.5; DB 3; Length 2907;
Best Local Similarity 20.8%; Pred. No. 5.4e+02;
RESULT 1373
ID ABM82857 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3106.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.2%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 50;
RESULT 1374
ID ABM83144 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3393.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.2%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 50;
RESULT 1375
ID AAB98978 standard; protein; 551 AA.
DE Rabbit PCIP1.
PN WO200134797-A1.
PD 17-MAY-2001.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.2%; Score 86; DB 4; Length 551;
Best Local Similarity 26.4%; Pred. No. 62;
RESULT 1376
ID ADD18594 standard; protein; 601 AA.
DE Human disease related protein Seqid25.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 5.2%; Score 86; DB 7; Length 601;
Best Local Similarity 22.0%; Pred. No. 69;
RESULT 1377
ID AAY05477 standard; protein; 750 AA.
DE C. albicans Rbt1 protein sequence.
PN WO9918115-A1.
PD 15-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.2%; Score 86; DB 2; Length 750;
Best Local Similarity 23.4%; Pred. No. 94;
RESULT 1378
ID AAB19499 standard; protein; 905 AA.
DE Amino acid sequence of the R591 form of the human EAA3 receptor.
PN US6136544-A.
PD 24-OCT-2000.
PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 5.2%; Score 86; DB 4; Length 905;
Best Local Similarity 22.4%; Pred. No. 1.2e+02;
RESULT 1379
ID ADB79822 standard; protein; 1080 AA.
DE Mouse putative deubiquitinating enzyme 8, SEQ ID 62.
PN EP1279744-A2.
PD 29-JAN-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 5.2%; Score 86; DB 7; Length 1080;
Best Local Similarity 20.2%; Pred. No. 1.6e+02;
RESULT 1380
ID ABG28388 standard; protein; 1086 AA.
DE Novel human diagnostic protein #28379.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 86; DB 4; Length 1086;
Best Local Similarity 19.8%; Pred. No. 1.6e+02;
RESULT 1381
ID ABG05675 standard; protein; 1190 AA.
DE Novel human diagnostic protein #5666.

PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEC INC.
Query Match 5.2%; Score 86; DB 4; Length 1190;
Best Local Similarity 19.8%; Pred. No. 1.8e+02;
RESULT 1382
ID AAG23116 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26303.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.2%; Score 85.5; DB 3; Length 193;
Best Local Similarity 20.9%; Pred. No. 16;
RESULT 1383
ID AAG23115 standard; protein; 199 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26302.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.2%; Score 85.5; DB 3; Length 199;
Best Local Similarity 20.9%; Pred. No. 17;
RESULT 1384
ID AAB09826 standard; protein; 346 AA.
DE Endoglucanase protein sequence 6.
PN WO200024879-A1.
PD 04-MAY-2000.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 3; Length 346;
Best Local Similarity 22.4%; Pred. No. 36;
RESULT 1385
ID AAO15057 standard; protein; 346 AA.
DE Phycomyces nitens endoglucanase-related protein.
PN WO200242474-A1.
PD 30-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 36;
RESULT 1386
ID ABB08065 standard; protein; 346 AA.
DE P. nitens CP99002 PCEI protein.
PN WO200238754-A1.
PD 16-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 36;
RESULT 1387
ID ADA37114 standard; protein; 346 AA.
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO:6.
PN WO2003052105-A1.
PD 26-JUN-2003.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 6; Length 346;
Best Local Similarity 22.4%; Pred. No. 36;
RESULT 1388
ID AAR57350 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO9415627-A1.
PD 21-JUL-1994.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 2; Length 354;
Best Local Similarity 26.2%; Pred. No. 37;
RESULT 1389
ID ABB93134 standard; protein; 649 AA.
DE Herbicidially active polypeptide SEQ ID NO 2345.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 85.5; DB 5; Length 649;
Best Local Similarity 23.4%; Pred. No. 86;
RESULT 1390
ID ABB78250 standard; protein; 652 AA.
DE Amino acid sequence of a human heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 652;
Best Local Similarity 22.4%; Pred. No. 87;
RESULT 1391
ID ABB15839 standard; protein; 686 AA.
DE Protein encoded by Prokaryotic essential gene #1366.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 85.5; DB 6; Length 686;
Best Local Similarity 24.2%; Pred. No. 93;
RESULT 1392
ID ADN47243 standard; protein; 695 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1121.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.2%; Score 85.5; DB 8; Length 695;
Best Local Similarity 20.6%; Pred. No. 94;
RESULT 1393
ID ADD47689 standard; protein; 780 AA.
DE Human Protein XP_027074, SEQ ID NO 13385.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 85.5; DB 7; Length 780;
Best Local Similarity 23.2%; Pred. No. 1.1e+02;
RESULT 1394
ID ADD47692 standard; protein; 780 AA.
DE Human Protein XP_027074, SEQ ID NO 13388.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 85.5; DB 7; Length 780;
Best Local Similarity 23.2%; Pred. No. 1.1e+02;
RESULT 1395
ID AAB07743 standard; protein; 781 AA.
DE A snake venom protease (SVPH-4) polypeptide variant SVPH-4b.
PN WO200043525-A2.
PD 27-JUL-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 5.2%; Score 85.5; DB 3; Length 781;
Best Local Similarity 17.9%; Pred. No. 1.1e+02;
RESULT 1396
ID ADE71292 standard; protein; 781 AA.
DE Novel human protein #46.
PN JP2002345493-A.
PD 03-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 5.2%; Score 85.5; DB 7; Length 781;
Best Local Similarity 23.2%; Pred. No. 1.1e+02;
RESULT 1397
ID ABB78248 standard; protein; 841 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 841;
Best Local Similarity 22.4%; Pred. No. 1.2e+02;
RESULT 1398
ID ABB71012 standard; protein; 843 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39828.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.2%; Score 85.5; DB 4; Length 843;
Best Local Similarity 22.5%; Pred. No. 1.2e+02;
RESULT 1399
ID ABB78249 standard; protein; 977 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.

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PA (GEHO ) GEN HOSPITAL CORP.
  Query Match      5.2%; Score 85.5; DB 5; Length 977;
  Best Local Similarity 22.4%; Pred. No. 1.5e+02;
RESULT 1400
ID ABUS4710 standard; protein; 1784 AA.
DE Human CA125 protein amino terminal sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
  Query Match      5.2%; Score 85.5; DB 6; Length 1784;
  Best Local Similarity 27.2%; Pred. No. 3.4e+02;
RESULT 1401
ID ABUS4858 standard; protein; 1794 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
  Query Match      5.2%; Score 85.5; DB 6; Length 1794;
  Best Local Similarity 27.2%; Pred. No. 3.5e+02;
RESULT 1402
ID ABUS4707 standard; protein; 1821 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
  Query Match      5.2%; Score 85.5; DB 6; Length 1821;
  Best Local Similarity 27.2%; Pred. No. 3.5e+02;
RESULT 1403
ID ADE40509 standard; protein; 2055 AA.
DE Human nuclear receptor coactivator ARAP3.
PN DE10135787-A1.
PD 13-FEB-2003.
PA (JENP ) JENAPHARM GMBH & CO KG.
  Query Match      5.2%; Score 85.5; DB 8; Length 2055;
  Best Local Similarity 20.5%; Pred. No. 4.2e+02;
RESULT 1404
ID ABG95034 standard; protein; 2311 AA.
DE Human translocation (4; 11)(q21; q23) protein #1.
PN WO200265900-A2.
PD 12-SEP-2002.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
  Query Match      5.2%; Score 85.5; DB 5; Length 2311;
  Best Local Similarity 24.3%; Pred. No. 4.9e+02;
RESULT 1405
ID ABG31317 standard; protein; 2586 AA.
DE Human S-3 corrected OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
  Query Match      5.2%; Score 85.5; DB 5; Length 2586;
  Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1406
ID ABG32891 standard; protein; 2586 AA.
DE Human osteoclast protein (OCP) #1.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
  Query Match      5.2%; Score 85.5; DB 5; Length 2586;
  Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1407
ID ADL02231 standard; protein; 2586 AA.
DE Human OCP protein #1.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
  Query Match      5.2%; Score 85.5; DB 8; Length 2586;
  Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1408
ID ADL02234 standard; protein; 2586 AA.
DE Human CA125 protein sequence SeqID 5.
DE Human OCP protein #2.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
  Query Match      5.2%; Score 85.5; DB 8; Length 2586;
  Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1409
ID AAB47935 standard; protein; 2587 AA.
DE Human OCP.
PN US2002022026-A1.
PD 21-FEB-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
  Query Match      5.2%; Score 85.5; DB 5; Length 2587;
  Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1410
ID ABG32896 standard; protein; 2587 AA.
DE Human osteoclast protein (OCP) #2.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
  Query Match      5.2%; Score 85.5; DB 5; Length 2587;
  Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1411
ID ADL02236 standard; protein; 2587 AA.
DE Human OCP protein #3.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
  Query Match      5.2%; Score 85.5; DB 8; Length 2587;
  Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1412
ID ABG31323 standard; protein; 2589 AA.
DE Human OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
  Query Match      5.2%; Score 85.5; DB 5; Length 2589;
  Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1413
ID ADL02244 standard; protein; 2589 AA.
DE Human OCP protein #5.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
  Query Match      5.2%; Score 85.5; DB 8; Length 2589;
  Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1414
ID AAE34702 standard; protein; 5877 AA.
DE Human mucin (MUC-16B).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
  Query Match      5.2%; Score 85.5; DB 6; Length 5877;
  Best Local Similarity 27.2%; Pred. No. 1.8e+03;
RESULT 1415
ID ABUS4721 standard; protein; 11721 AA.
DE Human CA125 full length protein sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
  Query Match      5.2%; Score 85.5; DB 6; Length 11721;
  Best Local Similarity 27.2%; Pred. No. 4.6e+03;
RESULT 1416
ID ADP84155 standard; protein; 22157 AA.
DE Human CA125 protein sequence SeqID 5.
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PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 8; Length 22157;
Best Local Similarity 27.2%; Pred. No. 1.1e+04;
RESULT 1417
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 85; DB 3; Length 280;
Best Local Similarity 23.2%; Pred. No. 30;
RESULT 1418
ID ABB71546 standard; protein; 326 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41430.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 85; DB 4; Length 326;
Best Local Similarity 22.8%; Pred. No. 37;
RESULT 1419
ID ADQ25899 standard; protein; 472 AA.
DE B amyloidofaciens dipeptide synthesising protein SEQ ID NO: 7.
PN EP1433791-A2.
PD 30-JUN-2004.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.1%; Score 85; DB 8; Length 472;
Best Local Similarity 20.3%; Pred. No. 62;
RESULT 1420
ID ABR33289 standard; protein; 576 AA.
DE Protein sequence #SEQ ID 1443.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 5.1%; Score 85; DB 6; Length 576;
Best Local Similarity 21.0%; Pred. No. 81;
RESULT 1421
ID ADK63572 standard; protein; 576 AA.
DE Disease treating protein complex-derived protein #867.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 5.1%; Score 85; DB 7; Length 576;
Best Local Similarity 21.0%; Pred. No. 81;
RESULT 1422
ID ABB55236 standard; protein; 627 AA.
DE Lactococcus lactis protein yfC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.1%; Score 85; DB 5; Length 627;
Best Local Similarity 21.5%; Pred. No. 91;
RESULT 1423
ID ADS29466 standard; protein; 627 AA.
DE Bacterial polypeptide #18499.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.1%; Score 85; DB 8; Length 627;
Best Local Similarity 21.5%; Pred. No. 91;
RESULT 1424
ID ADA55053 standard; protein; 637 AA.
DE Human protein, SEQ ID 2621.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.1%; Score 85; DB 6; Length 637;

Best Local Similarity 21.7%; Pred. No. 93;
RESULT 1425
ID AAB29654 standard; protein; 667 AA.
DE Human membrane-associated protein HUMAP-11.
PN WO200065054-A2.
PD 02-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.1%; Score 85; DB 3; Length 667;
Best Local Similarity 21.7%; Pred. No. 1e+02;
RESULT 1426
ID ABB60387 standard; protein; 1049 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7953.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 85; DB 4; Length 1049;
Best Local Similarity 22.1%; Pred. No. 1.9e+02;
RESULT 1427
ID AAU14240 standard; protein; 1061 AA.
DE Human novel protein #111.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 85; DB 4; Length 1061;
Best Local Similarity 20.2%; Pred. No. 1.9e+02;
RESULT 1428
ID AAU14241 standard; protein; 1091 AA.
DE Human novel protein #112.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 85; DB 4; Length 1091;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1429
ID ABB69973 standard; protein; 1354 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36711.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 85; DB 4; Length 1354;
Best Local Similarity 19.4%; Pred. No. 2.6e+02;
RESULT 1430
ID AAE17600 standard; protein; 1438 AA.
DE Human extracellular messenger (XMES)-2 protein.
PN WO200194587-A2.
PD 13-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.1%; Score 85; DB 5; Length 1438;
Best Local Similarity 20.2%; Pred. No. 2.9e+02;
RESULT 1431
ID ADM47185 standard; protein; 1671 AA.
DE Neurexin III-alpha membrane-bound type I precursor like NOVX 3a protein.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 85; DB 7; Length 1671;
Best Local Similarity 21.7%; Pred. No. 3.5e+02;
RESULT 1432
ID ADO26854 standard; protein; 196 AA.
DE Human receptors and membrane-associated protein, REMAP-44.
PN WO2004044159-A2.
PD 27-MAY-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.1%; Score 84.5; DB 8; Length 196;
Best Local Similarity 23.1%; Pred. No. 21;
RESULT 1433
ID AAW25156 standard; protein; 562 AA.
DE HIV-1 Rev/HTLV-1 Rex activation domain binding protein.
PN WO9706257-A1.
PD 20-FEB-1997.
PA (UYDU-) UNIV DUKE.
Query Match 5.1%; Score 84.5; DB 2; Length 562;
Best Local Similarity 23.4%; Pred. No. 88;


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RESULT 1434
ID AAW63285 standard; protein; 562 AA.
DE Human h-RAB.
PN WO9846744-A1.
PD 22-OCT-1998.
PA (EUON-) IST EURO DI ONCOLOGIA SRL.
Query Match 5.1%; Score 84.5; DB 2; Length 562;
Best Local Similarity 23.4%; Pred. No. 88;
RESULT 1435
ID ADM05676 standard; protein; 569 AA.
DE Human protein of the invention SEQ ID NO:4361.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.1%; Score 84.5; DB 7; Length 569;
Best Local Similarity 23.4%; Pred. No. 89;
RESULT 1436
ID ADS44145 standard; protein; 658 AA.
DE Bacterial polypeptide #22575.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.1%; Score 84.5; DB 8; Length 658;
Best Local Similarity 19.3%; Pred. No. 1.1e+02;
RESULT 1437
ID ABB60849 standard; protein; 826 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9339.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 5.1%; Score 84.5; DB 4; Length 826;
Best Local Similarity 20.9%; Pred. No. 1.5e+02;
RESULT 1438
ID AAR99638 standard; protein; 1011 AA.
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit.
PN WO9614077-A1.
PD 17-MAY-1996.
PA (TROP-) TROPHIX PHARM INC.
PA (UYNY ) UNIV NEW YORK STATE RES FOUND.
Query Match 5.1%; Score 84.5; DB 2; Length 1011;
Best Local Similarity 20.5%; Pred. No. 2e+02;
RESULT 1439
ID AAR99639 standard; protein; 1984 AA.
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit.
PN WO9614077-A1.
PD 17-MAY-1996.
PA (TROP-) TROPHIX PHARM INC.
Query Match 5.1%; Score 84.5; DB 2; Length 1984;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1440
ID ADE54547 standard; protein; 1984 AA.
DE Rat Protein AAB50403, SEQ ID NO 350.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.1%; Score 84.5; DB 7; Length 1984;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1441
ID ADE54551 standard; protein; 1984 AA.
DE Rat Protein AAB50403, SEQ ID NO 354.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.1%; Score 84.5; DB 7; Length 1984;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1442
ID ADE63027 standard; protein; 1984 AA.
DE Rat Protein AAB50403, SEQ ID NO 8961.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.1%; Score 84.5; DB 7; Length 1984;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1443
ID AAR92317 standard; protein; 1989 AA.
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit.
PN WO9614077-A1.
PD 17-MAY-1996.
PA (TROP-) TROPHIX PHARM INC.
PA (UYNY ) UNIV NEW YORK STATE RES FOUND.
Query Match 5.1%; Score 84.5; DB 2; Length 1989;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1444
ID ABB65890 standard; protein; 2015 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24462.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 5.1%; Score 84.5; DB 4; Length 2015;
Best Local Similarity 19.0%; Pred. No. 5.1e+02;
RESULT 1445
ID ADJ66747 standard; protein; 2234 AA.
DE Human Muc16 GST fusion protein amino acid sequence SeqID20.
PN WO2004005470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
Query Match 5.1%; Score 84.5; DB 8; Length 2234;
Best Local Similarity 27.2%; Pred. No. 5.8e+02;
RESULT 1446
ID ABM70225 standard; protein; 2466 AA.
DE Photorhabdus luminescens protein sequence #3322.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match 5.1%; Score 84.5; DB 6; Length 2466;
Best Local Similarity 23.7%; Pred. No. 6.7e+02;
RESULT 1447
ID ABUI5838 standard; protein; 2481 AA.
DE Protein encoded by Prokaryotic essential gene #1365.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.1%; Score 84.5; DB 6; Length 2481;
Best Local Similarity 24.2%; Pred. No. 6.7e+02;
RESULT 1448
ID ABR62804 standard; protein; 2481 AA.
DE Methicillin resistant Staphylococcus aureus ORF SAI964-fmtB (mrp).
PN WO2003062466-A2.
PD 31-JUL-2003.
PA (UYBR-) UNIV BRISTOL.
Query Match 5.1%; Score 84.5; DB 7; Length 2481;
Best Local Similarity 24.2%; Pred. No. 6.7e+02;
RESULT 1449
ID ADR72871 standard; protein; 22152 AA.
DE Human ovarian cancer-related tumour marker CA125 protein.
PN WO2004075113-A2.
PD 10-SEP-2004.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Query Match 5.1%; Score 84.5; DB 8; Length 22152;
Best Local Similarity 27.2%; Pred. No. 1.4e+04;
RESULT 1450
ID AAB11729 standard; protein; 216 AA.
DE Cryptosporidium parvum Iowa isolate GP900, domain 2.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC ) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 3; Length 216;
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Best Local Similarity 26.7%; Pred. No. 26;
RESULT 1451
ID AAB11734 standard; protein; 216 AA.
DE Cryptosporidium parvum NINC isolate GP900, domain 2.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 3; Length 216;
Best Local Similarity 26.7%; Pred. No. 26;
RESULT 1452
ID ABJ04047 standard; protein; 216 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 8.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 5; Length 216;
Best Local Similarity 26.7%; Pred. No. 26;
RESULT 1453
ID ABB59598 standard; protein; 330 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5586.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 84; DB 4; Length 330;
Best Local Similarity 30.8%; Pred. No. 47;
RESULT 1454
ID ADO61979 standard; protein; 335 AA.
DE Transcription factor G2571, SEQ ID 446.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MENDEL) MENDEL BIOTECHNOLOGY INC.
Query Match 5.1%; Score 84; DB 8; Length 335;
Best Local Similarity 26.4%; Pred. No. 48;
RESULT 1455
ID ADM05769 standard; protein; 420 AA.
DE Human protein of the invention SEQ ID NO:4454.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.1%; Score 84; DB 7; Length 420;
Best Local Similarity 19.5%; Pred. No. 66;
RESULT 1456
ID ABB67668 standard; protein; 459 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29796.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 84; DB 4; Length 459;
Best Local Similarity 24.2%; Pred. No. 74;
RESULT 1457
ID ABB47318 standard; protein; 793 AA.
DE Listeria monocytogenes protein #22.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.1%; Score 84; DB 5; Length 793;
Best Local Similarity 22.4%; Pred. No. 1.6e+02;
RESULT 1458
ID ABU32765 standard; protein; 793 AA.
DE Protein encoded by Prokaryotic essential gene #18292.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.1%; Score 84; DB 6; Length 793;
Best Local Similarity 22.4%; Pred. No. 1.6e+02;
RESULT 1459
ID AAB41835 standard; protein; 833 AA.
DE Human ORFX ORF1599 polypeptide sequence SEQ ID NO:3198.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 84; DB 3; Length 833;
Best Local Similarity 20.0%; Pred. No. 1.7e+02;

RESULT 1460
ID ADH71762 standard; protein; 834 AA.
DE Human protein of the invention NOV28k SEQ ID NO:658.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 84; DB 8; Length 834;
Best Local Similarity 23.3%; Pred. No. 1.7e+02;
RESULT 1461
ID ADC30924 standard; protein; 845 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1006.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 84; DB 7; Length 845;
Best Local Similarity 19.5%; Pred. No. 1.7e+02;
RESULT 1462
ID AAU91290 standard; protein; 905 AA.
DE Human NOV51 protein.
PN WO200216600-A2.
PD 28-FEB-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 84; DB 5; Length 905;
Best Local Similarity 23.2%; Pred. No. 1.9e+02;
RESULT 1463
ID AAR11993 standard; protein; 920 AA.
DE Glutamate receptor 5-1.
PN WO9106648-A.
PD 16-MAY-1991.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.1%; Score 84; DB 2; Length 920;
Best Local Similarity 22.2%; Pred. No. 1.9e+02;
RESULT 1464
ID ADO67713 standard; protein; 933 AA.
DE Novel human protein sequence #2379.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.1%; Score 84; DB 8; Length 933;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1465
ID ADI27184 standard; protein; 996 AA.
DE Mouse LRP binding family protein #20.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 5.1%; Score 84; DB 8; Length 996;
Best Local Similarity 22.7%; Pred. No. 2.1e+02;
RESULT 1466
ID ADS43638 standard; protein; 1075 AA.
DE Bacterial polypeptide #22068.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.1%; Score 84; DB 8; Length 1075;
Best Local Similarity 24.2%; Pred. No. 2.4e+02;
RESULT 1467
ID ADN33134 standard; protein; 1084 AA.
DE Human transporter and ion channel (TRICH) protein SeqID19.
PN WO2004035755-A2.
PD 29-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.1%; Score 84; DB 8; Length 1084;
Best Local Similarity 19.4%; Pred. No. 2.4e+02;
RESULT 1468
ID ABP73029 standard; protein; 1228 AA.
DE Amino acid sequence of the GuxA polypeptide.
PN WO2003012109-A1.
PD 13-FEB-2003.

PA (MIDE) MIDWEST RES INST.
Query Match 5.1%; Score 84; DB 6; Length 1228;
Best Local Similarity 22.1%; Pred. No. 2.9e+02;
RESULT 1469
ID ADH36636 standard; protein; 1228 AA.
DE Acidothermus cellulolyticus glycoside hydrolase, GuxA.
PN US2003104522-A1.
PD 05-JUN-2003.
PA (DING/) DING S.
PA (ADNE/) ADNEY W S.
PA (VINZ/) VINZANT T B.
PA (HIMM/) HIMMEL M E.
PA (DECK/) DECKER S R.
Query Match 5.1%; Score 84; DB 8; Length 1228;
Best Local Similarity 22.1%; Pred. No. 2.9e+02;
RESULT 1470
ID ABB70925 standard; protein; 1291 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39567.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 84; DB 4; Length 1291;
Best Local Similarity 19.3%; Pred. No. 3.1e+02;
RESULT 1471
ID AAB96091 standard; protein; 1362 AA.
DE Putative P. abyssi amylopullulanase.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 5.1%; Score 84; DB 4; Length 1362;
Best Local Similarity 26.5%; Pred. No. 3.3e+02;
RESULT 1472
ID AAW48299 standard; protein; 1721 AA.
DE Cryptosporidium parvum GP900 antigen.
PN WO9806430-A1.
PD 19-FEB-1998.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 2; Length 1721;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 1473
ID AAB11727 standard; protein; 1721 AA.
DE Portion of Cryptosporidium parvum NINC isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 3; Length 1721;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 1474
ID ABJ04045 standard; protein; 1721 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 6.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 5; Length 1721;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 1475
ID AAB11726 standard; protein; 1837 AA.
DE Cryptosporidium parvum iowa isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 3; Length 1837;
Best Local Similarity 26.7%; Pred. No. 5e+02;
RESULT 1476
ID ABJ04044 standard; protein; 1837 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 5.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 5; Length 1837;
Best Local Similarity 26.7%; Pred. No. 5e+02;
RESULT 1477

ID ABUS3165 standard; protein; 143 AA.
DE Human testes-derived DKFzphtes3_2a11 homologue #25.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 143;
Best Local Similarity 30.7%; Pred. No. 17;
RESULT 1478
ID ABUS3163 standard; protein; 247 AA.
DE Human testes-derived DKFzphtes3_2a11 homologue #23.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 247;
Best Local Similarity 30.7%; Pred. No. 35;
RESULT 1479
ID ABUS3158 standard; protein; 260 AA.
DE Human testes-derived DKFzphtes3_2a11 homologue #18.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 260;
Best Local Similarity 30.7%; Pred. No. 38;
RESULT 1480
ID ADD55680 standard; protein; 352 AA.
DE Thalecress environmental stress-related protein #19.
PN US2003131386-A1.
PD 10-JUL-2003.
PA (SAMA/) SAMAHA R.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (KEDD/) KEDDIE J.
PA (RATC/) RATCLIFFE O.
PA (PIIG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (ZHAN/) ZHANG J.
Query Match 5.0%; Score 83.5; DB 7; Length 352;
Best Local Similarity 19.8%; Pred. No. 57;
RESULT 1481
ID ADO01723 standard; protein; 352 AA.
DE Thalecress transcription factor protein #68.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PIIG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 5.0%; Score 83.5; DB 8; Length 352;
Best Local Similarity 19.8%; Pred. No. 57;
RESULT 1482
ID ABUS3157 standard; protein; 368 AA.
DE Human testes-derived DKFzphtes3_2a11 homologue #17.
PN WO200112659-A2.
PD 22-FEB-2001.

PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 368;
Best Local Similarity 30.7%; Pred. No. 61;
RESULT 1483
ID ABUS3156 standard; protein; 385 AA.
DE Human testes-derived DKFZphtes3_2all homologue #16.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 385;
Best Local Similarity 30.7%; Pred. No. 65;
RESULT 1484
ID ABUS3159 standard; protein; 386 AA.
DE Human testes-derived DKFZphtes3_2all homologue #19.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 386;
Best Local Similarity 30.7%; Pred. No. 65;
RESULT 1485
ID ABUS3161 standard; protein; 387 AA.
DE Human testes-derived DKFZphtes3_2all homologue #21.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 387;
Best Local Similarity 30.7%; Pred. No. 65;
RESULT 1486
ID AAM50241 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase.
PN US6297055-B1.
PD 02-OCT-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.0%; Score 83.5; DB 4; Length 393;
Best Local Similarity 26.5%; Pred. No. 67;
RESULT 1487
ID AAU76423 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase clone wrl.pk0059.g9.
PN US2002009801-A1.
PD 24-JAN-2002.
PA (FALC) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (OROZ/) OROZCO E R.
Query Match 5.0%; Score 83.5; DB 5; Length 393;
Best Local Similarity 26.5%; Pred. No. 67;
RESULT 1488
ID ABUS3160 standard; protein; 395 AA.
DE Human testes-derived DKFZphtes3_2all homologue #20.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 395;
Best Local Similarity 30.7%; Pred. No. 67;
RESULT 1489
ID ABB69710 standard; protein; 399 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35922.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.0%; Score 83.5; DB 4; Length 399;
Best Local Similarity 26.2%; Pred. No. 68;
RESULT 1490
ID ADA19428 standard; protein; 498 AA.
DE Mouse CD30 amino acid sequence.
PN WO2003066674-A2.
PD 14-AUG-2003.
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
Query Match 5.0%; Score 83.5; DB 6; Length 498;
Best Local Similarity 20.5%; Pred. No. 92;
RESULT 1491
ID ABB10349 standard; protein; 553 AA.
DE Human cDNA SEQ ID NO: 657.
PN WO200154474-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 83.5; DB 4; Length 553;
Best Local Similarity 22.9%; Pred. No. 1.1e+02;
RESULT 1492
ID ABP66936 standard; protein; 553 AA.
DE Human polypeptide SEQ ID NO 657.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.0%; Score 83.5; DB 5; Length 553;
Best Local Similarity 22.9%; Pred. No. 1.1e+02;
RESULT 1493
ID AAM12713 standard; protein; 562 AA.
DE hRIP, a protein critical for HIV replication.
PN WO9701648-A1.
PD 16-JAN-1997.
PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
Query Match 5.0%; Score 83.5; DB 2; Length 562;
Best Local Similarity 23.4%; Pred. No. 1.1e+02;
RESULT 1494
ID ADO00991 standard; protein; 562 AA.
DE Human homologue of Fruit fly AD-related protein CG3365.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 5.0%; Score 83.5; DB 8; Length 562;
Best Local Similarity 23.4%; Pred. No. 1.1e+02;
RESULT 1495
ID ADP55222 standard; protein; 562 AA.
DE Human PRO protein sequence SEQ ID NO:1198.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 83.5; DB 8; Length 562;
Best Local Similarity 23.4%; Pred. No. 1.1e+02;
RESULT 1496
ID ADP04689 standard; protein; 643 AA.
DE Sea squirt protein with tissue specific expression in development Seq284.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 5.0%; Score 83.5; DB 8; Length 643;
Best Local Similarity 21.9%; Pred. No. 1.3e+02;
RESULT 1497
ID AAU33234 standard; protein; 644 AA.
DE Novel human secreted protein #3725.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.0%; Score 83.5; DB 4; Length 644;
Best Local Similarity 23.4%; Pred. No. 1.3e+02;
RESULT 1498
ID ABUS3144 standard; protein; 717 AA.
DE Human testes-derived DKFZphtes3_2all homologue #4.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 717;
Best Local Similarity 30.7%; Pred. No. 1.5e+02;
RESULT 1499
ID AAR77024 standard; protein; 879 AA.
DE Canine herpesvirus gb homologue.
PN WO9526751-A1.
PD 12-OCT-1995.
PA (VIRO-) VIROGENETICS CORP.
Query Match 5.0%; Score 83.5; DB 2; Length 879;
Best Local Similarity 30.9%; Pred. No. 2e+02;
RESULT 1500
ID AAO16418 standard; protein; 2759 AA.
DE Human nucleic acid-associated protein (NAAP) - SEQ ID NO 15.

PN WO2003000864-A2.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.0%; Score 83.5; DB 6; Length 2759;
Best Local Similarity 20.2%; Pred. No. 9.7e+02;